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QY 363 AGGATATATATGACATATTTTGCATACGACAGACATCTTCAGGCAAGCTATCA 422
DB 317 AAGCTCAATATGATATATTTTGCCTATGACAGACATCTTCAGGCAAGCTATCA 376
QY 423 TGATGGGAAACCAATTCATTTGGGCAATATATCCCAAGCCATACAGAAATTTTAAA 482
DB 377 TGATGGGTTCCAGAAATCATTTGGGAGTTATACCCAGGCAATTCATGACATTTTCAA 436
QY 483 TTATTCAGAGATCCGAAAGAGAGATTTCTTAAAGTTCTTATATGAGATTTTACA 542
DB 437 AATTTAAGAGTTCTGATAGGAAATTTCTTACGATATCTTACATGAGAAATATACA 496
QY 543 ATGAACCTGTGAAGACCTACTGTGTATGACAGAGAAAGAACCCCTGGAAATTCGCG 602
DB 497 ATGAACCATTTACAGATTTACTCTGTGCACTCAAAAATGAAACCTTTATTTATGAG 556
QY 603 AGGATTTTATAGAAAGTGTATTTGCTGACCTGACGAAAGAACTTTGATATGCTTCTG 662
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QY 663 AACATGTAATACAGTGAATCAAAAAGGTGAAAAGAAACAGACATATGAGAGACTAAA 722
DB 617 AATATGCTTTGAAATGAAATTCAAAAGGAGAAAGACAGCAATTTATGAGAAACAAA 676
QY 723 TGAATGATCATAGTATGCTTCAATCAATATTTAGATGATTTGAAAGCCGAGACA 782
DB 677 TGAATCAAGAGAGAGTCTTCTATCAATCTTTAGATGATTTTGAAGACAGAGAGA 736
QY 783 GAAATGATCCCAAAATTCAGAGAACTGTGATGAGCTGTATGATGATTTCTACTGAAAT 842
DB 737 AGGATGAACTTTTAAAT-----TGTAAGGATCTGTAAAGTATCCCATTTGAAAT 787
QY 843 TGGATGATCTTGTGCGAGTGAAGAGACAGCCAAATGAGAGCTGAAGGTGAGACTTA 902
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QY 903 AGGAAGCTCAACATCAACGAGCTTGTATTCCTTGGACAGTATTTAAGAGCTTA 962
DB 848 AGGAAGCTGTAAATATATATGAAGCTTATTTATTTGGGACAAAGTATGAAGAACTTA 907
QY 963 GCGAGCGGCGAGCTGTGATTTTAACTACAGAGACAGAACTCAGCAAAATTTCTC 1022
DB 908 GTATGAGCAAGTTGGTGTTCATTAATATGAGATGACAGATTTAACAGAAATCTTC 967
QY 1023 AAAATTCATTTGGGAGGAAATGCTAAACGCTTAAATTTGCAAAATTAAGCCGTTCTT 1082
DB 968 AGAATTCCTTGGAGGAAATCCAAAGACAGCTATTTCTGCAAAATTAATCTCCAGTA 1027
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QY 1203 TGGATTTTAAAGAAATTTAGAGATTTAGAGTATGATGATGATGATGATGATGAT 1262
DB 1148 TGGATCTTAAAGAAATTTAGAG-----GAGGTTCTTTAGAGAGCGGCTCAGAGCA 1201
QY 1263 TGGCTTAAAGAGACATACAGCTTGTAGCTGATGATGATGATGATGATGATGATG 1322
DB 1202 TGGAAAGAGCAATATGAGCCCACTTTTGGAGAAAGAAATTTGCTTCAAGAAAGTACA 1261
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DB 1262 ATGAGAAATTTGAAATCTTAAACAGAGATGCTGTGACCTTCTTCCCTCAGCTTCAAC 1321
QY 1380 AGGACAAAGGCTCAACAGAAAGAGTTAGCTGTGGGCGCAGGAAAGATCCAAATTA 1439
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DB 1382 TGAAGAA-----CTCAAACTATGACAGATCAATTTATATACCAAAATATTA 1429
QY 1500 GCAAGAGCGCAAGTCTCTGACATGCTTCAATTTCCAGAAATGATGACTCTTTGTA 1559
DB 1430 CAACAAAGAAACATTAAGCTTTCTATTAATTTATGAGAAATGATGATCTGTCTGTT 1489
QY 1560 CAGAGTTTCTGATTTTGAATGAGCGCCT 1587
DB 1490 CAGAGTCTGATGTTTCAAGTAAACATCTT 1517

RESULT 2
US-09-620-312D-130
; Sequence 130, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pf-fl_genes Version 1.0
; SEQ ID NO 130
; LENGTH: 8503
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (91)..(8082)
US-09-620-312D-130

Query Match 6.4%; Score 620.4; DB 4; Length 8503;
Best Local Similarity 65.5%; Pred. No. 2,2e-143;
Matches 1001; Conservative 0; Mismatches 491; Indels 36; Gaps 5;

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Db 496 AACACAGTATGTTGGGCGCAAGAAATGCCATGTGGAGATGACGTGAAGTATGAT 555
QY 677 TGGATCAAAAAGGTGAAAAAACGACATTAATGAGAGACTAAATGATGATCACT 736
Db 556 CTTTGGAGATGGGGAATGCGAGCAGCATACAGTACCACTCAAAATGAGTACCTCC 615
QY 737 AGTCGTTACATCAATATTTAGATGATTTGAAAGCCGAGACAGAAAT-----GAT 790
Db 616 AGCAGATCAGATGCAATTTTACATCAGCATTTTCAATTTCAATTAATATGAGGCA 675
QY 791 CCCACAATTCAGAGAACTGTGATGAGCTGTCAATGATTCATCTTGAATTTGATGAT 850
Db 676 GCTGAAGATGATCATGATGATTCCTCCGCAATATTTGTCCTCAAGTTCCACTTTGAT 725
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QY 911 TGCACATCAACGCGACCTGTTTATCTTGAACAGGTTATTAAGAACTTTAGCGAG-- 968
Db 796 ATTCAAATCAATAGTATGATTTGCTGCTTTAGAAATTTAAGCGCTCTTTGGGAGCCA 855
QY 969 -GCCAGGCTGTGATTTATTAACCTACAGACAGCAAACTCACAGAAATTCCTCAAAAT 1027
Db 856 CCGAGGAAGATTCACATATTCATATAGGATGCTAAATTTACCGGCTTCTGAAGAT 915
QY 1028 TCATTGGGAGAAATGCTAAACGGTTATTAATTTGCAATTTACCGCAGTTTCT--T 1081
Db 916 TCTCTGGAGGAGCTGTAAGCTGATCATGATCATGATGTCAGCCCTCTCTCGAAT 975
QY 1082 TTTGATGAGACTTAAGTACATTTGCTGCTGAGTACTGCCAAACATGTGAGAAATACT 1141
Db 976 TTTGATGAGCTCTTAATTTCTTCAATATGCGAACAGCAGCAAGCAATTAGAAACAA 1035
QY 1142 CCCCATGTTAA 1152
Db 1036 CCCACTGTAAA 1046

RESULT 4
US-09-641-807A-1
; Sequence 1, Application US/09641807A
; Patent No. 6440731
; GENERAL INFORMATION:
; APPLICANT: Berand, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6440731el motor proteins and methods for
; FILE REFERENCE: 1031
; CURRENT APPLICATION NUMBER: US/09/641.807A
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3837
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1226) ... (1336)
; OTHER INFORMATION: n = a, t, c, or g
US-09-641-807A-1

Query Match 1.5%; Score 147.4; DB 4; Length 3837;
Best Local Similarity 51.3%; Pred. No. 2,2e-26;
Matches 467; Conservative 0; Mismatches 411; Indels 33; Gaps 4;

QY 275 TTCAATTTGATGCTGATTTAATCTCAGAAATCAACAGTCAATTTTCCAGAAATA 334
Db 136 TTCACTTTGATTTTGTGTTTGGCAAAAATTCACCTCAATAGATTTAATCAACATGT 195
QY 335 GCAGTACTATCATAGATCAGCTTTGACAGGATATATGCAAAATTTGATACGCA 394

Db 196 ATAAAGCCCCAGTATGTTGCTCACTATGAGGCGTATTAATGCACTGTTTTCCTATGGA 255
QY 395 CAGACATCTTCAGGAGAGCGTACCAATGATGGGAAACCAATTCATT----- 444
Db 256 CAAACTGATCTGGGAGACATACACATGAGAGGGGGCCATATTTCTTCAAGTTGGAG 315
QY 445 -----GGGCAATATACCCCAAGCCATACAGAAATTTTAAATTAATTCAGAGATA 496
Db 316 GGGCAAAAGGATATCTTCTCGAGTATTCAGAAATTTTCAAAAGCATCTGTAAACAT 375
QY 497 CCGAAGAGAGTCTTCTTAAGATTTCTTAATGAGATTTTACATATAAACTGTGAA 556
Db 376 CTTAGCATTTGATTTATATTAAGATCTTATATAGAGTACAGGAAACCTTAA 435
QY 557 GACCTATCTGTGATGACAGAAAGAAAGCCCTTGAAATTCGGAGATTTTATATA 616
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QY 617 AACGTGTATGTTGCTGACCTGACCTGAGAACTTGAATGTTCTGAACTGTAATACAG 676
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QY 677 TGGATCAAAAAGGTGAAAAAACGACATTAATGAGAGACTTAAATGATGATCACT 736
Db 556 CTTTGGAGATGGGAGATGACCCAGACATACAGGATCCATCAATGATGAGCAGCTCC 615
QY 737 AGTCGTTACATCAATATTTAGATGATTTGTAAGCCGAGACAGAAAT-----GAT 790
Db 616 ACAGATCAATGACATTTTCAATACAGCAATTTGCAAGTTCAATTAATATGAGGCA 675
QY 791 CCCACAATTCAGAGAACTGTGATGAGCTGTCAATGATTTCTCACTGTAATTTGATGAT 850
Db 676 GCTGAAGATGATCATGATTTCCCTGGCATATTTGTCAAAGTTTCACTTTGATGAT 735
QY 851 CTTCGTCGAGTGAAGAGCAAGCCAACTGAGCTGAAGGTGTGAGACTTAAGAGAGC 910
Db 736 TTGGCAGGATCAGAAAGATTAACAAACGGGGAATCTGTGAACGGTTCAAGATATC 795
QY 911 TGCACATCAACCGGAGCTGTTTATCTTGAACAGGTTATTAAGAGTTAGCGAG-- 968
Db 796 ATTCAAATCAATAGTATGATTTGCTGCTTGAAGAAATTAATAGCGCTTTGGGAGCCA 855
QY 969 -GCCAGGCTGTGATTTTAACTACAGAGACAGCAAACTCACAGAAATTCCTCAAAAT 1027
Db 856 CCGAGGAAGATTCACATATTTCCATATAGGATGCTAAATTAACCGGCTTCTGAAGAT 915
QY 1028 TCATTGGGAGAAATGCTTAAACGGTTATTAATTTGCACAATTAACCGCAGTTTCT--T 1081
Db 916 TCTCTGGAGGAGAGCTGTAAGCTGATCATGATCATGATGTCAGCCCTCTCTCGAAT 975
QY 1082 TTTGATGAGACTTAAGTACATTTGCTGCTGAGTACTGCCAATCATGTGAGAAATACT 1141
Db 976 TTTGATGAGCTCTTAATTTCTTCAATATGCGAACAGCAGCAAGCAATTAGAAACAA 1035
QY 1142 CCCCATGTTAA 1152
Db 1036 CCCACTGTAAA 1046

RESULT 5
US-09-723-096-1
; Sequence 1, Application US/09723096
; Patent No. 6448026
; GENERAL INFORMATION:
; APPLICANT: Berand, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6448026el motor proteins and methods for
; FILE REFERENCE: 1031
; CURRENT APPLICATION NUMBER: US/09/723.096
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: US/09/641.807
; PRIOR FILING DATE: 2000-08-17

NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 3837
 TYPE: DNA
 ORGANISM: Human
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1228)...(1337)
 OTHER INFORMATION: n = a, t, c, or g
 US-09-723-096-1

Query Match 1.5%; Score 147.4; DB 4; Length 3837;
 Best Local Similarity 51.3%; Pred. No. 2.2e-26;
 Matches 467; Conservative 0; Mismatches 411; Indels 33; Gaps 4;

QY 275 TTCATTTTCGATGCTGATTTAATTCACGAATCAACAAGTCAAAATTTACCAAGAATA 334
 DB 136 TTCACCTTTGATTTGTTTGGCAAAAATTCACCTCAAGATGAAGTTTAAACACATGT 195
 QY 335 GCAGTACCTATCATACGATCAGCTTGCAGGATATATGACACATATTTGCATACGGA 394
 DB 196 ATAAAGCCCCCTAGTGTGTCACCATGAGGGCTATATGCAACTGTTTTGCCATGGA 255
 QY 395 CAGACATCTTCAGGCAAGATGATGAGGAAACCAAAATTCAT-----444
 DB 256 CAACTGATCTGGAGACATACACCATGAGGGGCCATTTGCTTACGTTGGAG 315
 QY 445 -----GGGCAATTAACCCCAAGCCATACAGAAATTTTAAATTTACGAGATA 496
 DB 316 GGCCAAAAGGATTCATCTCGAGCTATTCAGAAATATTTCAAGCATCTGAAACAT 375
 QY 497 CCGAACAAGAGATTCTTCTTAAGATTCTTATATGAGATTTCATTAACCTGTAAG 556
 DB 376 CTTAGCATTCATTTAATGTAAGATCTTATATAGAGTGAAGGAAAGACCTAAGA 435
 QY 557 GACCTACTGTGATGACAGAAAGAACCCCTGGAAATGGCAGGATTTTAAATAGA 616
 DB 436 GATCTTCTAGAAATGGAGACATCATGAAGATCTTCACATCCGAGAAAGTGAAGAA 495
 QY 617 AACGTATGTTGCTGACCTGACGAAAGCTTGTATGTTCTGTAACATGTAATACAG 676
 DB 496 AACACAGTATTTTGGGCGCAAGAAATGCCATGTGAGAGTGCAGTGAAGTGAAGT 555
 QY 677 TGGATCAAAAAGGTTAAAAAAGACATATGAGAGACTAAATGAATGATCATAGT 736
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 QY 737 AGTCGTTACATACATATTTAAGATGATTTGAAAAGCCGAGACGAAT-----GAT 790
 DB 616 AGCAGATCACATCAATTTTACATCAGCATTTGTCMAATTCATAAATATGAGGCA 675
 QY 791 CCCCAAAATTCAGAGAACTGTATGAGCTGTATGATCTCACTTGAATTTGTATAGAT 850
 DB 676 GCTGAAGATGATCATGATTTCCCTCGGCATATTTCTCAAGTTCCACTTTGTGAT 735
 QY 851 CTTGCTGGCAGTAAAGAGCAAGCCAAATGAGCTGAGAGTGTGAGACTTAAAGAGGC 910
 DB 736 TTGGCAGGATCAAGAAAGATTAACAAAAGGGAATCTGTGAACGGTTCAAAAGATCC 795
 QY 911 TGAACATCAACCGCAGCTTTTATCTTGGACAGTTATTAAGAACTTACGAGC-- 968
 DB 796 ATTCAATCAATGTGATTTGCTGCTTAAAGAAATGTAATTAAGCGCTCTTGGGAGCCCA 855
 QY 969 -GCCAGCTGCTGATTTATTAATCAAGAGACAGCAAACTCACGAATTTCTCAAAAT 1027
 DB 856 CCGAGAAAGATTCATATATTCATATAGGATGCTTAATTAACCCGGCTTCTGAAAGAT 915
 QY 1028 TCATTTGGAGAAATCTAAACGTTATTAATTTGACCAATTAAGCCGAGTTTC-----T 1081
 DB 916 TCTCTGGAGGAGCTGTAGATGATGATGATGATGATGATGATGATGATGATGATGAT 975
 QY 1082 TTTGATGAGACTAAGTACATTCAGTTTCCAGTATGCGCAAAATGAGAAATACT 1141

DB 976 TTTGATGAGCTCTTAATTTCTCAATATATGCCAAGAGCAAGCAATTAAGAAACAA 1035
 QY 1142 CCCCATGTTAA 1152
 DB 1036 CCCCATGTTAA 1046

RESULT 6
 US-09-724-517-3
 ; Sequence 3, Application US/09724517
 ; Patent No. 6379941
 ; GENERAL INFORMATION:
 ; APPLICANT: Beraud, Christophe
 ; APPLICANT: Freedman, Richard
 ; TITLE OF INVENTION: No. 6379941el motor proteins and methods for
 ; FILE REFERENCE: 1031
 ; FILE REFERENCE: their use
 ; CURRENT APPLICATION NUMBER: US/09/724,517
 ; PRIOR APPLICATION NUMBER: US/09/641,807
 ; PRIOR FILING DATE: 2000-08-17
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 1023
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-724-517-3

Query Match 1.5%; Score 140; DB 4; Length 1023;
 Best Local Similarity 51.0%; Pred. No. 7.3e-25;
 Matches 456; Conservative 0; Mismatches 405; Indels 33; Gaps 4;

QY 275 TTCATTTTCGATGCTGATTTAATTCACGAATCAACAAGTCAAAATTTACCAAGAATA 334
 DB 130 TTCACCTTTGATTTGTTTGGCAAAAATTCACCTCAAGATGAAGTTTAAACACATGT 189
 QY 335 GCAGTACCTATCATACGATCAGCTTGCAGGATATATGCAACATATTTGCATACGGA 394
 DB 190 ATAAAGCCCCCTAGTGTGTCACCATGAGGGCTATTAAGCAACTGTTTTGCCATGGA 249
 QY 395 CAGACATCTTCAGGCAAGATGATGAGGAAACCAAAATTCAT-----444
 DB 250 CAACTGATCTGGAGACATACACCATGAGGGGCCATATTTGCTCAGTTGGAG 309
 QY 445 -----GGGCAATTAACCCCAAGCCATACAGAAATTTTAAATTTACGAGATA 496
 DB 310 GGCCAAAAGGATTCATCTCGAGCTATTCAGAAATATTTCAAGCATCTGAAACAT 369
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 DB 370 CTTAGCATTCATTTAATGTAAGATCTTATATGAGATGTAAGAAAGACCTAAGA 429
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 DB 430 GATCTTCTAGAAATGGAGACATTCATGAAGATCTTCACATCCGAAATGAAAGAA 489
 QY 617 AACGTATGTTGCTGACCTGACGAAAGCTTGTATGTTCTGTAACATGTAATACAG 676
 DB 490 AACACAGTATTTTGGGCGCAAGAAATGCCATGTGAGAGTGCAGTGAAGTGAAGT 549
 QY 677 TGGATCAAAAAGGTTAAAAAAGACATTAAGAGACTTAAATGAATGATCATAGT 736
 DB 550 CTTTGGAGATGGGAAATGACGCAAGACATACAGGATCAACATCAATGATGAGCACTCC 609
 QY 737 AGTCGTTACATACATATTTAAGATGATTTGAAAAGCCGAGACGAAT-----GAT 790
 DB 610 AGCAGATCACATCAATTTTACATCAGCATTTTGTCAAGTTCTAATTAATTAAGAGCA 669
 QY 791 CCCCAAAATTCAGAGAACTGTATGAGCTGTATGATGATGATGATGATGATGATGATGAT 850
 DB 670 GCTGAAGATGATCATGATTTCCCTCGGCATATTTGCTCAAGTTCCACTTTGTGAT 729

QY 851 CTGGCTGGCAGTGAAGAGCAAGCAAGCTGAGGTGTGAGACTTAAAGAGGC 910
Db 730 TTGGCAGGATCAGAAAAGATTAACCAAGGGAATCTGTGAACGGTTTAAAGATCC 789
QY 911 TGCACATCAACCGCAGCTTGTATCTTGGACAGGTATTAAAGAGCTTGGACGC-- 968
Db 790 ATTCAATCAATAGTGAATGTGGCTTTAGGAATGTATAAGGCTCTTGGGACCCA 849
QY 969 -GCCAGGCTGTGATTTTAACTACAGACAGCAAACTACCAAGATTCTCCAAAT 1027
Db 850 CCGAGGAAGATTCACATATTCATATAGGATGCTAAATTAACCCGCTTGTGAAGAT 909
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Db 910 TCTCTGGGAGGAGCTAGCTAGACTGTCAATGATCATATGTGACCCCTCTCTCGAAT 969
QY 1082 TTTGATGAGCTCTAAGTACCTTGAATTTGGCAGTACTGCCAAACATGTGAGA 1135
Db 970 TTTGATGAGTCTTAAATTTCTCTCAATATGCAACAGACGGAACATTAGA 1023

RESULT 7
US-09-641-807A-3

; Sequence 3, Application US/09641807A
; Patent No. 6440731
; GENERAL INFORMATION:
; APPLICANT: Berard, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6440731el motor proteins and methods for
; FILE REFERENCE: 1031
; CURRENT APPLICATION NUMBER: US/09/641.807A
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Human
US-09-641-807A-3

Query Match 1.5%; Score 140; DB 4; Length 1023;
Best Local Similarity 51.0%; Pred. No. 7.3e-25;
Matches 456; Conservative 0; Mismatches 405; Indels 33; Gaps 4;
QY 275 TTCAATTCGATCGTATTTAATTTCCAGCAATCAACAGCAATTTTACCAAGAAATA 334
Db 130 TTCACTTTGATTTTGTGGCAAAATTTCCATCAAGATGAAGTTTATTAACACATGT 189
QY 335 GCAGTACATATCAATGATCAGTTTGCAGAGATATATGSCAATATTTGCATACGA 394
Db 190 ATTAAGCCCCCTAGTGTGTCTACTCATTTAGGGCTATATAGCAATGTTTTGCTATGSA 249
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Db 250 CAAACTGATCTGGGAAGACATACACATTGAGGGGGCCATATGCTTCAGTTGTGAG 309
QY 445 -----GGGATAATATACCCCAAGCCATACAGGAATTTTAAATTTTACAGAGATA 496
Db 310 GGCAGAAAGGATTCATCTCTGAGCTATTCAGAAATTTTCAAGCATCTCTGAACAT 369
QY 497 CCGAAGAGAGATTTTCTTAAGATTTTATATGAGATTTTACATGAAGAACTGTGAAA 556
Db 370 CCTAGATTTGATTTATATGATAAGATCTTATATGAGATTTTACAGGAAGAACTAGA 429
QY 557 GACCTACTGTGATGACAGAGAAAGAAAGCCCTTGAATTTGGGAGATTTTATATGA 616
Db 430 GATCTTTGATTTGAGATTCATTCATGAAGATCTTCAATCCGAGGAAGTGAAGAAAGGA 489
QY 617 AAGGTATATGTTGCTGACCTGACAGAACTTGTATGTTTCTGAACATGTAATACAG 676
Db 490 AACAGATGATTTGTTGGGGCCAAAGAAATGCCATGTGAGAGATGCGAGTGAAGTATGAGT 549

QY 677 TGGATCAAAAAGGGTGAAGAAAAACAGACATTTATGAGAGACTTAAATGATCATAGT 736
Db 550 CTTTGTGAGATGGGAATGAGCCACATACAGGTACATCTCAATGATATAGCACTCC 609
QY 737 AGTCGTTACATACAAATTTTATGATGATTTGTAAGCCGAGACGAAT-----GAT 790
Db 610 AGCAGATCACATGCAATTTTTCATATCAGCATTTGTCAAGTTTCATATAAATATGAGGCA 669
QY 791 CCCAGAAATTCAGAGAACTGTATGAGAGCTGTATGATCTTCATCTGTAATTTGTAGAT 850
Db 670 GCTGAAGATGATCATGTATTTCCCTCGCATATTTCTTCAAGTTCTCATCTTTGTGAT 729
QY 851 CTGGCTGGAGAGTGAAGAGCAAGCCAACTGAGCTGAAGGTGAGACTTAAAGAGGC 910
Db 730 TTGGCAGATTCAGAAAAGATTAACCAAGGGAATCTGTGGAACGGTTCAAGAAATCC 789
QY 911 TGCACATCAACCGCAGCTTGTATCTTGGACAGTTTATTAAGAGCTTAGCGAGC-- 968
Db 790 ATTCAATCAATAGTGAATTTGCTGTAGGAAATGTATTAAGCGCTTTGGGAGCCA 849
QY 969 -GCCAGGCTGTGATTTTAACTACAGACAGCAAGCAAGTACAGAAATTTCTCCAAAT 1027
Db 850 CCGAGGAAGATTCACATATTTCCATATAGGATGCTTAAATTAACCCGCTTGTGAAGAT 909
QY 1028 TCATTGGGAGAAATGCTTAAACGGTTTATTTGCAACATTAAGCCGAGTTTC-----T 1081
Db 910 TCTCTGGGAGGAGCTAGCTAGCTGTCAATGATCATATGTGACGCCCTCTCTCGAAT 969
QY 1082 TTTGATGAGCTCTAAGTACCTTCAATTTGCGAGTACTGCCAAACATGTGAGA 1135
Db 970 TTTGATGAGTCTTAAATTTCTCTCAATATGCAACAGACGGAACATTAGA 1023

RESULT 8
US-09-723-096-3

; Sequence 3, Application US/09723096
; Patent No. 6448026
; GENERAL INFORMATION:
; APPLICANT: Berard, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6448026el motor proteins and methods for
; FILE REFERENCE: 1031
; CURRENT APPLICATION NUMBER: US/09/723.096
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: US/09/641.807
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Human
US-09-723-096-3

Query Match 1.5%; Score 140; DB 4; Length 1023;
Best Local Similarity 51.0%; Pred. No. 7.3e-25;
Matches 456; Conservative 0; Mismatches 405; Indels 33; Gaps 4;
QY 275 TTCAATTCGATCGTATTTAATTTCCAGCAATCAACAGCAATTTTACCAAGAAATA 334
Db 130 TTCACTTTGATTTTGTGGCAAAATTTCCATCAAGATGAAGTTTATTAACACATGT 189
QY 335 GCAGTACATATCAATGATCAGTTTGCAGGATATATGSCAATATTTGCATACGA 394
Db 190 ATTAAGCCCCCTAGTGTGTCTACTCATTTAGGGCTATATAGCAATGTTTTGCTATGSA 249
QY 395 CAGACATTTTCAGGCAAGCGTACATATGATGGGAACCAATTCATT----- 444
Db 250 CAAACTGATCTGGGAAGACATACACATTGAGGGGGCCATATGCTTCAGTTGTGAG 309
QY 445 -----GGGATAATATACCCCAAGCCATACAGGAATTTTAAATTTTACAGAGATA 496

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Db      310 GGGCAAAAGGATTCATCTCCGAGCTATTCAGAAATATTTCAAGACATCTCTGAACAT 369
QY      497 CCGAAGAGAGATTTCTCTTAAGATTTCTTAATGAGATTTCAATGAAGCTGTGAAA 556
Db      370 CTTAGCATTTACTTAATGTAAGATTTCTTAATGAGATTTCAAGAGAACTGTAGA 429
QY      557 GACTTACTGTGTATGACAGAAAGAAAGCCCTTGAAATTTGCCAGATTTTAAATAGA 616
Db      430 GATCTTCTAGAAATTTGAGACATCATGAAAGATCTTCACATCCGAGAAAGTGAAGAAAGGA 489
QY      617 AACGTATGTTGCTGACCTGACGAAAGCTGTATGTTGCTGCTGAAACATGTAATACAG 676
Db      490 AACACAGTATTTGTTGGGGCCAAAGAAATGCCATGTGAGAGTGCAGGTGAAGTATGAT 549
QY      677 TGGATCAAAAAGGGTGAAGAAAAAGACATTTATGAGAGACTAAATGAATGATCATAGT 736
Db      550 CTTTGGAGATGGGGAATGACGACAGCATACAGGTACCACTCAATGAATGAGCACTCC 609
QY      737 AGTCCTTCACTACATTTATTAATGATTTGAAAGCCGAGACAGAAAT-----GAT 790
Db      610 AGCAGATCATCTCAATTTTTCACATCAGCATTTGTCAGTTGATTAATAAATATGAGAGCA 669
QY      791 CCCCAAAATCAGAGAACTGTATGAGCTGTATGATCTGATCTGATCTGAATTTGATAGT 850
Db      670 GCTGAAGATGATCATGTATTTCCCTCGGACATTTGTCTCAAGTTCCACTTTGTGAT 729
QY      851 CTTCGTGAGAGTAAAGAGACCAACCACTGAGCTGAAAGTGTAGACTTAAGAGAGC 910
Db      730 TTGGCAGAGATCAGAAAGATGACCAAAACGGGGATCTGTGAAACGGTTCAAAAGATCC 789
QY      911 TGCACATCAACCGCAGCTTTTATCTCTTGACAGGTTTAAAGAGCTTACGAGC-- 968
Db      790 ATTCAATCAATGATGATGATGCTGCTTTAGGAAATGTAAGCCCTCTTGGGAGCCCA 849
QY      969 -GCCAGCTGGTGGATTTATTAACCTACAGAGACAGCAACTCAGCAAGATTTCCAAAT 1027
Db      850 CGCAGAAAGATTCACATATTCATATAGGAGTCTTAATTAACCGGCTTCTGGAAGAT 909
QY      1028 TCATTGGAGGAATGCTAAACGGTTATTAATTTGCAATTTAGCGCCAGTTTC-----T 1081
Db      910 TCTCTGGAGGAGCTGTAGATCTGTATGATGATGATGATGATGATGATGATGATGAT 969
QY      1082 TTTGATGAGACTTAAGTACATTCAGTTGCTGCAAGTACGCCAAACATGTGAGA 1135
Db      970 TTGTAGAGAGCTTAATATCTCTCAATATGATGCCAAGACGAGCAACATTTAGA 1023

RESULT 9
US-09-592-054-5
; Sequence 5, Application US/09592054
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Finet, Jeffrey
; APPLICANT: Sakowicz, Roman
; APPLICANT: Wood, Kenneth
; TITLE OF INVENTION: No. 6440684el motor proteins and methods for
; FILE REFERENCE: 1016
; CURRENT APPLICATION NUMBER: US/09/592.054
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1421
; TYPE: DNA
; ORGANISM: Human
US-09-592-054-5

Query Match      1.4%; Score 135.2; DB 4; Length 1421;
Best Local Similarity 50.6%; Pired. No. 1,3e-23;
Matches 468; Conservative 0; Mismatches 408; Indels 48; Gaps 4;
```

```

QY      257 GTTGATGGGACAAAGCTTTCAATTTGATTCGATTCGTTATTTAATTTCTCAGCAATCAACAAGT 316
Db      123 GTTGTGACAGATTAATCTTACCTACCTACGATTTGTTATTTGATCCCTCTACTGAACAGAA 182
QY      317 CAATTTTACCAAGAAATAGCAGTACCTATCATACGATTCAGCTTTGAGGAGATTAATGAGC 376
Db      183 GAAGTCTTCAATACACAGATAGCGCACATTAAGAGTATTTAAAGATTAATGAGC 242
QY      377 ACAATATTTGATACGACAGACATCTTCAAGGCAAGAGTACCAATGATGGAAACCA 436
Db      243 ACGGTCTGGCTTATGAGGACAGATGAGCTCTGGAAGAAACCTATTTCAATGAGAGGTGATAT 302
QY      437 AATTCATTTG-----GGCATATACCCCAAGCCATACAGAAAGT 475
Db      303 ACTGACAGACAGAGAAATGACCAACACAGTTGGGTTATTTCTTAGGTAATACATGCTCTC 352
QY      476 TTTAAATTAATTCAGAGATACCGAAACAGAGACTTTCTTAAGATTTCTTAATGAG 535
Db      363 TTCAAGAAATTTGATTAAGAAAGATGACTTTGAATTTACTGTGAAGTGTCTTACTTAGAG 422
QY      536 ATTTACATGAACCTGTGAAGACCTACTGTGTGATGACAGAAAGAAAGAAAGCCCTTGAA 595
Db      423 ATTTACATGAAGAAATTTGATCTTATGCTATGCCATCTCTGTGAGAAAGCTCAAAATTAAT 482
QY      596 ATTGGGAGGATTTTAATGAAGAGTATTTGCTGACCTGACCTGAAGAACTGTATAG 655
Db      483 ATACGAGAGATCTTAAGAGAGGATTAAGATTTGAGACTCATCTGAAGAACTGTTTGG 542
QY      656 GTTCTGAAACATGTAATACAGTGTATCAAAAAGGTTGAAAGAAAGAAAGACATTTATGAGAG 715
Db      543 GTTGCTTGGATATCTGTTTCTGTTTGGAAACAGGAGCAACACTGTGAGACTGTGGCTCC 602
QY      716 ACTTAAATGATGATCATGATGATGCTTCAATCAATATTTGAATGATTTGAAAGC 775
Db      603 ACGGTATGAACTCCAGTCTGCTCCGATCTCATGCCATCTTTAACAAT--CTCCTTAGAGC 660
QY      776 CGAGACAGAAATATATCCCAAAATTCAGAGAACTGTGATGAGCTGTATGATCTCAC 835
Db      661 AAGAAAGAAAGATGACCAAGAAATAGAG-----CTTTCGCTCCAG 701
QY      836 TTGAATTTGATGATCTTCTGTCAGTGAAGAGCAAGCAACTGAGCTGAAGGTGTG 895
Db      702 CTGATCTTGTAGACTCTGCTGATCAGAAAGACAGAAAGAAACAAAGCTGAAGGGAT 761
QY      896 AGACTTAAGAGAGCTGCAACATCAACCGCAGCTTGTATTCCTTGACAGGTTATTAAG 955
Db      762 CGCTAAAGAGGATTTATATTAATTAACGAGGCTCTCTATGCTTGGGAAATGTAATCAGT 821
QY      956 AAGCTTAGGAGCGGACAGGCTGTGATTTATTAATCAAGACAGCAACCACTCACAGA 1015
Db      822 GCTCTTGGAGATGACAAAGAGGTGCTTTGCTCCTACAGAAATTTCAAGTTGACTCGA 881
QY      1016 ATTCTCCAAATTCATTTGGAGGAATGCTTAACGGTTATTAATTTGCAATTTAGCGCC 1075
Db      882 CTGCTTCAAGATTTCTAGAGGTAATAGCAATCTTATGATGATGATGATGATGATGAT 941
QY      1076 GTT-----TCTTTTATGAGACTTAAGTACATTCAGTTGCTGAGTACTGCAACAT 1129
Db      942 GCTGATCCCAATTTAGAGAAACATTAATACCTTCGCTATGCTGACAGAGCAAGAAAA 1001
QY      1130 GTGAGAAATATCTCCCATGTTAAT 1153
Db      1002 ATCAAGAACAAACCTATGTTAAT 1025

RESULT 10
US-09-592-054-3
; Sequence 3, Application US/09592054
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Finet, Jeffrey
```

APPLICANT: Sakowicz, Roman
 APPLICANT: Wood, Kenneth
 TITLE OF INVENTION: No. 6440684el motor proteins and methods for
 FILE REFERENCE: 1016
 CURRENT FILING DATE: 2000-07-20
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 3
 LENGTH: 1569
 TYPE: DNA
 ORGANISM: Human
 US-09-592-054-3

Query Match 1.4%; Score 135.2; DB 4; Length 1569;
 Best Local Similarity 50.6%; Pred. No. 1.4e-23;
 Matches 468; Conservative 0; Mismatches 408; Indels 48; Gaps 4;

257 GTTGATGGACAAAGCTTTCAATTGCGTGTATTTAAATCTCAGCAATCAACAGT 316
 187 GTTGTACAGATTAATCTTCACTACATTTTGTATTTGATCCCTACTGAAACAGAA 246
 317 CAAATTACCAAGAAATAGCAGTACCTATACATGATCAGCTTTGACGGATATATGCG 376
 247 GAAGTCTTAATACAGCAGTACGCGCAGCTATTAAGGTATTTAAAGATATATGCA 306
 377 ACAATTATTGATACAGCAGCATCTTACAGCAGAGCTACACATGATGGGAACCA 436
 307 ACGGTCTGGCTATGAGGAGAGCTGCTGTAAGAAACCTTAAAGGAGGAGCTAT 366
 437 AATTCATG-----GGCATATATCCCAAGCCATACAGGAAGT 475
 367 ACTGAGAGCAAGAGATGAACCAACAGTTGGGGTTATTTCTAGGATATACATGCTC 426
 476 TTTAAATATTATTCAGAGATACCAACAGAGATTTCTTCAAGATTTCTTATATGAG 535
 427 TTCAAGAAATTGATTAAGAGAGTGAATTTACTGTAAGGTCTTACTTATGAG 486
 536 ATTTACATGAACTGTGAAGAACCTTACTGTGATGACAGAAAGAAAGCCCTTGAA 595
 487 ATTACATGAAAGAAATTTGGATCTTATGCCATCTGTGAGAAAGCTCAATTAAT 546
 596 ATTGCGAGATTTTAAATAGAAAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 655
 547 ATACGAGAGATCTTAAGAGAGCATTAAGATTTGGAGCTCAGAGAGCTGTTTG 606
 656 GTTCTGAACATGTAATACAGTGCATCAAAAGGAGTGAAGAAAGAGACATTAATGAGAG 715
 607 GTTGCCTTGGATCTGTTCTCTGTTGGAAAGGGAACAACCTTAGACCTGTGCTCC 666
 716 ACTAAATGTAATGATATAGTCTGCTACATCAATTTAGAAATGATTTGAAAGC 775
 667 ACGGCTATGAATCCAGCTGCTCCGATCTCAAGCATCTTAAAT--CTCCTTAGAGC 724
 776 CGAGACAGAAATGATCCCAATTCAGAGAACTGTGATGAGCTGATGTAATCTAC 835
 725 AAAGAAAGAAAGTGAAGAAATAGAG-----CTTTCGCTCCAG 765
 836 TTGAATTTGATATTTCTGCTGCACTGTAAGAGCAAGCAAACTGAGCTGAAGGTG 895
 766 CTGCACTTGTAGACCTCGCTGATCAGAAAGACAGAAAGAAACCAAGCTGAAGGGAT 825
 896 AGACTTAAGAGAGCTGCAACATCAACGCAAGCTTGTATCTTGTGACAGCTTAATAG 955
 826 CGTCTTAAGAGAGATTAATTAATTAACGAGGCTCTATGCTTGGAAATGTAATAGT 885
 956 AAGCTTAGGAGCGGCTGCTGATTTTAACTACAGACAGCAAACTGACAGA 1015
 886 GCTCTTGAAGATGACAAAGAGGTGCTTTGGCTTACAGAGATTCAGAGTGAATCTGA 945
 1016 ATTCCAAATTTCAATTTGGAGAAATGCTAAAGGTTAATTTGCAATTAACGCA 1075

Db 946 CTGCTCAAGATCTCTAGAGGAAATAGCCACTTATATGATACCTGTGACTCT 1005
 Oy 1076 GTT-----TCTTTGATGAGATCTTAAGTACCTTCACTTGGCCAGTACGCCAACAT 1129
 Db 1006 GCTACTCCATCTAGAGGAAACATTAAATACCTTCGCTATGCTGACAGACAAAGAAA 1065
 Oy 1130 GTGAGAAATATCCCATGTTAAT 1153
 Db 1066 ATCAAGAAACCACTAATTTGTAAT 1089

RESULT 11 US-09-595-684B-22

Sequence 22, Application US/09595684B
 Patent No. 6544766
 GENERAL INFORMATION:
 APPLICANT: Beraud, Christophe
 APPLICANT: Ohashi, Gara
 APPLICANT: Sakowicz, Roman
 APPLICANT: Vaisberg, Eugeni
 APPLICANT: Wood, Kenneth
 APPLICANT: Yu, Ming
 TITLE OF INVENTION: Human kinesins and methods of producing
 FILE REFERENCE: cyclopo36
 CURRENT FILING DATE: 2002-06-24
 PRIOR APPLICATION NUMBER: 09/295,612
 PRIORITY FILING DATE: 2000-04-20
 NUMBER OF SEQ ID NOS: 105
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 22
 LENGTH: 4348
 TYPE: DNA
 ORGANISM: Human
 US-09-595-684B-22

Query Match 1.4%; Score 133.6; DB 4; Length 4348;
 Best Local Similarity 50.5%; Pred. No. 6.1e-23;
 Matches 467; Conservative 0; Mismatches 409; Indels 48; Gaps 4;

257 GTTGATGGACAAAGCTTTCAATTTGATGCTGCTGCTGCTGCTGCTGCTGCTG 316
 187 GTTGTACAGATTAATCTTCACTACATTTTGTATTTGATCCCTACTGAAACAGAA 246
 317 CAAATTACCAAGAAATAGCAGTACCTATACATGATCAGTTCGAGGATATATGCG 376
 247 GAAGTCTTAATACAGCAGTACGCGCAGCTATTAAGGTATTTAAAGATATATGCA 306
 377 ACAATATTGATACAGCAGCATCTTACGCAAGAGCTTCTTAAAGATTTCTTATATGAG 436
 307 ACGTCTGCTTATGAGGAGAGCTGCTGTGAAAGAACTTAAATGAGGAGTCAAT 366
 437 AATTCATG-----GGCATATATCCCAAGCCATACAGAACTT 475
 367 ACTGAGACAGAGATGAACCAACAGTTGGGTTATTTCTAGGATATCACTGCTC 426
 476 TTTAAATATTACAGAGATACCAACAGAGATTTCTTAAAGATTTCTTATATGAG 535
 427 TTCAAGAAATGATTAAGAAAGAGTACTTGAATTTACTGAAAGGTCTTACTTAGAG 486
 536 ATTTCAATGAATCTGTGAAGAGCTACTGTGTATGACAGAAAGAAAGAGCCCTTGAA 595
 487 ATTACATGAAGAAATTTGGATTTCTATGCTCATCTCGTGAAGAGCTCAATTAAT 546
 596 ATTGCGAGATTTTAAATAGAAAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 655
 547 ATACAGAGAGATCTTAAGAGAGCATTAAGATTTGGAGCTCACTGAAAGAGCTGTTTG 606
 656 GTTCTGAACATGTAATACAGTGCATCAAAAGGAGTGAAGAAAGAGACATTAATGAGAG 715
 607 GTTGCCTTGGATCTGTTCTCTGTTGGAAAGGGAACAACCTTAGACCTGTGCTCC 666

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Qy 716 ACTAAATGATGATCATAGTACGTTCCATCATCATATTTAGATATGTTGAAGC 775
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 667 ACCGCTATGAATCTCCAGTGTCTCCGATCTCATGCCATCTTTACAT--CTCCTAGAGC 724
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 776 CGAGACGAAATGATCCACAAATTCAGAGAACTGTGAGAGCTGTATGATCTCAC 835
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 725 AAGGAAAGAAAGTACAGAAATGACAG-----CTTCGCTCAAG 765
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 836 TTGAATTTGATGATCTTCTGCGACGAGAAAGCAAGCAAGCAAGTGAAGCTGAAAGTGTG 895
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 766 CTGCATCTTTGATGACCTGCTGATCAGAAAGACAGAAACCAAGGCTGAAGGGGAT 835
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 896 AGACTTAAGGAGGCTGCAATCAACCGAGCTTTGTTATCTTGGACAGTTATTAAG 955
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 826 CGTCTAAAGAGGATATTAATTAACCGAGGCTCTTATGCTTGGAAATGTAATAGT 885
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 956 AAGCTTAGCGACGCGCGAGCTGTGATTTAATACTACAGACAGCAAACTCACAGA 1015
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 886 GCTCTTGAGATGACAAAAGGGTGGCTTGGCGCTACAGAGATTCAGATTGACTCGA 945
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1016 ATTCTCCAAATTCATTGGAGAGAAATGCTAAAACGGTTATTAATTGGACAATTACGCCA 1075
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 946 CTGCTTCAGATTCCTAGAGAGTAATAGCCATATCTTATGATAGCTGTGTGAGTCTT 1005
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1076 GTT-----TCTTTGATGAGACTCTAAGTACCTTCACTTGGCAGTACTGCAAAAT 1129
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1006 GCTGACTCCCATTTAGAGAAACATTAATACCTTTCCTATGCTGACAGACAGAAAA 1065
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1130 GTGAGAAATACCTCCCATGTTAAT 1153
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1066 ATCAGAACAAACCTATTGTTAAT 1089
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 12

```

US-09-592-054-7
; Sequence 7, Application US/09592054
; Patent No. 6440684
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Finer, Jeffrey
; APPLICANT: Sakowicz, Roman
; APPLICANT: Wood, Kenneth
; TITLE OF INVENTION: No. 6440684e1 motor proteins and methods for
; FILE REFERENCE: 1016
; CURRENT APPLICATION NUMBER: US/09/592.054
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FaetsEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 4127
; TYPE: DNA
; ORGANISM: Human
US-09-592-054-7

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Query Match 1.3%; Score 127.2; DB 4; Length 4127;
Best Local Similarity 50.1%; Pred. No. 2.3e-21;
Matches 463; Conservative 0; Mismatches 413; Indels 48; Gaps 4;

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Qy 257 GTTGATGGGACAAAGTCTTCAATTTGATCGTGTATTTAATCTCAGCAATCAACAGT 316
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 229 GTTGTGACTGATTAATCTTACCTACCTAGATTTGTGTTTACCCTGTACTGACAGAA 288
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 317 CAAATTTACCAAGAAATAGCAGTACCTATCATAGTACAGCTTTGACAGGATATAATGCG 376
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 289 GAAGTCTTCAATAAGAGAGTACGCGCTCATATAAGGCAATTTAAAGATATAATGCA 348
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 377 ACAATATTGTCATAGCAGACATCTTCAGGCAAGCGTACCAATGATGGAAACCA 436
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 349 ACCGTCTGGCTTATGGGAGACTGGCTCGGAAAAACCTATTCAATGGAGGTGATAC 408
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 437 AATT-----CATTGGCATATATACCAAGCATACAGAAAGT 475
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 409 ACTGCGAGACGAGAGATGACCAACAGTTGCAATTATCTAGGTAATACAACTGCTC 468
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 476 TTTAAATTTATAGAGATACCGAAGAGAGTCTTCTTAAGATTTCTTATATGAG 535
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 469 TTTAAAGAAATTTGATCAAAAGAGTCTTGAATTTACTGTGAAGTCTTATAGAG 528
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 536 ATTTCAATGAACTGTGAAGACCTACTGTGTATGACAGAAAGAAAGAGCCCTTGAA 595
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 529 ATTTACATGAAATAATTTTGGATCTTTATGCCCCATCTCTGAGAAAGCTCAATTAAT 588
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 596 ATTGCGAGATTTTAATAGAAACGTATATGTTGCTGACCTGATGAAGACTTGTAAAG 655
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 589 ATACGGAGAGATCTTAAGAAAGCATAAAGATTGTGGACTCACTGAAAGACTGTTTA 648
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 656 GTTCTGAACTATATACAGTGAATCAAAAAGGGTGAAGAAAAACGACTTTATGAGAG 715
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 649 GTTGCTTGGATCTGTTTCTGTTGGAGCAGGGAACAACTGTGAGACTGTGCTCC 708
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 716 ACTAAATGATGATGATAGTACGTTGCAATACATATTTAGAAATGATTTGAAAGC 775
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 709 ACAGCTATGAATCTCCAGTCGTCCGATCTCATGCCATCTTTACAT--CTCCTTAGAGC 766
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 776 CGAGACGAAATGATCCCAAAATTCAGAGAACTGTGATGAGACTGTATGATCTCAC 835
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 767 AAGGAAAGAAAGTGAACAAGATAGCAG-----CTTCGCTCAAG 807
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 836 TTGAATTTGATGATTTGCTGCGACGTGAAGAGCAAGCAAGCTGAGAGTGAAGTGTG 895
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 808 CTGCATCTTGTAACTCTGCTGATCAGAAAGCAGAAAGAAACCAAGCTGAAGGGAT 867
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 896 AAGCTTAAGGAGGCTGCAACATCAACCGAGCTGTTTATCTTGGACAGTATTAATG 955
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 868 CGTCTAAAGAGGATTAATTAATTAACAGGCTCTCTATGCTTGGAAATGTAATCAGT 927
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 956 AAGCTTAGCGACGCGCGAGCTGTGATTTAATACTACAGACAGCAAACTCACAGA 1015
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 928 GCTCTTGAGATGACAAAAGGGTAGCTTTGTCCCTACAGAGATTCAAAGTTAACTCGA 987
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1016 ATTCTCCAAATTCATTGGAGAGAAATGCTAAAACGGTTAATTTGACAAATTAACGCCA 1075
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 988 CTGCTCAAGATTCCTAGAGGTAAACAGCCACACTTATGATACCTGTGTGAGTCTCT 1047
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1076 GTT-----TCTTTGATGAGACTCTAAGTACCTTCACTTGGCAGTACTGCAAAAT 1129
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1048 GCTGACTCCCATTTAGAGAAACATTAAGTACCTTTCCTATGCTGACAGACAGAAAA 1107
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1130 GTGAGAAATACCTCCCATGTTAAT 1153
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1108 ATCAGAACAAACCTATTGTTAAT 1131
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 13

```

US-09-592-054-1
; Sequence 1, Application US/09592054
; Patent No. 6440684
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Finer, Jeffrey
; APPLICANT: Sakowicz, Roman
; APPLICANT: Wood, Kenneth
; TITLE OF INVENTION: No. 6440684e1 motor proteins and methods for
; FILE REFERENCE: 1016
; CURRENT APPLICATION NUMBER: US/09/592.054
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FaetsEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4308
; TYPE: DNA
; ORGANISM: Human
US-09-592-054-1

```

Query Match 1.2%; Score 116; DB 4; Length 4308;
 Best Local Similarity 49.4%; Pred. No. 1.4e-18;
 Matches 456; Conservative 0; Mismatches 420; Indels 49; Gaps 4;

QY 257 GTTGATGGGCAAAAGCTTTCAATTTGATGCTGATTTAATTCACGAATCAACAAGT 316
 DB 187 GTTGTGACAGATTAATCCCTTCACTACGATTTTGTATTTGATCCCTACTAACAAGAA 246
 QY 317 CAAATTTACCAAAATAGCAGACCTATCATACATGCTTTGAGAGATATATGCG 376
 DB 247 GAAGTCTTCAATACAGCAGTACGACCTATCAATAAAGTATTAAGAAATATATGCA 306
 QY 377 ACAATATTTGATACAGCAGACATCTTCAGCAGAGTACACATGATGAGAAACCA 436
 DB 307 ACGGTCTGGCCTATAGGAGAGCTGGCTCTGAAAAACCTATTCATGAGAGGTGATAT 366
 QY 437 AATTCATTG-----GGCATTAATCCCAAGCCATACAGAAATT 475
 DB 367 ACTGACAGCAAGAAATGAAACCAAGTTGGGGTTATTCCTAGGGTAAATCAACTGCTC 426
 QY 476 TTTAAATTTATTCAGAGATACCAACAGAGATTTCTTAAAGTTCTTATATGAG 535
 DB 427 TTCAAGAATTTGATTAAGAAAGTACCTTTGATTTACTTGAAAGTGTCTTACTTATGAG 486
 QY 536 ATTTACATGAACCTGTGAAAGCTTCTGTGTATGACAGAAAGAAAGCCCTTGAA 595
 DB 487 ATTTACAAATGAAGAAATTTGGATCTTATGTCCATCTGTGAAAGATCAATTGAG 546
 QY 596 ATTGCGAGGATTTTATAGAAACGTATGTGCTGACTGATGAAGAACTTTATATG 655
 DB 547 ATTTACATGAAGAAATTTGGATCTTATGTCTGATCTGCTGAAAGCTCAAGTTTG 606
 QY 656 GTTCCGAACTGTAAATACAGTGTATCAAAAAGGGTAAAAAACAACATTTATGAGAG 715
 DB 607 GTTCCCTTGATCTGTTTCTGTTTGGAAAGGGAACAACCTAGAGACTGTGGCTCC 666
 QY 716 ACTAAATTTGATGATCAATAGTCTGCTGATCAATCAATTTTGAATGATTTGTAAGC 775
 DB 667 ACGGCTTGAACCTCCAGTGTCCGATCTCATGCCATCTTAACAAT--CTCCCTAGAGC 724
 QY 776 CGAGACAGAAATGATCCCAAAATTCAGAGAACTGTATGAGAGCTGTCAATGATCTAC 835
 DB 725 AAGGAAGAAAGTGAACAAGATAGCAG-----CTTGGCTCAAG 765
 QY 836 TTGAATTTGATGATCTTGTGCTGCAATGAAGCAAGCCAACTGAGCTGAGAGTGTG 895
 DB 766 CTGATCTTGTAGACCTGCTGATCAGAAAGACAGAAAGAAACCAAGGCTGAAGGGAT 825
 QY 896 AGACTTAAGAGAGCTGCAACATCAACCGAGCTGTTTATCTTGTGACAGTTTATAG 955
 DB 826 CGTCTAAAGAGGTATTAATTAACCGAGGCTCTCTATGCTTGGAAATGTAAATCAGT 885
 QY 956 AAGCTTAGCAGCGGCGAGCTGTGATTTAATTAACCTAGACAGACAGCAATCCACGGA 1015
 DB 886 GCTCTTGAGATGACAAAAAGGTGTGGCTTGCGCCTACAGAGATTCCAAAGTTGACTGA 945
 QY 1016 ATTCTCCAAATTTGAGAGAAATGCTAAACCGTTATATATTGCAATTAACGCCA 1075
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 QY 1076 GTT-----TCTTTGATGAGACTTAAGTACACTGATGCTGAGTATGAGTATGAG 1129
 DB 1006 GCTGACTCAATCTAGAGAAACATTAATACCTTTCGCTATGAGACAGAGCAAGAAA 1065
 QY 1130 GTGAGAAATCTCCCATGTTAAT 1153
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RESULT 14
 US-09-641-806-3
 ; Sequence 3, Application US/09641806
 ; Patent No. 6395527

GENERAL INFORMATION:
 ; APPLICANT: Beraud, Christophe
 ; APPLICANT: Freedman, Richard
 ; TITLE OF INVENTION: No. 6395527e1 motor proteins and methods for
 ; TITLE OF INVENTION: their use
 ; FILE REFERENCE: 1034
 ; CURRENT APPLICATION NUMBER: US/09/641,806
 ; NUMBER OF SEQUENCE: 4
 ; CURRENT FILING DATE: 2000-08-17
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 1011
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-641-806-3

Query Match 1.0%; Score 98; DB 4; Length 1011;
 Best Local Similarity 48.3%; Pred. No. 1.8e-14;
 Matches 346; Conservative 0; Mismatches 355; Indels 15; Gaps 2;

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 DB 214 TTGAGAGGCTTCAATGACCACTGTCTTGTCTATGTGACAGGCTCAGGAAAGCATAC 273
 QY 419 ACAATGATGGGAACACCAA-----ATTCAITGGCATTAATCCCAAGCCATA 466
 DB 274 ACCATGGGGAGGACCACTCCCTCTGAGATGAGCAGGAGCATTTGCCAGAGGCCATG 333
 QY 467 CAGAAATTTTAAATTTATTCAGAGATACCGAACAGAGTCTTCTTAAGTTTCT 526
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 QY 527 TATATGATTTTCAATGAATCTGTGAAGACCTTCTGTGTATGACAGAAAGAAAG 586
 DB 394 TACTGGAAGGTATCAAGAGAGAGTCCGAACTGTCTGAGGTGGGCACTGCCAGCCGT 453
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 ; Sequence 3, Application US/09723129
 ; Patent No. 6551787

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/ GENERAL INFORMATION:
/ APPLICANT: Beraud, Christophe
/ APPLICANT: Freedman, Richard
/ TITLE OF INVENTION: No. 6551787el motor proteins and methods for
/ FILE OF INVENTION: their use
/ FILE REFERENCE: 1034
/ CURRENT APPLICATION NUMBER: US/09/723,129
/ CURRENT FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 09/641,806
/ PRIOR FILING DATE: 2000-08-17
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 1011
/ TYPE: DNA
/ ORGANISM: Human
US-09-723-129-3
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Query Match      1.0%; Score 98; DB 4; Length 1011;
Best Local Similarity 48.3%; Pred. No. 1.8e-14;
Matches 346; Conservative 0; Mismatches 355; Indels 15; Gaps 2;
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GenCore version 5.1.6
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(without alignments)
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Gapop 10.0, Gapext 1.0

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Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Published Applications_NA:
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SUMMARIES

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1	620.4	6.4	8491	12 US-10-133-013-260	Sequence 260, App
2	620.4	6.4	8493	13 US-10-071-766-51	Sequence 51, App1
3	620.4	6.4	8503	14 US-10-037-270-130	Sequence 130, App
4	615.2	6.4	7992	11 US-09-893-519A-140	Sequence 140, App
5	206.6	2.1	581	9 US-09-833-790-351	Sequence 351, App
6	147.8	1.5	3505	12 US-09-814-353-21787	Sequence 155, App
7	146.6	1.4	501	9 US-09-833-790-167	Sequence 167, App
8	138.2	1.4	3753	12 US-10-116-712-668	Sequence 668, App
9	135.2	1.4	4348	12 US-10-116-712-661	Sequence 661, App
10	133.6	1.4	4348	12 US-10-116-712-667	Sequence 667, App
11	133.6	1.3	9240	14 US-10-198-846-13194	Sequence 13194, A
12	124.4	1.3	1726	12 US-10-133-013-263	Sequence 263, App
13	122.8	1.2	3366	10 US-09-938-842A-2651	Sequence 2651, App
14	117.6	1.0	4858	10 US-09-954-456-733	Sequence 733, App
15	95.8	0.9	29793	10 US-09-973-451-38	Sequence 38, App1
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17	85.6	0.9	501	9 US-09-833-790-329	Sequence 329, App
18	82	0.9	4775	14 US-10-146-473-81	Sequence 81, App1
19	81.2	0.8	6586	10 US-09-954-456-1115	Sequence 1115, App
20	81.2	0.8	6586	10 US-09-954-456-1790	Sequence 1790, App
21	81.2	0.8	6586	14 US-10-157-031-37	Sequence 37, App1
22	73.8	0.8	3348	10 US-09-954-456-90	Sequence 90, App1
23	73.8	0.8	3348	10 US-09-954-456-727	Sequence 727, App1
24	68.2	0.7	3376	13 US-10-071-766-80	Sequence 80, App1
25	68	0.7	5361	10 US-09-742-096-2	Sequence 2, App1
26	68	0.7	6152	10 US-09-742-096-1	Sequence 1, App1
27	67.8	0.7	5848	13 US-10-044-090-299	Sequence 299, App
28	67.6	0.7	3930	10 US-09-847-874A-2	Sequence 2, App1
29	66.6	0.7	410	14 US-10-106-698-2537	Sequence 2537, App
C 30	66.6	0.7	14006	12 US-10-311-455-1931	Sequence 1931, App
C 31	62.8	0.7	6668	12 US-10-311-455-1670	Sequence 1670, App
C 32	61.8	0.6	3673778	12 US-10-312-841-2	Sequence 2, App1
C 33	61	0.6	1171	14 US-10-198-846-12848	Sequence 12848, A
C 34	59	0.6	9539	12 US-10-240-453-54	Sequence 54, App1
C 35	59	0.6	9539	14 US-10-239-676-52	Sequence 52, App1
C 36	58.6	0.6	113515	12 US-10-311-455-2147	Sequence 2147, App
C 37	58.4	0.6	1002	10 US-09-879-536-442	Sequence 442, App
C 38	58.2	0.6	498	10 US-09-738-973-345	Sequence 345, App
C 39	58.2	0.6	498	10 US-09-854-133-345	Sequence 345, App
C 40	58.2	0.6	498	14 US-10-144-642A-345	Sequence 345, App
C 41	58	0.6	529	10 US-09-983-965-2109	Sequence 2109, App
C 42	57.4	0.6	446	10 US-09-960-352-3400	Sequence 3400, App
C 43	56.4	0.6	6668	12 US-10-311-455-1669	Sequence 1669, App
C 44	56.2	0.6	5750	12 US-10-311-455-1981	Sequence 1981, App
C 45	56	0.6	1395	12 US-10-161-051-120	Sequence 120, App

ALIGNMENTS

RESULT 1
US-10-133-013-260
Sequence 260, Application US/10133013
Publication No. US2003016903A1
GENERAL INFORMATION:
APPLICANT: Astromoff, Anna
APPLICANT: Bandman, Olga
APPLICANT: Cocke, Benjamin G.
FILE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
TITLE REFERENCE: PA-0049 US
CURRENT APPLICATION NUMBER: US/10/133, 013
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 60/287, 067
PRIOR FILING DATE: 2001-04-27
NUMBER OF SEQ. ID NOS: 271
SOFTWARE: PERL Program
SEQ. ID NO 260
LENGTH: 8491
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. US2003016903A1 441283.5
US-10-133-013-260

Query Match 6.4%; Score 620.4; DB 12; Length 8491;
Best Local Similarity 65.5%; Pred. No. 2.6e-131;
Matches 1001; Conservative 0; Mismatches 491; Indels 36; Gaps 5;
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17 GCGGCTGTGAGCGCCGTGAAGTCCGCGCGGAGAGGCTCCGTCATTTCGTGGACAG 76
QY 129 TAATCGGTCTCAAAATGTCGAGAGGAGTCACTTAAAGTGTGTGAGGCTTCGCGCC 188
DB 77 TTCAGCTATAGATGAGGCGGAGAGGAGGCTTCGCTGCGTGTGCGGCTCGCGCC 136
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Db      197 ATGTCAATTTATCAAGTTGATGGAGAAATCCTTCAATTTTGTATGTCTTTCAATGTA 256
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Qy      603 AGGATTTTAAATGAACGTATATGTTGCTGACCTGACAGAAATCTTGAATGTTCTG 662
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Qy      783 GAAATGATCCCAAAATTCAGAGAACTGTATGAGCTGATGATGATCTTCACTGAT 842
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Qy      843 TGTAGATCTTTGCTGAGATGAAAGACAAAGCCAACTGAGCTGAAGCTGTAGACTTA 902
Db      788 TGGTGTATCTTTGACGAGATGAAAGAGCTCTCAAAACAGGCTGAGAGTGTGCGCTCA 847
Qy      903 AGGAAGCTGCAACATCAACGAGCTTTGTTATCTTGGAGAGGTATTTAAGAACTTA 962
Db      848 AGGAAGCTGTAATATATATGAAAGCTATTTATTTGGAGCAAGATCAAGAACTTA 907
Qy      963 GCGACGCGCGAGCTGTGATTTATATATCAAGAGACAGCAAACTCACAGAAATTC 1022
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RESULT 2

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; Sequence 51, Application US/10071766
; Publication No. US20020192678A1
; GENERAL INFORMATION:
; APPLICANT: Huel-Mei Chen
; TITLE OF INVENTION: GENES EXPRESSED IN SENESENCE
; FILE REFERENCE: PA-0043 US
; CURRENT APPLICATION NUMBER: US/10/071.766
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PERL Program
; SEQ ID NO 51
; LENGTH: 8493
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
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Query Match 6.4%; Score 620.4; DB 13; Length 8493;

Best Local Similarity 65.5%; Pred. No. 2.6e-131;

Matches 1001; Conservative 0; Mismatches 491; Indels 36; Gaps 5;

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Qy 1023 AAAATTGATGGAGAGAAATGCTAAACGGTTATTAATTGACAAATTAAGCCATTTCT 1082
Db 968 AGAATTCCTTGGAGAGAAATCCAAAGACAGTATTTCTGCAAAATTAATCTCCAGTAT 1027
Qy 1083 TTGATGAGACTTAAGTACATCTCACTTGGCAGTCTGCAAGCAAGTGTGAGAAATCTC 1142
Db 1028 TTGATGAAACTCTTACTGCTCTCCAGTGTGCAAGTCTGTAATATATAGAAATATCTC 1087
Qy 1143 CCCATGTTATGAGTCTGATGATGAGAGCTGTCTAAAGGTTACAGAAAGAAATCT 1202
Db 1088 CTTATGTTATAGAGTATCACTGATGAGAGCTCTCTGAAAGGTTATAGAAAGAAATAA 1147
Qy 1203 TGGATTTTAAAGAAACAATTAGAGAAATTAAGTCACTGTCTGAAACAAAGCTCAAGCA 1262
Db 1148 TGGATCTTAAAGAAACAATTAGAG-----GAGGTTCTTTAGAGAGCGGCGCTCAAGCA 1201
Qy 1263 TGGGTTAAAGAGAGCATACAGTGTGCTGAAATCAAAACAACATCAAAAGAGAG 1322
Db 1202 TGGAAAAAGACCAATTTGGCCCACTTTTGAAGAAAAAGATTTGCTTCAAGAAAGTACAG 1261
Qy 1323 AAGATGATATGAGCACTGACAAATATTTGTTGTTG---CTTCATCCCAAGATCTCAAC 1379
Db 1262 ATGAGAGAAATTTGAAATCTTAACACGAGTGTGTGACCTTCTTCTCCACAGTTGCAAC 1321
Qy 1380 AGGACCAAAAGGCTCAACGAGAAAGGTTACGTGGGCGCCAGAGAAATTCAAATA 1439
Db 1322 AGGAATTTAAAGGCTTAAAGAAAAAGAAAGTTACTTGTCCTGCAAAATTAACAAA 1381
Qy 1440 GTTTACATGCTCTGTGTGTTCTGACTTGTGATATGATATCCAGATCTGCGCAATTTA 1499
Db 1382 TGAAGAA-----CTCAACTATGACAGATCAATTTATATATCAACAACAAATATA 1429
Qy 1500 GCAAGAGGCAAAAGTTCTGTGACATGCTTCATTTCCAGAAATGTGATGATCTGTTGTA 1559
Db 1430 CAACAAAAACATATAGCTTTCTATTAATTTATTCGAGAAATGATGATCTGTCTGTT 1489

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Qy 1560 CAGAGTTTCTGATTTTGTATGACGCGCT 1587
Db 1490 CAGAGTCTGATGTTTTCAGTAACACTCT 1517

RESULT 3
US-10-037-270-130
; Sequence 130, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungding
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Tillinghast, John
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/10/037,270
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pc_FL_genes Version 1.0
; SEQ ID NO 130
; LENGTH: 8503
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (91)..(8082)
; US-10-037-270-130

Query Match 6.4%; Score 620.4; DB 14; Length 8503;
Best Local Similarity 65.5%; Pred. No. 2,6e-131;
Matches 1001; Conservative 0; Mismatches 491; Indels 36; Gaps 5;

Qy 69 GCCGCCAAAGGAGCTAAAGTACAGAGACAGAGAGCGGTGTCGTACCGATTTCTCCAC 128
Db 17 GCGGCGTGTGAGACCCCTGAAGTCCGCCGCGGAGGGTCTGCGCAATTTTGGTGGAGCCAG 76
Qy 129 TTAATGGGTCTCAAAATGTCGAGGAGATGCACTTAAAGTGTGTGTGAGGGTTCGGCCCC 188
Db 77 TTCACCTGATATGAGATGGCGGAGGAAGAGCGTGCCTGTGCGTGTGCGAGTGTGCGCCCC 136
Qy 189 TTATACAGAGAGAACAA-----GGGATCAAGCCAACTGCAATGGAAGGCTGGAACA 242
Db 137 TGAACGACGAGAGAGATCACTTGAAGAACTGCCCAAGTTTACTGGAACCTGACAAATA 196
Qy 243 ACACATTTTCCCAAGTTGATGAGACAAAGCTTTCAATTTGATGATGATTTAAATTTCTC 302
Db 197 ATGCTATTTATCAAGTGTATGAGAGTAATCTTCAATTTGATGATGATGATGATGATG 256
Qy 303 AGCAATCAACAGTCAAAATTTTACAGAAATATGCGATCTATCATATGATGATGATGATG 362
Db 257 ATGAACCTTACCAAAATGTGTATGAAAGAAATGCGACGACCAATTCATTCGATTCATAC 316
Qy 363 AGGATATATATGCAACAATATTGATGATACGAGACAGACATCTTCAGGCAAGAGCTACAAA 422

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Db 317 AAGGTACATGCTACTATATTTGCTTATGACAGACCTGCTTACAGAAAAACATATCCCA 376
Qy 423 TGATGGAAACACCAATTCATTTGGGCAATATACCCAGCATACAGAACTTTTAA 482
Db 377 TGATGGGTTAGAAATCATTTGGAGTTATACCCAGGCAATTCATGACATTTCCAA 436
Qy 483 TTATTCAGAGATTCAGAAACAGAGATTTCTTCAAGATTTCTTATATGAGATTTACA 542
Db 437 AAATTTAAGAGTTCTTGATAGGAAATTTCTTACCTGTATCTTACATGAAATATACA 496
Qy 543 ATGAACTGTGAAAGACCTACTGTGTATGACAGAAAGAAAGCCCTTGAATTCGG 602
Db 497 ATGAAACCATTACAGATTTACTGTGGCACTCAAAAAAGAACTTTATTTATTCGAG 556
Qy 603 AGATTTTAAATAGAAAGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 662
Db 557 AAGATGCTCATAGAAATGTTATGTTGCTGATCTCAGAGAAAGTTGTATATACATCAG 616
Qy 663 AACCTGTAATACAGTGTATCAAAAAAGGTTGAAAAAAGAGCAATTAAGAGACTTAAA 722
Db 617 AAATGCTTTGAATGATTAACAAGGAGAAAAAGAGAGCAATTAAGAGAAAAA 676
Qy 723 TGAATGATCAATAGTATCTTCTTCAATCAATTTTGAATGATGTTGAAAGCCAGACA 782
Db 677 TGAATCAAGAGAGAGAGTCTTCTTCAATCCTTTAGAGATTTTGAAGCAGAGAGA 736
Qy 783 GAAATATCCCAAAATTCAGAGAACTGTGATGAGCTGTGATGCTGCTGCTGCTGCTG 842
Db 737 AAGGTGAACTTCTTAAAT-----TGTGAAAGATCTGTTAAGGTATCCCATTTGATTT 787
Qy 843 TGGTATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 902
Db 788 TGGTATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 847
Qy 903 AGGAAGCTGCAACATCAACGAGCTGTTTATCTTGAAGTATTAAGAGCTTA 962
Db 848 AGGAAGCTGTAATTAATGAAGCTTATTTATTTGGGCAAGATGATCAAAAACTTA 907
Qy 963 GCGAGCGGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1022
Db 908 GTGATGCAAGAGTTGGTGGTTTCAATTAATATGAGATGCAAGTAAACGAAATCTTC 967
Qy 1023 AAAATTCATTTGGAGAAATGCTTAAACGGTTAATTTGCAATTTAGCCAGTTCTT 1082
Db 968 AGAATTCCTTGGAGAAATCCAAAGACGTTATTTCTGCACAATTTACTCCAGATCTT 1027
Qy 1083 TTGATGAGCTCTTAAGTACACTTCAAGTTTCCAGTACGCAAAACATGAGAAATCTC 1142
Db 1028 TTGATGAACTCTTAAGTACACTTCAAGTTTCCAGTACGCTAAATATATGAGAAATCTC 1087
Qy 1143 CCCATGTTAATGAGTCTGCTGATGAGAGCTTGTATAAAGGTAAGAGAAATCT 1202
Db 1088 CTTATGTTAATGAGTATCACTGATGAAGCTTCTGTAAGAAAGGTAAGAAATTA 1147
Qy 1203 TGGATTTAAAGAAACATTTAGAGAAATTTAGATCACTGCTGAAACAAAGCTCAAGCA 1262
Db 1148 TGGATCTTAAAGAAACATTTAGAG-----GAGGTTCTTTAGAGCGGGCTCAAGCA 1201
Qy 1263 TGGCTAAAGAGACATACAGTGTGCTAGTGAATCAAAACATACAAAGAGAG 1322
Db 1202 TGGAAAGAGACAAATTTGGCCCACTTTTGAAGAAAAAGATTTCTTCAAGAAATGACA 1261
Qy 1323 AAGATGATATAGCACTTGACAAATATTTGTTGTTG---CTTCAATCCCAAGAAATCTCAAC 1379
Db 1262 ATGAGAAAAATGAAAACTTAAACAGAGTGTGAGTCTGCTTCTTCTTCTTCTTCTTCTTCAAC 1321
Qy 1380 AGGACCAAGGCTCAAGAAAGAGAGAGTACGCTGGCGCCAGAGAAATCAAAATA 1439
Db 1322 AGGATTTAAGGCTTAAAGAAAGAGAGAGTACGCTGGCGCCAGAGAAATCAAAATA 1381
Qy 1440 GTTATACATGCTTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1499

Db 1382 TGAGAA-----CTCAACTATGACAGATCAATTTAATATCAACAAATATA 1429
Qy 1500 GCAAGAAAGCAAGTCTCTGACATGCTTCAATTTCCAGAAATGATGACTGTTTGA 1559
Db 1430 CAACAAAAACATACAGTCTTCTAATAATTTATATGAGAAATGATGATCTGCTGTT 1489
Qy 1560 CAGAGTTTCTGATTTTGTATGACGCCCT 1587
Db 1490 CAGAGTCTGATGTTTCTTCAATACATCT 1517

RESULT 4
US-09-893-519A-140
; Sequence 140, Application US/09893519A
; Publication No. US20030027243A1
; GENERAL INFORMATION:
; APPLICANT: ANADYS PHARMACEUTICALS, INC.
; APPLICANT: THOMPSON, Craig
; APPLICANT: MOORE, Jeffrey
; APPLICANT: BURMAN, Ed T.
; APPLICANT: BRADLEY, John
; APPLICANT: DESTIVA, Thamara
; APPLICANT: HARRIS, Sandra
; APPLICANT: KOMARNITSKY, Svetlana
; APPLICANT: MENDILLO, Marc
; APPLICANT: MOORE, Daniel
; APPLICANT: MCCOY, Melissa
; APPLICANT: SANDERSON, Karen
; APPLICANT: HAO, Taiq
; APPLICANT: ZHU, Shuhao
; APPLICANT: LONG, Fan
; APPLICANT: DAVIDOV, Eugene
; TITLE OF INVENTION: ANTIFUNGAL COMPOUNDS AND METHODS OF USE
; FILE REFERENCE: 0342/1G548-US2
; CURRENT APPLICATION NUMBER: US/09/893,519A
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 60/215,164
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/224,457
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 140
; LENGTH: 7992
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER:
; DATABASE ENTRY DATE: 1993-01-10
; RELEVANT RESIDUES: (1)..(7992)
US-09-893-519A-140

Query Match 6.4%; Score 615.2; DB 11; Length 7992;
Best Local Similarity 66.7%; Pred. No. 3.9e-130;
Matches 970; Conservative 0; Mismatches 448; Indels 36; Gaps 5;
Qy 143 ATGTCGAGGGAGATGCAATTAAGTGTGTGAGGGTTGCGCGCTTATACAGAGAA 202
Db 1 ATGCGGAGAGAGAGCGCGTGGCCGTGCGTGGAGTGGCGCGCTGAACACAGAGAA 60
Qy 203 CAA-----GGGAGTCAAGCAACCTGCAATGAGAGCTGGAACAACAACATTTCCAA 256
Db 61 GAATCACTTGGAGAACTGCCCAAGTTTACTGAAAACTGACAAATATGTCAATTTATCAA 120
Qy 257 GTGATGGGCAAAAGTCTTTCAATTTGATGCTGTATTTAATTTCTACAGAAATCAACAGT 316
Db 121 GTTATGAGATTAATCTTCAATTTTGAATCGTCTTTCAATGTAATGAATCACTAACAA 180
Qy 317 CAAATTTACCAAGAAATAGCAGTACCTATCATACATGCTTTGAGAGATATATGCGC 376
Db 181 AATGTGATGAAGAAATAGCAGCAACCAATCATGATTCGCCATCAAGGCTACAAATGT 240
Qy 377 ACAATATTTGCAATGCGAGACATCTTCAGGCAAGAGTACACAAATGATGAGAAACACCA 436

Db 241 ACTATATTTGCTTATGACAGACTGCTTCAGAAAAACATATACATGATGGGTTGACA 300
 Qy 437 AATTCATGGGCAATTAATACCCAGCAATACAGAAATTTTAAATTAATTCAGAGATA 496
 Db 301 GATCATTTGGAGTTATACCCAGGCAATTCATGACATTTTCCAAAAAATTAAGAGATT 360
 Qy 497 CCGAAGAGAGCTTTCTTCAAGATTTCTTATATGAGATTTTACATGAACTGTGAAA 556
 Db 361 CCGATAGGAAATTTCTTCAAGATTTCTTATATGAGATTTTACATGAACTGTGAAA 420
 Qy 557 GACCTACTGTGATGACAGAAAGAAAGCCCTTGAAATTTGCGAGATTTTAAATAGA 616
 Db 421 GATTTACTGTGACACTCAAAAAATGAAACCTTTATTTTGAAGAGATGTCATAGG 480
 Qy 617 AACGTGTATGTTGCTGACCTGACTGATGAAATCTTGAATGTTCTGAACATGTAATACAG 676
 Db 481 AATGTGTATGTTGCTGATCTCAGAGAAAGTTGTAATATACATGAAATGCTTGAAA 540
 Qy 677 TGGATCAAAAAGGTTGAAAAAAGACACATATATGAGAGCTTAAATGATGATCATAGT 736
 Db 541 TGGATTAAGAGGAGAAAAAGACAGGCAATATGAGAAAAAATGAATCAAGAAAGC 600
 Qy 737 AGTCGTTACATCAATATTTAGATGATGTTGAAGCCGAGACAGAAATGATCCACA 796
 Db 601 AGTCGTTCTCATACCATTTTAGATGATTTTGAAGACAGAGAGAGGTTGAACCTTCT 660
 Qy 797 AATTCAGAACTGTGATGAGAGCTGTCATGTAATCTCACTTGAATTTGTTGATCTTGT 856
 Db 661 AAT-----TGTGAAGATCTGTTAAGTATCCCATTTGAATTTGGTTGATCTTGCA 711
 Qy 857 GGCAGTGAAGAGCAAGCCAACTGAGCTGAAGGTTGAGATTTAAGAAAGCTGCAAC 916
 Db 712 GGCAGTGAAGAGCTGCTCAAGAGGCTGAGGCTGAGGCTCAAGAAAGCTGTATAT 771
 Qy 917 ATCAACCGAGCTGTTGTTATCCCTTGACAGGTTATTAAGAAAGCTTGCGACGCGAGCT 976
 Db 772 ATTAATCGAAGCTTATTTATTTTGGACAGATGATCAAGAACTTATGATGACAAAGTT 831
 Qy 977 GGTGATTTATTAATACAGAGACAGCAAACTGACAGAAATTTCCAAATTTGATGGGA 1036
 Db 832 GGTGATTTATTAATATGAGATGACAAAGTTAACAAGATTTCTGCAATTTCTTGGA 891
 Qy 1037 GGAATATGCTAAAAAGGTTATATTTGACAAATTAACCGAGTTCTTTTGAAGACTCTTA 1096
 Db 892 GGAATATGCTAAAAAGGTTATATCTGACAAATTAACCGAGTTCTTTTGAAGACTCTT 951
 Qy 1097 AGTACACTTCAGTTGCCAGTACTGCAAAATGATGAGAAATCTCCCACTGTTAATGAG 1156
 Db 952 ACTGCTCTCAAGTTGCGAGTACTGCTAAATATATGAGAAATCTCTTATGTTAATGAG 1011
 Qy 1157 GTCTGATGATGAGAGCTGTTGCTTAAAGAGTACAGAAAGAAATCTTGATTTAAAGAA 1216
 Db 1012 GATATCAACGATGAGAGCTCTCGTGAAGAGTATAGAAAGAAATTAATGATCTTAAAGAA 1071
 Qy 1217 CAATTTGAGAAATTTAGAGTATGCTGAAACAAAGCTCAAGCAATGCTTAAAGAGAG 1276
 Db 1072 CAATTTAGAG-----GAGGTTCTTTAGAGACCGGAGCTCAGGCAATGGAAGAACAA 1125
 Qy 1277 CATPACAGATTTGCTACTAGAAATCAAAACAATPACAGAAAGAGAGATGATTAATGAG 1336
 Db 1126 TTGGCCCAACTTTTGAAGAAAGATTTGCTTCAAGAAATGACAGATGAGAAATTTGAA 1185
 Qy 1337 CACTTGACAAATATTTGTTGT---TGCTTCATCCCAAGAAATCTCAAGAGCAAGAGGCT 1393
 Db 1186 AACTTAAACGAGATGCTGAGACCTCTTCTTCCCTCAAGTGAACAGAGATTTAAAGGCT 1245
 Qy 1394 AAAAGAAAAGAGATTAAGTGGGCGCAGAGAAATTCAGAAATGCTTACATGCTTCT 1453
 Db 1246 AAAAGAAAAGAGATTAAGTGGGCGCAGAGAAATTCAGAAATGCTTACATGCTTCT 1305
 Qy 1454 GGTGTTTCTGACTTTATATGCTATCAGATTAACCTGGCAATTTTGAAGAGAGCAAG 1513

Db 1306 TATGACATCAATTTAATATACACACA-----AATATAACAAACAAACAT 1353
 Qy 1514 TTCTGACATGCTTCAATTTCCAGAAATTTGATGACTGTTTGTACAGAGTTTCTGAT 1573
 Db 1354 AACCTTTCAATTAATTTAATTAACAGAAATTTGAGAAATGATGAAATGCTGTTGATGAT 1413
 Qy 1574 TTGATGAGGCTT 1587
 Db 1414 TTCAGTAACTCT 1427

RESULT 5
 US-09-833-790-351
 ; Sequence 351, Application US/09833790
 ; Patent No. US2002068288A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Wang, Tonglong
 ; APPLICANT: Secretist, Heather
 ; APPLICANT: Mohamath, Radooh
 ; APPLICANT: Indriah, Carol Y.
 ; APPLICANT: Fan, Liqun
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121.512
 ; CURRENT APPLICATION NUMBER: US/09/833,790
 ; NUMBER OF SEQ ID NOS: 440
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 351
 ; LENGTH: 581
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-833-790-351

Query Match 2.1%; Score 206.6; DB 9; Length 581;
 Best Local Similarity 68.4%; Pred. No. 5.8e-37;
 Matches 333; Conservative 0; Mismatches 144; Indels 10; Gaps 3;

Qy 955 GAAGCTTACGACGCGCAGCTGTTGATTTATTAATTAATCAAGAGACAGAACTCACAG 1014
 Db 72 GAAACTTATGATGACCAAGTTGTTGTTCAATTAATGAGATGACAAAGTTAACAG 131
 Qy 1015 AATTCCTCAAAATTTCTTTGGAGAAATGCTTAAACGGTTATATTTGCACAAATTACGC 1074
 Db 132 AATTCCTCAAAATTTCTTTGGAGAAATGCTTAAACGGTTATATCTGCAAAATTACTCC 191
 Qy 1075 AGTTCTTTGATGAGACTCTTAAGTACCTTCAGTTGTCAGTACGCAAAACATGAGAG 1134
 Db 192 AGTATCTTTGATGAGAAACCTTAAGTCTTCAGTTGTCAGTACGCTTAATATATGAA 251
 Qy 1135 AATATCTCCCATGTTAATGAGTCTCGATGATGAGAGGCTGCTTAAAGAGTACAGAA 1194
 Db 252 GATATCTCTTATGTTAATGAGATTAATGAGTATCAACTGATGAGAGCTCTCCGAAAGGATAGAA 311
 Qy 1195 GGAATCTTTGATTTAAGAAACATTAAGAAATTTAGATCATGCTCTGAAACAAAGC 1254
 Db 312 AGAAATTAATGATCTTTAAAGAAACAAATTAAG-----GAGGTTCTTTAGAGACGCGGAG 365
 Qy 1255 TCAGCAATGAGCTTAAAGAGAGATPACAGATTTGCTAGCTGTAATCAAACTACACAA 1314
 Db 366 TCAGCAATGAGAAAGAAACCAATTTGCCCACTT-TTGAAGAAAGAAATTTGCTTACAGAA 424
 Qy 1315 AGAGAGAGAGATGAGATATGACACTTGAACAATATGTTGT---TGCTTCATCCCAAGA 1371
 Db 425 AGTACGATGAGAAATTTGAAACCTTAACAGAGATGCTGAGACTCTTCTTCCCTCAG 484
 Qy 1372 ATCTCAACGAGCAAGAGGCTCAAGAGAAACGAGAGATTTAGTGGGCGCAGAGAAAT 1431
 Db 485 GTTGACACGAGATTAAGGCTTAAAGAAAGAAAGAGATTTAGTGGGCGCAGAGAAAT 544
 Qy 1432 CCAAAAT 1438

D6 545 ACCCAAT 551

```

RESULT 6
US-10-175-523-155
/ Sequence 155, Application US/10175523
/ Publication No. US20030096264A1
GENERAL INFORMATION:
/ APPLICANT: Brockman, Jeffrey
/ APPLICANT: Evans, David
/ APPLICANT: Hook, Derek
/ APPLICANT: Klimczak, Leszek
/ APPLICANT: Laeng, Pascal
/ APPLICANT: Palfreyman, Michael
/ APPLICANT: Rajan, Priti
/ TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
/ FILE REFERENCE: 3235/11795-US3
/ CURRENT APPLICATION NUMBER: US/10/175,523
/ PRIOR FILING DATE: 2002-06-18
/ PRIOR APPLICATION NUMBER: US 60/299,151
/ PRIOR FILING DATE: 2001-06-18
/ PRIOR APPLICATION NUMBER: US 60/317,828
/ PRIOR FILING DATE: 2001-09-07
/ PRIOR APPLICATION NUMBER: US 60/325,150
/ PRIOR FILING DATE: 2001-09-25
/ PRIOR APPLICATION NUMBER: US 60/333,047
/ PRIOR FILING DATE: 2001-11-14
/ PRIOR APPLICATION NUMBER: US 60/349,936
/ PRIOR FILING DATE: 2002-01-18
/ PRIOR APPLICATION NUMBER: US 60/361,834
/ PRIOR FILING DATE: 2002-03-04
/ NUMBER OF SEQ ID NOS: 197
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 155
/ LENGTH: 2109
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-175-523-155

```

Query Match	1.5%	Score 147.8;	DB 14;	Length 2109;
Best Local Similarity	51.8%;	Pred. No. 4.2e-23;		
Matches 530; Conservative	0;	Mismatches 452;	Indels 41;	Gaps 7

OY	224	CTGGAACAACACCATTTCCCAAGTTATGAGCAAAAGTCTTCAATTTGCATCGTGAT	293
Db	140	CTGTCATATAAGCTGATTTCTTCCAAATGAACCTCCAAAAGACATTTACTTTGATACGT	199
OY	294	TTAATTTCAAGATCAACAAGTCAAAATTTACCAAGAAATPACAGTACTATCATACAT	353
Db	200	TTGAGCCAGAGAGTAACCACTTGATGTTTTATATCTGAACCTGAACCTATATATGAT	255
OY	354	CAGCTTTCAGGGATATTAATGAGCAAAATTTGCATACGACAGACATCTTCAGGACAGA	413
Db	260	CTGACTTGAAGGCTCAATGAGGACTATTTTTCATATGAGCAAAACCGAACAGGCAAAA	319
OY	414	CGTACACAATGATGGG-----AACCAACAATTCATTGGGCATTAATACCCCAAGCA	464
Db	320	CTTTTACATGAGAAAGGTTTGCAGCAATTCCTGAACCTTAGAGAAATTAATTCCCAATTCAT	379
OY	465	TA---CAGGAGTTTTTAAATAATTCACAGAGATACCGAACAGAAAGTTTCTTTAAGAG	521
Db	380	TTGCTCACAATATTGGTCATATTGGCAAAACCGGAGGTGATACAAAGTTTTTGGTTGAG	439
OY	522	TTTCTTATATGAGATTTACAATGAAACTGTGAAGACCTACTGTGTATGACACAGAAGA	581
Db	440	TGCTTATTTGGAAATATATTAATGAAGAAGTTTCGTGACCTTTTGGGCAAGATATGACAC	499
OY	582	AGAGACCCCTTGGAATTTCCGAGAGATTTTAATAGAAACGTGATGTGTCGACCTGACTG	641
Db	500	AAAGG---TTAGCGGTTAAAGAAAGACCTGATGTGGAGTTTATATCAAAAGATTTATCAG	556
OY	642	AAGACCTTGAATGCTTCTGGAACATGTAAATCACTGAGATCAAAAAGGCTGAAAAAACA	701

Db	557	CTTATGCGTAATTAATGCGTGAATATGATATGATTAATATGAGCTTAGGCCAATAAATC	616
Qy	702	GACATTATGAGAGACTTAAATAATGAATCATATGATGCTGTTACATATATTTAGAA	761
Db	617	GTTCTTTGGTGGACATTAATGAAAGAAACATAGTTCGCCGTTCCATGCGCATCTTACAA	676
Qy	762	TGATTGTTGAAAGCCAGACAGAAATGATATCCCAATTCAGAGACTGATGAGAGCTG	821
Db	677	TTACTATAGAAATSCAATGA-----AAAGCATTTGATGGTATCATGCATG	721
Qy	822	TCAATGATCTCACTTGAAATTTGATGATCTTGTGCGAGTGAAGAAGCAAGCCAACTG	881
Db	722	TGAGATGCGGAAGCTCCACTCTTGATGATCTGTGTTCAAGAAAGACAGGCAAAACTG	781
Qy	882	GAGCTGAAGGTGAGACTTAAAGGAAGGCTGCACATCAACCGCACTGTTATCTCTTG	941
Db	782	GAGCTACTGSAACAGCCCTTAAGGAAGCTACAAAATCATCTTTCACTTTCACCCCTTG	841
Qy	942	GACAGGTTATTTAAGAGCTTACCGACGCGCAGCTGTGATTTTAACTACAGAGACA	100
Db	842	GTAATGTAATTTCTGCTGTTGTTATGGAAGAAAGACATCA---TGTGCTTATGTA	898
Qy	1002	GGAATCTACCAAGATTTCTCCAAAATTCATTGGGAGGAATGCTAAACGTTATPATTT	106
Db	898	CTAAACTGCTGCTCTTCTTCAAGATTCCTTAAGGAGAAATTCAAAAACATGATGTGTG	958
Qy	1062	GCACATTTACGCGCAG-----TTTCTTTGATGAGACTCTAGTACCTTCACTTGTGCA	111
Db	958	CAATATTTGGGCGACAGCATTAACATTTATGATGAAACTATCAGTACATTCAGTATGCCA	1018
Qy	1116	GTACTGCCAAACATGTGGAATACTCCCACTGTTAATGAGTCTCTGATGATGAAGCGT	1175
Db	1019	ATCGCTCAAAATTAATTAATAAAGCTAGAAATTAAGAAGATCCAAAGCATGCTTTGC	1078
Qy	1176	TGCTAAAGGTACAGAAAGAAATCTTGATTTAAGAAACATTTAGAAATTTAGCT	1235
Db	1079	TGC--GTAGTTCAGAAAGAAATAGAAAGAACTGAAAAAGAGCTTGAAGAGGTGAAGA	1138
Qy	1236	CAT 1238	
Db	1137	AAT 1139	

; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 3503, 3504, 3505
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-814-353-21787

Query Match 1.5%; Score 146.6; DB 12; Length 3505;
 Best Local Similarity 51.1%; Pred. No. 1.1e-22;
 Matches 523; Conservative 0; Mismatches 459; Indels 41; Gaps 6;

QY 234 CTGGAACAACACACATTCCCAAGTTGATGAGCAAAAGCTTTTCATTTTGCATGCTGAT 293
 DB 303 CTGTACATAGACTGATTTCTTCCATGACCTCCAAAGAAATTTACTTTGATACGTGTT 362
 QY 294 TTAATTCACGATCAACAGTCAAAATTTACCAAGAAATAGCAGTACTATCATAGAT 353
 DB 363 TTGACACAGAGATTAACAATTGATGTTATATTAATTAACTTAACTGCAAGACTATTGATT 422
 QY 354 CAGCTTGCAGGATATATGACCAATATTGCTATCGACACACATCTTCAGCGAAGA 413
 DB 423 CTGTACTTGAAGCTCAATGAGGACTATTTTGCATATGACCAACCGAAGCGCAAAA 482
 QY 414 CGTACCAATGATGGGAACCAAAATTCATGGGCATATATCCCAAGCCATACAGGAG 473
 DB 483 CTTTTCATGGAAGGTGTTGAGCTATCTCTGACTTAAGGAATTAATCCCAATTCAT 542
 QY 474 TTTTAAATTTATTCAGAGATACCGAACAGAG-----TTTCTTCAAG 521
 DB 543 TTGCTCAATATTTGGCATATTTGCAAAAGCGAGGTGATACAAAGTTTTTGGTTGAG 602
 QY 522 TTTCTTATATGAGATTTACATGAACTGTGAAGACCTACTGTGTGATGACAGAA 581
 DB 603 TGTCTTATTTGGAATATATATATGAAAGAGTCTGTGACCTTTTGGGCAAGATCAGAC 662
 QY 582 AGAAGCCCTTGGAAATTCGGAGGATTTTATAGAAACGTATNGTGTGACTGACTG 641
 DB 663 AAAAG--TTAGCGTTAAAGAAAGACCTGATGTGGAGTTTATATCAAAATTTATCAG 719
 QY 642 AAGAACTTGTATGTTCTCTGAAATGTATATAGATGATCAAAAAGGTGAAAAAACA 701
 DB 720 CTATATGTGTAATATATGCTGATGATATGATATGAAATATAGAGCTAGGCAAAAATC 779
 QY 702 GACATTATGAGAGACTAAATGATGATCATAGTACTGTTCACTACATATTTTGA 761
 DB 780 GTTCTGTGTGCAACTAATATATGAAACCATAGTTCCTCCATGCCATCTTTTACA 839
 QY 762 TGAATTTGAAACCGAGACAGAAATGATCCCAAAATTGAGAACTGTGATGAGCTG 821
 DB 840 TTAATTAAGATGACAGTGA-----AAAAAGCATTTGATGTAACATGCATG 884
 QY 822 TCATGTATCTCACTTGAATTTTGTAGATCTTCTGCGACGTAAAGAGCAAGCAAACTG 881
 DB 885 TCGAGATGGGAGAGCTCCATCTTGTATGATCTTGTGCTTCAAGAAAGACAGCAAAAATG 944
 QY 882 GAGCTAAGGTGTGAGACTTAAGAAAGCTGCAACATCAACCGACGTTGTATCTG 941
 DB 945 GAGCTACTGAGACGCGCTTAAGAAAGCTCAAAAATCAATCTTTCACCTTCCACCCTG 1004
 QY 942 GACAGTTATTAAGAAAGCTTACGAGCGGCGACGCTGTGATTTTAACTACAGAGCA 1001
 DB 1005 GTATATTAATTTTGTGCTTGTGATGAAAAAGCACTCA--TGTCCTTATCTGTAAT 1061
 QY 1002 GCAAACTACACAGAAATCTCCAAATTCATTTGGAGAGAAATGCAAAAAGGTATATTT 1061
 DB 1062 CTAACTGACTGCTCTTCTTCAAGATTCCTTAAAGAAATTTCAAAAACATGATGTGTG 1121
 QY 1062 GCACAAATTAAGCAG-----TTTCTTTGATGAGACTTAAGTACATTTCAAGTTTCCA 1115
 DB 1122 CAATATTTGGGCGACGAGATTAATCAATATGATAAATCATACATCTACATTCGGTATGCCA 1181
 QY 1116 GTACTGCCAAACATGTAGAAAAATATCCCATGTTAATGAGTCTCGAGATGAAAGCT 1175

DB 1182 ATCGTGTAGATATTTAAATAAAGCTAGAAATTAATGAAGATCCAAAGAGCTTTGC 1241
 QY 1176 TGCTAAAAAGTACAGAAAGAAATCTTGATTTAAAGAAACAATTAGAGATTTAGACT 1235
 DB 1242 TGC--GTCACTTCAGAAAGAAATAGAAAGACTGAAAAAGAGCTTGAAAGGTGAAGA 1299
 QY 1236 CAT 1238
 DB 1300 AAT 1302

RESULT 8

US-09-833-790-167
 ; Sequence 167, Application US/09833790
 ; Patent No. US200206828BA1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Wang, Tonglong
 ; APPLICANT: Secret, Heather
 ; APPLICANT: Mohamath, Raedoh
 ; APPLICANT: Inditias, Carol Y.
 ; APPLICANT: Fan, Liqun
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121.512
 ; CURRENT APPLICATION NUMBER: US/09/833.790
 ; CURRENT FILING DATE: 2001-04-11
 ; NUMBER OF SEQ ID NOS: 440
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 167
 ; LENGTH: 501
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-833-790-167

Query Match 1.4%; Score 138.2; DB 9; Length 501;
 Best Local Similarity 57.7%; Pred. No. 2.7e-21;
 Matches 266; Conservative 0; Mismatches 193; Indels 2; Gaps 1;

QY 2844 AAATGAAAGCTGATTTGCAAGAAAGAGTGCAGAAAGCTTTTAAATGAGATTAAGTAA 2903
 DB 1 AAATGCAAGTGTATCGGAAAGAAATTAACAATCTGTTTAAATGAGATTAACAAGTCA 60
 QY 2904 ATGCGCTTCTGCGAGGAAAGGTCCCAAGATTTGCTTCTGCTGTGAATTGAGAAAA 2963
 DB 61 CTCCTCTTATATGATGCAAAAGTTCAAAAGATTTGCTGTGTAATTTGGAATTTGGAAGCA 120
 QY 2964 AGGTTCTGAGCTCTCAAGACAGCTTGAGAAAGCA--TTGGAAGAAAAAATGCGTTGA 3021
 DB 121 AGATTAATGATCTTCAAGAAAGAACTAAATTAAGAAAGTTGAAAGAAATGAACTTTGCC 180
 QY 3022 GAATGAAGTACTTGGCTTACAGAAATACAAATTTTGGCCAAATGAAGTGAATGCTTTGA 3081
 DB 181 GGAAGAAATGATTTTGTGCTTCAAGATTTGAATCTTTTACCTTCTGAAAGTAAAGCGCTGAG 240
 QY 3082 AAATCAATCAGACGAAGGCTTCTGAAGATATATGTTATTAAGCAAGAAAGAGAACATTC 3141
 DB 241 GAAAGAGATCAAGAACAAATCTGAAAGGCTCATATATATCACTGAAAAAAGATTAATT 300
 QY 3142 TGATCTATATTAAGCAACAGAGATTAATGACAGAGCAATCTGAGCAATTTTACA 3201
 DB 301 GTTTTCTGAAGTATGTTCAATAGAGAGTGAAGTCAAGGTTTACTTGAAGAAATTTGGGA 360
 QY 3202 ACTGATGACGAGTACACACACAGTCAAAAGTGCAGACAGTGAAGAGCAATCTT 3261
 DB 361 AAGAAAGATGACTGACGAACTACACAGTGAATTTAAAGCACTGATGAAGATTTCCA 420
 QY 3262 GAGATGAAGAAAAATGATGATGATCTTTTGAAGATTA 3302
 DB 421 AAATTTCAAAACCTTCATATGAGACTTTGAGCAAAAGTATA 461

RESULT 9
US-10-116-712-668
; Sequence 668, Application US/10116712
; Publication No. US20030194764A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Bangur, Chaitanya S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.568
; CURRENT APPLICATION NUMBER: US/10/116,712
; NUMBER OF SEQ ID NOS: 670
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 668
; LENGTH: 3753
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-116-712-668

Query Match 1.4%; Score 135.2; DB 12; Length 3753;
Best Local Similarity 50.6%; Pred. No. 4.7e-20;
Matches 468; Conservative 0; Mismatches 408; Indels 48; Gaps 4;

```
QY 257 GTTGATGGACAAAGTCTTTCAATTGCGATGATTTAAATTCACGAATCAACAAGT 316
DB 154 GTTGATGGACAAAGTCTTTCAATTGCGATGATTTAAATTCACGAATCAACAAGT 213
QY 317 CAATTTACCAAGAAATGACAGTACCTATCATAGATGAGTTGCGAGGATTAATGCG 376
DB 214 GAGTCTTCAATACAGCAGTACGCGCTACTATTAAGGTGATTTAAAGATTAATGCA 273
QY 377 ACAATATTGCAATACGACAGACATCTTCAGCAGCAAGCTACACATGATGGAAACCA 436
DB 274 ACGGTCTCGGCTATGGGACAGCTGCTCTGAAAAAACCATTCAAGGAGGCTATAT 333
QY 437 AATTCATTG-----GGCATATACCCCAAGCCATACAGAAAGT 475
DB 334 ACTGACAGCAAGAAATGAACCAACAGTTGGGTTATCTTGGGTAATACAACTGCTC 393
QY 476 TTTAAATTTATTCAGAGATACCGACAGAGATTTCTTCAAGATTTCTTATGAG 535
DB 394 TTTCAAGAAATGATTAAGAGAGTCTTGAATTTACTGAAAGTGTCTTATCTTATGAG 453
QY 536 ATTACATGAATACTGAAAGACCTACTGCTGATGACAGAAAGAAAGCCCTTGAA 595
DB 454 ATTACATGAATACTGAAAGACCTACTGCTGATGACAGAAAGAAAGCCCTTGAA 513
QY 596 ATTGCGAGGATTTTAATGAAGAGTATGCTGACCTGACCTGAACCTTGTATG 655
DB 514 ATACGAGAGATCTTAAGAGAGCATTAAGATTTGAGACTCACTGAGAAAGCTGTTTG 573
QY 656 GTTCTGGAACATTAATACAGTGGATCAAAAAGGTGAAGAAAGAAAGCAATATGAGAG 715
DB 574 GTTGCCTGGATATCTGTTCTGTTTGGAAAGGGCAACACTAGAGCTGTGCTCC 633
QY 716 ACTAATATGAATGATGATGATGCTGCTTCAATACATATTTGAATGATGTTGAAAGC 775
DB 634 ACGGCTATGAATCTCCAGTGTGCTGATCTGATGCTATCTTACAT--CTCCTTAGAGC 691
QY 776 CGAGACAGAAATGATCCCAAAATTCAGAAAGCTGATGAGCTGATGATGATGATGATG 835
DB 692 AAAGAAAGAAAGTGAAGAAATGAGAG-----CTTTCGCTCCAG 732
QY 836 TTGAATTTGGTATGATCTTCTGCTGAGTGAAGAGCAAGCAACGAGCTGAAGTGTG 895
DB 733 CTGCTATCTTGTAGACCTGCTGATCAGAAAGCAAGAAAGAAAGCAAGCTGAAGGAGAT 792
QY 896 AGACTTAAAGAGCTGCAACATCAACGAGCTGTTATCTTCTTGAAGCTTATTAAG 955
DB 793 CGTAAAAAGAGGATTAATTAATTAACGAGAGCTCTTATGCTTGGGAAATGATACAGT 852
QY 956 AAGCTTAGCAGCGGCAAGGCTGTGATTTTAACTACAGAGACAGCAAACTCAGCAGA 1015
```

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DB 853 GCTCTTGAGATGACAAAGAGGCTGTTGCTCCCTACAGAGATTCAGATGACTCGA 912
QY 1016 ATTTCACAAATTCATTTGGAGAAATGCTTAAACGGTTATATTTGACAAATTAAGCA 1075
DB 913 CTGCTTAAAGATTTCTAGAGAGTAAATAGCAATCTATATGATAGCTGTGTGAGTCT 972
QY 1076 GTT-----TCTTTGATGAGACTTAAGTACCTTCACTTTGCCAGTACTGCCAAACAT 1129
DB 973 GCTGATCCCATATTAAGAGAAACATTAATACCTTCTGCTATGCTGACAGCAAGAAAA 1032
QY 1130 GTGAGAAATCTCCCATGTTAT 1153
DB 1033 ATCAAGAAACAACTATGTTAT 1056
```

RESULT 10
US-10-116-712-661

; Sequence 661, Application US/10116712
; Publication No. US20030194764A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Bangur, Chaitanya S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.568
; CURRENT APPLICATION NUMBER: US/10/116,712
; NUMBER OF SEQ ID NOS: 670
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 661
; LENGTH: 4348
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-116-712-661

Query Match 1.4%; Score 133.6; DB 12; Length 4348;
Best Local Similarity 50.5%; Pred. No. 1.2e-19;
Matches 467; Conservative 0; Mismatches 409; Indels 48; Gaps 4;

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QY 257 GTTGATGGACAAAGTCTTTCAATTGCGATGATTTAAATTCACGAATCAACAAGT 316
DB 187 GTTGATGGACAAAGTCTTTCAATTGCGATGATTTAAATTCACGAATCAACAAGT 246
QY 317 CAATTTACCAAGAAATGACAGTACCTATCATAGATGAGTTGCGAGGATTAATGCG 376
DB 247 GAACTCTTCAATACAGCAGTACGCGCATTAAGGTGATTTAAAGATTAATGCA 306
QY 377 ACAATATTGCAATACGACAGACATCTTCAGGCAAGCAACGATGATGAGAAACCA 436
DB 307 ACGGTCTCGGCTATGGGACAGCTGCTCTGAAAAAACCATTCAATGAGAGTGCATAT 366
QY 437 AATTCATTG-----GGCATATACCCCAAGCCATACAGAAAGT 475
DB 367 ACTGACAGCAAGAGATGAACCAACAGTTGGGTTATCTTGAAGTATTAACATGCTC 426
QY 476 TTTAAATTTATTCAGAGATACCGAACAGAGTTCTTCAAGAGTTCTTATGAG 535
DB 427 TTTCAAGAAATGATTAAGAGAGTGAATTTACTGTAAGAGTGTCTTATGAG 486
QY 536 ATTACATGAATACTGTAAGAGCTGATGATGACAGAAAGAAAGCCCTTGAA 595
DB 487 ATTACATGAATACTGTAAGAGCTGATGATGACAGAAAGCCCTTGAA 546
QY 596 ATTGCGAGGATTTTAATGAAGAGTATGCTGACCTGACCTGAAGAACTTGTATG 655
DB 547 ATACGAGAGATCTTAAGAGAGCATTAAGATTTGAGAGCTCACTGAGAAAGCTGTTTG 606
QY 656 GTTCTGGAACATTAATACAGTGGATCAAAAAGGTGAAGAAAGAAAGCAATATGAGAG 715
DB 607 GTTGCCTGGATATCTGTTCTGTTTGAAGAGGCAACACTTGAAGCTGTGAGCTCC 666
QY 716 ACTAATATGAATGATGATGATGCTGCTTCAATACATATTTGAATGATGTTGAAAGC 775
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Db      667  AGCGCTATGAACTCCAGTGTGCCGATCTCATGCCATCTTTAACAAT--CTCCTTAGAGC 724
Qy      776  CGAGACAGAAATATATCCCAAAATTGAGAGAACTGTGATGAGCTGTGATATCTCAC 835
Db      725  AAGGAAAGAAAGTGAACAAGAAATAGCAG-----CTTTGCTCCAG 765
Qy      836  TTGAATTTGCTAGATCTGTGCAAGTGAAGCAAGCAAGCAAGCTGAGAGTGAAGTGTG 895
Db      766  CTGCATCTTGTAGACCTCGCTGATCAGAAAGACAGAAAGCAAGGCTGAAGGGGAT 825
Qy      896  AGACTTAAGGAAGCTGCAACATCAACCGAGCTTGTATCTTGGACAGTTAATTAAG 955
Db      826  CGCTTAAGAGAGGATTAATTAATTAACCGAGGCTCTATGCTTGGAAATGTAATCAGT 885
Qy      956  AAGCTTAGCGACGGCCAGGCTGTGATTAATACTACAGAGACAGCAAACTCACCAGA 1015
Db      886  GCTCTTGAGATGACAAAAAGGGTGGCTTGCGCCCTACAGAGATTCCAAGTTGACTCGA 945
Qy      1016  ATTCTCCAAATTCATTGGAGGAATGCTAAACGGTTAATTTGGCAATTAAGGCCA 1075
Db      946  CTGCTTCAAGATTCTCTAGAGGTAATAGCCATCTTATGATAGCTGTGTAGTCTT 1005
Qy      1076  GTT-----TCTTTGATGAGACTTAAGTACACTTCAGTTTGCAGTACTGCCAAACAT 1129
Db      1006  GCTGACTCCAAATCTAGAGAAACATTAATTAATCCCTTCGCTATCTGACAGAGCAAGAAA 1065
Qy      1130  GTGAGAAATACCTCCCATGTTAAT 1153
Db      1066  ATCAAGAACAAACCTATTGTTAAT 1089

RESULT 11
US-10-116-712-667
; Sequence 667, Application US/10116712
; Publication No. US20030194764A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Switzer, Ann
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.568
; CURRENT APPLICATION NUMBER: US/10/116.712
; NUMBER OF SEQ ID NOS: 670
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 667
; LENGTH: 4348
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-116-712-667

Query Match      1.4%; Score 133.6; DB 12; Length 4348;
Best Local Similarity 50.5%; Pred. No. 1.2e-19;
Matches 467; Conservative 0; Mismatches 409; Indels 48; Gaps 4;

```

```

Db      427  TTCAAAGAAATGATTAATAAGAGTACTTTGATTTACTGTGAAGATGTCTTACTAGAG 486
Qy      536  ATTTACAAATGAACCTGTGAAGACCTACTGTGTGATGACAGAAAGAACCCCTTGAA 595
Db      487  ATTTACAAATGAAGAAATTTTGATCTTCTATGTCATCTCTGAGAAAGCTCAAAATTAAT 546
Qy      596  ATTGCGAGAGATTTTAATGAACGCTATGTTGCTGACCTGACCTGAAGAACTGTATATG 655
Db      547  ATTCGAGAGATCTTGAAGAGGCAATTAAGATTGTGGACTCACTGAGAAAGCTGTTTGG 606
Qy      656  GTTCTGGAACATGTAATTAATACAGTGCATCAAAAAGGTTGAAAAAACAAGACATTATGAGAG 715
Db      607  GTTGCCTTGATATCTGTTTCTGTTTGAAGAGGGAACAACAATCTATGAGACTGTGGCTCC 666
Qy      716  ACTAAATGAATGATCATATGATGCTGTTACATCAATATTTGAATGATTTGTTGAAGC 775
Db      667  ACGGCTATGAATCCCAAGTGTCCGATCTCATGCTCATTTTACAAT--CTCCTTAGAGC 724
Qy      776  CGAGACAGAAATGATCCCAAAATTCAGAGAACTGTGATGAGAGTGTATCTCAC 835
Db      725  AAGGAAAGAAAGTGAACAAGAAATAGCAG-----CTTTGCTCCAG 765
Qy      836  TTGAATTTGCTAGATCTTGTGCAAGTGAAGCAAGCAAGCAAGCTGAGAGTGTG 895
Db      766  CTGCATCTTGTAGACCTCGCTGATCAGAAAGACAGAAAGCAAGGCTGAAGGGGAT 825
Qy      896  AGACTTAAGGAAGCTGCAACATCAACCGAGCTTGTATATCTTGGACAGTTAATTAAG 955
Db      826  CGCTTAAGAGAGGTAATTAATTAATTAACGAGGCTCTATGCTTGGGAATGTAATCAGT 885
Qy      956  AAGCTTAGCGACGGCCAGGCTGTGATTAATACTACAGACAGCAAACTCACCAGA 1015
Db      886  GCTCTTGAGATGACAAAAAGGGTGGCTTGCGCCCTACAGAGATTCCAAGTTGACTCGA 945
Qy      1016  ATTCTCCAAATTCATTGGAGGAATGCTAAACGGTTAATTTGCAATTAAGGCCA 1075
Db      946  CTGCTTCAAGATTCTCTAGAGGTAATTAATTAATCCCTTCGCTATGATGAGCTGTGTAGTCTT 1005
Qy      1076  GTT-----TCTTTGATGAGACTTAAGTACACTTCAGTTTGCAGTACTGCCAAACAT 1129
Db      1006  GCTGACTCCAAATCTAGAGAAACATTAATTAATCCCTTCGCTATGCTGACAGAGCAAGAAA 1065
Qy      1130  GTGAGAAATACCTCCCATGTTAAT 1153
Db      1066  ATCAAGAACAAACCTATTGTTAAT 1089

RESULT 12
US-10-198-846-13194
; Sequence 13194, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198.846
; PRIOR FILING DATE: 2002-07-18
; NUMBER OF SEQ ID NOS: 60/306, 220
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13194
; LENGTH: 9240
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

```

LOCATION: 1, 9240
OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13194

Query Match 1.3%; Score 124.4; DB 14; Length 9240;
Best Local Similarity 50.3%; Pred. No. 2.5e-17;
Matches 438; Conservative 0; Mismatches 396; Indels 36; Gaps 4;

321 TTACCAAGAAATGACGATCTTATCATAGATGAGCTTTGACAGGATTAATAGGCACA 380
273 TTTTCAAGTGCTTGGAGAGATATCCGAGAAATGCTTTGATGAGCTACAAATGATGTA 332
381 TATTTGCATACGACAGACATCTTCAGCAAGAGCTACAGATGAGGAAACCAAT 440
333 TCTTGGCTATGACAGACAGCTGGCTCTGAAATCTTATACATGATGAGGACAGCTACC 392
441 CATTGGCATTAATCCCAAGCCATACAGAGATTTTAAATTAATTCAGAGATACCGA 500
393 AACCTGATTAATCCCAAGCTTTCAGAGTACTCTTTGAACGAACTCAGAAAGAGGAAA 452
501 ACAGAGG-----TTCTCTAAGAGTTCTTAATAGAGATTTTAAATGAACGCTGA 554
453 ATGAAAGACAGAGTTTAAAGTGAAGTGTCTACATGAAATTTATATGAAAGATTC 512
555 AAGACCTACTGTGTGATGACAGAGAAAGAGCCCTTGAATTCGCGAGATTTTATA 614
513 GAGACCTCTTGTATCCCAAGAGAGCCGTCAGACGTTGAAGTCAGAGACATAGTGT 572
615 GAAACGATATGTTGCTGACCTGACGAAACCTTGAATGTTCTGAAACATGTATAC 674
573 TGGAGCTTAATGTGAGAGGACTTCTAACTGCTGACCAAGCTACAAAGATATTGAGT 632
675 AGTGATCAAAAGAGGAGGAGAAAGAGACATTATGAGAGATTAATGAATGATCATA 734
633 CGTTGATGTGAGGAGTAAACATCTGCACTGTGCTGCAACCAATGAAAGAGAGAG 692
735 GTAGTGTGTACATACATATTTAGATGATTTGTAAGCCGAGACAGAAATGATCCCA 794
693 GTAGCGATCCCATGAGGTTCTCAAAATCACCT-----CACGATACCTCT 740
795 CAATTCAGAGAACTGTGATGAGAGCTGTCACTGTATCTCACTGAAATTTGATGATCT 854
741 ACAGTCAAGAGTGTGAGACATCTGAGAGAAAGTGGCAAACTCAGCTGTGATTTAG 800
855 CTGGCAGTGAAGAGCAAGCAAACTGAGCTGAGAGTGAAGCTTAAAGAGAGCTGCA 914
801 CTGGCAGTGAAGAGCAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 860
915 ACATCAACCGCAGCTGTTTATCTTGGACAGGTTATTAAGAGCTTAAAGAGAGAGAG 974
861 ACATTAACAAGTCCCTCACAACTCGGTCTGTTATCTCAGCTTTGACAGATCAGAGT 920
975 CTGG-----TGATTTATTAACATACAGAGAGCAAACTCAGCAATTCCTCC 1022
921 CTGGCAAAAACAGAAATTAATTTGTTCCATATGTAATCACTTCCATCTTGGCTGCTCA 980
1023 AAAATTCATTGGGAGAGAAATGTCTAAACGGTTTAAATTTGCACAATTAAGCCAGTTCT- 1081
981 AAGACAGCTCGGGGGTAAACAGAGACAGCCCATGCTGCTACTGATGCTTCGACGCTG 1040
1082 -----TTGATGAGACTCTTAAGTACACTTCAGTTTCCAGTACAGTCCCAAACTGTGAGAA 1136
1041 ATATCATATGATGAACCTCTCAACTCTGCGGTATCAGATGAGAGCAAGCATTTGTAA 1100
1137 ATATCTCCCATGTTATGAGAGTCTGTGAGAG 1166
1101 ACCAGCTGTGTGTAATGAGAGACCTTAATG 1130

RESULT 13
US-10-433-013-263
Sequence 263, Application US/10133013
Publication No. US2003016903A1

GENERAL INFORMATION:
APPLICANT: Astromoff, Anna
APPLICANT: Bandman, Olga
APPLICANT: Cocks, Benjamin G.
TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
FILE REFERENCE: PA-0049 US
CURRENT APPLICATION NUMBER: US/10/133,013
PRIORITY APPLICATION NUMBER: 60/287,067
PRIORITY FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 271
SOFTWARE: PERL Program
SEQ ID NO 263
LENGTH: 1726
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. US2003016903A1 441283.4
US-10-133-013-263

Query Match 1.3%; Score 122.8; DB 12; Length 1726;
Best Local Similarity 45.6%; Pred. No. 2e-17;
Matches 685; Conservative 0; Mismatches 787; Indels 30; Gaps 6;

4649 GAAAACTGAGCGAAATGATATTACTGGAAGATTCAGAGAAAGAAAGCTGGAAC 4708
213 GAGCAATTAACCCAGAGATTCAGACCTAATGAGATGAAATGAAATGCTCGGATTTG 272
4709 TCTAACAACTTGAAATCCTTCAGAAAGATGAGAGCGCTCCGTTCTATTAAGATGAC 4768
273 TCCAAAGACTTCAGAAAGATCATGATGAAATGAAATCTGTGCTTAAGAGAAAGATGAC 332
4769 CTGCAACAGAGCTGAAAAGCTTGTGAGTGAACATTAATTCATAAGAGAAATTTGAC 4828
333 CTACAGAGGCTCAAGAGATTTCTCAATCTGAAAGTGAACAGCTCAAGAAACATAAAA 392
4829 ACAACCTTAACATCATTCATCACTCAAGCTCAGCTGACAGAAACAGAGAGAGCTTA 4888
393 GAAATTTGATGCTTAACACCTGGAACCTGAGAGAACTTAAGTTGCTCATTTGTTGCTG 452
4889 CAGTTGGCTAAGATCTTGCATCGCTGCTTGAACAATGTCATTAATCAAGAAAG 4948
453 -----AAGAACAGAGAGAACTATTATAGATTAAGGTGAATCTTTCAGAGAG 503
4949 GAAACCTCTGCAAGTTGTGTGATCTCTGGAAGAAAGATTTGTTATTAACAGAGAA 5008
504 GAACTGAAATATCAACATTCAAAAGAGTGAAGCAATCAATGATTAATTAACAGAAC 563
5009 TTGCATCAAAAACATTAAGACAGAGAAATTAATCAATGAAAGAAATGAATGAAC 5068
564 AAGATCCAGAGATTTATGAGAAAGAGAA-----CAATTAATTAATTAACAAATTTAGTGA 620
5069 GCTCAGTTGAGCTAAAGTGGAGAGTGAACATCTGATGAAGAGATGATGAAATGGAAG 5128
621 GTTCAGGAAAAAGTGA-----TGAATGAACAATTCAGAGAGATTCGCAAGCCAGAGAT 677
5129 TCTCCTACTGAGTCTTTCAGAGATGAGAAATGATATCTGAACAAACATCTTCTGCTTT 5188
678 TCAGACCTAACAAGATTAAGAAAGTAAAGATGCTGCGATTGACCAACAGACTTCAAGAAAGT 737
5189 AAACAGCAGATGCAAGTATTAATCAAGAAAGAAAGAGCTGCAACAAACCATGAACAC 5248
738 CAGAGAAATTAACAAATTTATATTAAGAGAAAGAGAAATGAAAGAGTCAAGAGGCC 797
5249 TTAACAGCTGAGTGAACCATCTAAAGAGATTTGAAATTTGGTTGAAATTTTAAAT 5308
798 CTTCAGATAGAGAGAGCACTGAAGAAACCTAAAGAAATGTGTGCTTAATTAATGAAA 857
5309 GAAAGGAGCAAAAGAGCACTTAAGAGCAATGTCTGCTTAATGAGATTAAGAACTTGA 5368
858 GAATCTCAAGAAAGAAATATCAGTTTCTTAAGATGACAGCTGCTCAATGAGACTCAGAG 917


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/ APPLICANT: Young, Paul
/ TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
/ FILE REFERENCE: 689290-76
/ CURRENT FILING DATE: 2001-09-18
/ PRIOR APPLICATION NUMBER: US/09/954,456
/ PRIOR FILING DATE: 2000-09-18
/ PRIOR APPLICATION NUMBER: US/60/233,617
/ PRIOR FILING DATE: 2000-09-18
/ PRIOR APPLICATION NUMBER: US/60/234,052
/ PRIOR FILING DATE: 2000-09-20
/ PRIOR APPLICATION NUMBER: US/60/234,923
/ PRIOR FILING DATE: 2000-09-25
/ PRIOR APPLICATION NUMBER: US/60/235,134
/ PRIOR FILING DATE: 2000-09-25
/ PRIOR APPLICATION NUMBER: US/60/235,637
/ PRIOR FILING DATE: 2000-09-26
/ PRIOR APPLICATION NUMBER: US/60/235,638
/ PRIOR FILING DATE: 2000-09-26
/ PRIOR APPLICATION NUMBER: US/60/235,711
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: US/60/235,720
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: US/60/235,840
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: US/60/235,863
/ NUMBER OF SEQ ID NOS: 2276
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 733
/ LENGTH: 4858
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-954-456-733
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Query Match      1.0%; Score 95.8; DB 10; Length 4858;
Best Local Similarity 53.5%; Pred. No. 6,2e-11;
Matches 286; Conservative 0; Mismatches 222; Indels 27; Gaps 3;
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Search completed: October 23, 2003, 11:04:31
Job time : 2254 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 22, 2003, 19:44:52 ; Search time 308 Seconds
(without alignments)
4233.265 Million cell updates/sec

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Ygapop 10.0, Ygapext 0.5
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Searched: 569978 seqs, 220691566 residues
Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Issued Patents NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3615.5	24.5	8257	4	US-09-595-684B-30
2	3613.5	24.5	8503	4	US-09-620-312D-130
3	1153	7.8	10136	1	US-08-353-700-2
4	1153	7.8	10136	5	PCR-US95-16216-2
5	1061	7.2	8789	1	US-08-328-254-5
6	1051	7.1	4757	4	US-09-572-191-1
7	1051	7.1	4757	4	US-09-723-262-1
8	1051	7.1	4757	4	US-09-723-219-1
9	941.5	6.4	4348	4	US-09-595-684B-22
10	941	6.4	4127	4	US-09-592-054-7
11	915.5	6.2	4176	4	US-09-722-139-1
12	915.5	6.2	4176	4	US-09-721-832-1

13	915.5	6.2	4176	4	US-09-721-689-1	Sequence 1, Appl
14	909.5	6.2	4308	4	US-09-592-054-1	Sequence 1, Appl
15	867.5	5.9	3572	2	US-08-713-815A-2	Sequence 2, Appl
16	866	5.9	30549	4	US-09-134-001C-322	Sequence 322, App
17	848	5.7	6773	4	US-09-166-350-27	Sequence 27, Appl
18	841.5	5.7	3837	4	US-09-724-517-1	Sequence 1, Appl
19	841.5	5.7	3837	4	US-09-641-807A-1	Sequence 1, Appl
20	841.5	5.7	3837	4	US-09-723-096-1	Sequence 1, Appl
21	828	5.6	580073	4	US-08-545-528D-1	Sequence 1, Appl
22	776	5.3	8948	4	US-09-643-597-119	Sequence 119, App
23	776	5.3	8948	4	US-09-480-884A-119	Sequence 119, App
24	776	5.3	8948	4	US-09-542-615A-119	Sequence 119, App
25	776	5.3	8948	4	US-09-606-421B-119	Sequence 119, App
26	769.5	5.2	11091	4	US-09-134-001C-2243	Sequence 2243, App
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28	759	5.1	3319	1	US-08-282-845-1	Sequence 1, Appl
29	759	5.1	3319	2	US-08-428-414A-4	Sequence 4, Appl
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32	758.5	5.1	3709	4	US-09-723-820-7	Sequence 7, Appl
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35	756.5	5.1	4911	4	US-09-718-852-1	Sequence 1, Appl
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38	754	5.1	13977	4	US-09-484-970B-60	Sequence 60, Appl
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42	744.5	5.0	6306	1	US-08-470-950-3	Sequence 3, Appl
43	744.5	5.0	6306	1	US-08-467-781-3	Sequence 3, Appl
44	744.5	5.0	6306	2	US-08-483-924-3	Sequence 3, Appl
45	742	5.0	19307	3	US-08-836-022A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-595-684B-30
; Sequence 30, Application US/09595684B
; Patent No. 6544766
; GENERAL INFORMATION:
; APPLICANT: Bernad, Christophe
; APPLICANT: Oshahi, Cara
; APPLICANT: Sakowicz, Roman
; APPLICANT: Valsberg, Eugeni
; APPLICANT: Wood, Kenneth
; APPLICANT: Yu, Ming
; TITLE OF INVENTION: Human kinesins and methods of producing
; TITLE OF INVENTION: and purifying human kinesins
; FILE REFERENCE: cytop036
; CURRENT APPLICATION NUMBER: US/09/595,684B
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 09/295,612
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 8257
; TYPE: DNA
; ORGANISM: Human
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Pred. No.: 8.67e-283
Score: 3615.50
Percent Similarity: 50.34%
Best Local Similarity: 31.97%
Query Match: 24.48%
DB: 4
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Mismatch: 932
Indels: 615
Gaps: 86

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Qy 938 LeuGlnLysLysValSerGluPheSerLysGlnLeuGlnLysAlaLeuGlnGluLysAsn 957
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Db 2662 GATTGAGTTTGGTGCTTTGAAAGACCGAGCTTTCTTACAAAGCCCAAGAACTTCAGAG 2721

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Db 3178 ACTGCAGATGTTAAGATATGATGATTAATGAGCAACAAGAAAGAAATATTTCTTTAATA 3237
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Qy 1395 LeuLysSerMetLeuGluAsnLeuLysGlnAspAsnLeuValLeuLysGlnGlnAlaGlu 1414
Db 3703 CTAAAGGAATTAACAGAAAGTATTTGAAACAGAGAGAGACCACTTAAGAGATAT----- 3756

QY 1415 GluTyrSerSerLysGluAsnGlnPheSerLeuGluGluValPheSerGlySerGlnLys 1434
 Db 3757 -----ATAGAGAAATTGAAAGCTACAGCTACAA 3786
 QY 1435 LeuValAspGluIleGluValLeuLysAlaGlnLeuValAlaGlnGluTyrLeuGlu 1454
 Db 3787 ACCAAGAGAACTAAATAATGCTCATTTACCTTAAAGAAACACCAAACTATTGAT 3846
 QY 1455 IleLysAspArgAspTyrPheGlu--LeuValGlnThrAlaSerThrAsnLeuValGlu 1473
 Db 3847 GAACTAAGAAAGAGCTATCTGAGAGACAGCTCAAAATATTAATCTCAGACTTAAGA 3906
 QY 1474 GlyLysLeuGluThrProLeuGlnAlaAsp-----HisGlnGluAsp----- 1487
 Db 3907 ---AATCCCATTCCTCAATTAACAGAGAGATCCAGTGCCTTCATGAGAGAAACAAGATT 3963
 QY 1488 -----SerIleAspArgTyrSerGluMet---GluIleLysValLeu 1501
 Db 3964 CTGCCTTAATGTAAAAAGTCAAGTCACTCAGAAACAAATGAATGAATGAGATTATTA 4023
 QY 1502 GlyGluLys---LeuGluArgAsnGlnTyrLeuLeuGluTyrGluGlnGluLysLeu 1520
 Db 4024 ACAGAACAGTCCACAAACCAAGGACTCAACAACTGCAGCAAGAAATGAAGAAAGGCTC 4083
 QY 1521 GluLeuSerAsnLysLeuGluIleLeuGlnLysGluMetGluThrSerValLeuLys 1540
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 Db 4474 -----AAAGAAACATTAAGAAATTTAGCTAAACACCTGGAACCTGAAGAG 4521
 QY 1678 GlnLeu-----LeuAlaLeuLysGlnMetGlnValAlaThrGlnLys 1693
 Db 4522 GAACCTAAAGTTCATTTGCTGCTGAAGAAACAGAGAACTATTAAATGAGTTAGA 4581
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 Db 4630 TTAGAGCAATCAATGATTAATTAACAGAAACAGATCCAAAGATTTATGAAAGAGAA 4689
 QY 1733 CysLeuLeuAsnGluAsnLysGluLeuGlnGlnSerGlnHisArgLeuGlnCysGluIle 1752
 Db 4690 CAACCT-----AATATTAACCAATTAAGAGGTTCAAGAAACGGAAT---GAACTG 4740
 QY 4753 GluGluLeuMetLysSerLeuLysAspLysGluSerAlaLeuGlnThrLeuLysGluSer 1772

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 Db 4792 GAAGATGAAGTGTGCAAGTTGACCAACAGACTTCAAGAAAGTCAAGAAATCAAAATT 4851
 QY 1786 ValMetLeuGluMetGluLysLeuLysAsnSerGlnArgThrValIleAlaGluArgAsp 1805
 Db 4852 ATGATTAAAGAAAGAAAGAGAAATGAAGAAAGATACAGAGGCCCTTCAGATGAGAGAGAC 4911
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 QY 1826 ArgLysAlaGlnGluAlaLeuGlnGlnLysAspLysValGlnGluLeuThrSerGln 1845
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 QY 1846 IleSerValLeuGlnGlnLysIleSerLeu-----LeuGluAsn----- 1858
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 Db 5665 CAAGCTTAACCTGAGATTAATTA-----GAAATAGAG 5697
 QY 2061 AsnLeuThrAlaLysIleSerSerLeuGlnGluGluIleLeuGlnAsnAlaSerIleLeu 2080
 Db 5698 AATTTA-----AATTGGCTCAAGAACTTATGAAAACTTGAAGAAAG 5742
 QY 2081 AsnGluAlaValSerGluArgGluAsnLeuArgHisSerLysGlnGlnLeuValSerGlu 2100


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Db 5743 AAATCTGTAATGAAGAAAGAGTAATCTAAGAGAGTAGAGAGACTCAAACTGGAG 5802
Qy 2101 LeuGluGlnLeuSerLeuThrLeu-----LysSerArgAspHisAlaPheAlaGln 2117
Db 5803 AGAGACCAATCAAGGAAAGCCCTGCAAGAAACCAAGCTAGAGATCTGGAATACAAACAG 5862
Qy 2118 -----SerLysArgGluLys-----AspGlnAlaVal 2126
Db 5863 GAACCTAAAACTGCTGCTATGCTATCAAAAAGAACACAAAGAAACTGTTATTAACCTTAA 5922
Qy 2127 AsnLysIleAlaSerLeuAlaGluGlnIleLysIleLeuThrLysGluMetAspGlnPhe 2146
Db 5923 GAAAAAATTTCAAGAAAGCAATTCAAATTTTCAGACATTCAAAGAGATTAGATAA---- 5979
Qy 2147 ArgAspSerLysGluSerLeuGlnGlnGlnSerHisLeuSerGluGlnLeuGlnCysThr 2166
Db 5980 -----TCAAAAGATCAATTCACAGAAAAAGATCCAAAGACTTCAG----- 6018
Qy 2167 TyrLysThrGluLeuGlnMetLeuLysGlnGlnLysGlnAspIleAsnLysLeuAla 2186
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Qy 2187 GluLysValLysGluValAspGluLeu----- 2195
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Qy 2211 MetGluLeuArg---AsnGluLysLeuArgAsnTyrGluLeuGlnGlnLysMetAspIle 2229
Db 6190 ATTGTAAGCTAAAGAAAGAGATGAGCTTACAGAGAGATTAAGAAATCTCTCAAAATGGA--- 6246
Qy 2230 MetGluLysGluIleSerValLeuArgLysMet-----Gln 2241
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Qy 2242 AsnGluProGlnGlnGln-----GluAspAspValAlaGluArgMetAspIleLeuGln 2259
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Qy 2280 HisThrLeuSerLeuSerSerSerGlnLeuGlnLysGlnIleThrGlnAlaHisLysHis 2299
Db 6424 TATGAGTGTGTAATGATGTTGCTCTTGACTTGAGAGAAAGAAATTGCAATTCACAGA--- 6480
Qy 2300 CysMetLeuAsnIleLysGlnSerLeuSerThrLeuSerArgSerPheGlnSerLeu 2319
Db 6480 ----- 6480
Qy 2320 GlnThrGlnHisValLysLeuAsnThrGlnLeuGlnThrLeuLeuAsnLysPheLysVal 2339
Db 6481 -----ATCATGAAAGAACTGGAAGTAT 6501
Qy 2340 Val-----TyrArgThrAlaAlaValLysGluAspHisSerLeuIleLysAspTyrGln 2357
Db 6502 GTGTTAAGCTATGTTACAAAATTAAGAAAGAAACAACATGATGCATCAATAATTGAA 6561
Qy 2358 LysAspLeuAlaIleGlnGlnLysArgHisAspGluLeuArgLeuGlnLeuGlnCysLeu 2377
Db 6562 ATGGAATTTATGATGAAGTGAAGAAAGCAAAAGCAATTCCTAATTAATAACAGACCTT 6621
Qy 2378 GlnGlnHisGlyArgLysThrSerAspSerAlaSerGlnGlnLysPheCysGlnIle 2397
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Qy 2398 GlnPheLeuAsnGluLeuLeuPheLysValAsnIleIleGlnSerAlaGlnAspAsp 2417
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Db 6766 AATAGAAAGAAATGACACAGTTTTGGAAAGTGSTTAATATACCGTTTGTATATAGA 6825
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Qy 2535 LeuLeuGlyIleLeuLysThrValGlnAspGln-----SerLysLys 2548
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Qy 2549 LeuGln-----SerArgIleLysMetLeuGlnAsnGlnLeuAsnLeuValLysAsp 2565
Db 7102 ACACAGTTAACCACAGAGAAATTTGAGAGCTGGAAATTCATCTGCATCAAGACTAAAGAA 7161
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Qy 2585 AsnAlaGlnAlaGluLeuAsnAlaMetGlnValLysLeuThrLysLysGlnAspAsnLeu 2604
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Db 7393 AAAAATGCCAAAGAAATTTGAAAGGAAGAAATCGTGTACAAAAGCCATGTGAATATACA 7452
Qy 2665 GlnGlnGlnLysArgArgLeuLysGlnGlnLeuAspArgAlaGlnAlaAspAsnAspThr 2684
Db 7453 AAGGAAGTTATAGGCTATTTAGAGAAATCTCAGAAAGATCAACAGCCCAAGATACC 7512
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Db 7513 TCAGTATATACGAACATATGATCTCCAGCCTTCAATAAACCTTAACTTTGTGAGAGT 7572
Qy 2705 GlySerGlyIleValGlnSerThrAlaMetLeuValLeuGlnSerGlnLysAlaLeu 2724
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Qy 2725 GluArgGlnLeuSerHisTyrLysLysValTyrHisIleAspSerArgThrMetSerSer 2744
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Qy 2745 SerGluAspArgLysLysThrLysAlaLysSerAspAlaHisSerSerHisThrGlySer 2764
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QY 2765 SerHisArgGlySerProHisIleuThrGluThrArg-----HisGlyProVal 2781
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Db 7777 ACTGCTGAG-----AATCTCTCAAG----- 7797
QY 2802 SerThrIleuArgValIleuSerProAsnArgSerGluIleuSerGluIleuValMetSer 2821
Db 7798 ----- 7845
QY 2822 ProGlyLysThrGlyMetHisIleuSerProSerIleuValGlyLeuHisIleu 2841
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Db 8032 CCTTGGCAGCGCTCCTCAGGCAAGATGCTGCTGAGCAAACT 8076

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RESULT 2

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US-09-620-312D-130
Sequence 130, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Zhao, Qing-hong
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aldong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundong
APPLICANT: Wang, Dunhui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pl_FL_genes Version 1.0

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; SEQ ID NO 130
; LENGTH: 8503
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (91)..(8082)
US-09-620-312D-130

Alignment Scores:
Pred. No.: 1,31e-282
Score: 3613.50
Percent Similarity: 50.34%
Best Local Similarity: 31.97%
Query Match: 24.47%
DB: 4
Gaps: 86

US-09-724-584-1 (1-2954) x US-09-620-312D-130 (1-8503)

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QY 21 Gln-----GlyAspGlnAlaAsnLeuGlnTrpLysAlaGlyAsnAsnThrIleSerGln 38
Db 151 GATCATCTGGAGAACTGCCCAAGTTTACTGGAAACAGCAATATGCTCATTTATCA 210
QY 39 ValAspGlyThrLysSerPheAsnPheAspArgValPheAsnSerHisGluSerThrSer 58
Db 211 GTTATGGAAGTAAATCTTCATTTTGCATCGCTTTTCAAGTAAATGAACTCAAA 270
QY 59 GlnIleThrGlnGlnIleAlaValProIleIleArgSerAlaLeuGlnGlyTyrAsnGly 78
Db 271 AATGATGATAGAAATAGACAGACCAATCATCGATTGCGCATCAAGGCTACATGCT 330
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Db 331 ACTATATTGCTATGACAGACTGCTTCAGAAAAACATATACCATGATGGTTCAAA 390
QY 99 AsnSerLeuGlyIleIleProGlnAlaIleGlnGluValPheLysIleIleGlnGluIle 118
Db 391 GATCATTTGGAGATTATCCAGGCAATTCATGACATTTTCCAAAAATTAAGAGATT 450
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Db 451 CCTGATAGGGAATTTCTTACGTATCTTACATGGAATATATCAATGAACCATTAACA 510
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QY 159 AsnValTyrValAlaAspLeuThrGluGluLeuValMetValProGluHisValIleGln 178
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QY 179 TrpIleLysLysGlyGluLysAsnArgHisTyrGlyGluThrLysMetAsnAspHisSer 198
Db 631 TGGATTACAAAGGAGAAAGAGAGCATTAAGAGAAACAAATATGATCAAGAAC 690
QY 199 SerArgSerHisThrIlePheArgMetIleValGluSerArgAspArgAsnAspProThr 218
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QY 239 GlySerGluArgAlaSerGlnThrGlyAlaGluGlyValArgLeuLysGlnGlyCysAsn 258
Db 802 GCGAGTAAAGACCTCTCAACAGGCGCTGACAGGTGCGGCTCAAGAGAGGCTGTAAT 861
QY 259 IleAsnArgSerLeuPheIleLeuGlyGlnValIleLysLysLeuSerAspGlyGlnAla 278

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Db      922  GGTGGTTTCATTAATATGAGATAGCAAGTTAAACGAATTCCTCAGAAATTCCTTGGA  981
QY      299  G|Y|A|n|A|L|e|Y|T|V|a|I|L|e|I|e|C|Y|T|h|I|e|T|h|P|r|o|V|a|S|e|r|P|h|e|a|S|p|I|u|T|h|L|e|u  318
Db      982  GGAATTCGAACAGACAGCTATTATCTGCACAAATTAATCCAGATCTTTTATGAAACTCTT  1041
QY      319  S|e|r|T|h|L|e|u|G|I|n|L|e|u|G|I|n|S|e|r|T|h|A|L|y|S|I|s|V|a|L|A|S|n|T|h|P|r|o|H|I|s|V|a|L|e|u|G|I|n  338
Db      1042  A|C|T|G|C|T|C|C|A|G|T|T|G|C|C|A|G|T|A|T|A|T|A|T|A|G|A|A|T|A|C|T|C|T|T|A|T|G|T|T|A|T|G|A|G  1101
QY      339  V|A|L|L|e|u|S|e|r|P|S|p|I|u|A|L|e|u|L|e|u|Y|S|A|g|Y|T|A|G|Y|S|G|I|U|I|L|e|u|S|p|L|e|u|Y|S|  358
Db      1102  G|T|A|T|C|A|C|G|A|G|A|G|C|T|C|C|T|G|A|A|A|G|T|A|G|A|A|A|A|T|A|T|G|A|T|C|T|T|A|A|A|A|  1161
QY      359  G|I|N|L|e|u|G|I|A|S|n|L|e|u|S|e|r|S|e|r|S|e|r|I|U|T|h|L|y|S|A|I|G|I|A|L|A|S|e|r|A|L|y|S|G|I|U|I  378
Db      1162  C|A|T|T|A|G|A|C|-----G|A|G|T|T|C|T|T|A|G|A|C|G|G|G|C|T|C|A|G|C|A|T|G|A|A|A|A|A|G|C|A|  1215
QY      379  H|I|S|T|h|G|I|n|L|e|u|A|L|a|G|I|U|I|L|e|u|S|G|I|N|L|e|u|H|I|S|Y|S|G|I|U|A|G|I|U|A|S|P|A|G|I|E|T|P  398
Db      1216  T|T|G|G|C|C|C|A|C|T|T|T|G|G|A|G|A|A|A|A|A|G|T|T|G|C|T|C|A|G|A|A|G|T|A|C|A|A|T|G|A|A|A|T|T|G|A  1275
QY      399  H|I|S|L|e|u|T|h|A|S|n|I|L|e|V|a|I|A|L|A|S|e|r|S|e|r|G|I|N|L|e|u|S|e|r|-----G|I|N|G|I|A|S|P|G|I|N|A|G|Y|A|I  417
Db      1276  A|A|C|T|T|A|A|C|G|A|G|A|T|G|T|G|T|G|A|C|C|T|C|T|C|C|C|T|C|C|A|C|G|T|C|C|A|C|G|A|A|T|T|A|A|A|G|G|T  1335
QY      418  L|y|S|A|G|Y|S|A|G|A|X|V|a|I|T|h|T|h|P|A|L|P|r|o|G|I|U|Y|S|I|L|e|G|I|A|S|n|S|e|r|L|e|u|H|I|S|A|S|e|r  437
Db      1336  A|A|A|A|G|A|A|A|C|G|A|G|A|G|T|T|A|C|T|T|G|G|C|C|T|T|G|C|A|A|A|T|T|A|C|A|A|A|A|T|G|A|A|C|T|C|A|A|C  1395
QY      438  G|I|Y|A|I|S|e|r|A|S|P|P|h|e|A|S|P|L|e|u|S|e|r|A|G|I|U|S|P|P|r|o|G|I|U|A|S|n|P|h|e|S|e|r|L|y|S|A|L|y|S  457
Db      1396  T|A|T|G|A|G|A|T|C|A|T|T|A|T|-----A|T|A|C|C|A|A|A|A|T|A|T|A|C|A|A|C|A|A|A|A|C|A|C|A|T  1443
QY      458  P|h|e|S|e|r|A|S|P|P|r|o|S|e|r|P|h|e|P|r|o|G|I|U|I|L|e|A|S|P|A|S|e|r|V|a|I|C|Y|e|T|h|G|I|U|S|e|r|S|e|r|P  477
Db      1444  A|A|G|C|T|T|C|T|A|T|A|A|T|T|A|T|T|A|C|G|A|A|A|T|T|G|A|T|G|A|T|C|T|G|T|C|T|C|A|G|A|C|T|G|A|T|G|T  1503
QY      478  P|h|e|A|S|P|A|L|A|L|e|u|S|e|r|L|e|u|S|e|r|L|e|u|S|e|r|A|S|P|A|S|e|r|A|S|P|A|L|G|I|U|T|h|P|A|S|n|L|e|u|A|I  497
Db      1504  T|T|C|A|G|T|A|C|A|C|T|T|G|A|T|C|A|T|T|A|G|T|-----G|A|G|A|T|G|A|A|G|G|A|A|T|C|C|A|G|A  1551
QY      498  S|e|r|L|y|S|A|I|T|h|H|I|S|A|G|I|U|Y|S|T|h|S|e|r|L|e|u|H|I|S|G|I|n|S|e|r|L|e|u|S|e|r|P|h|e|G|I|G|I|N  517
Db      1552  A|C|A|A|G|C|T|A|C|T|A|A|T|C|A|G|A|G|-----  1572
QY      518  I|L|e|S|e|r|A|S|P|S|e|r|V|a|I|G|I|N|P|h|e|H|I|S|A|S|P|S|e|r|L|y|S|G|I|U|A|S|n|G|I|N|L|e|u|G|I|N|T|Y|L|e|u|P|r|o  537
Db      1572  -----  1572
QY      538  L|y|S|A|S|P|S|e|r|G|I|Y|A|S|P|L|a|G|I|U|C|Y|S|A|G|Y|S|A|L|A|S|e|r|P|h|e|G|I|U|S|G|I|U|I|e|T|h|S|e|r  557
Db      1572  -----  1572
QY      558  L|e|u|G|I|N|G|I|N|L|e|u|G|I|n|S|e|r|L|y|S|G|I|U|G|I|U|Y|S|G|I|U|L|e|u|V|a|I|G|I|n|S|e|r|P|h|e|G|I|  577
Db      1572  -----  1572
QY      578  L|e|u|Y|I|L|e|A|G|I|U|L|e|u|G|I|U|G|I|n|L|e|u|S|e|r|V|a|I|L|y|S|A|L|y|S|n|L|e|u|G|I|U|S|e|r|V|a|I  597
Db      1573  -----A|A|T|A|G|A|A|A|G|T|G|A|  1587
QY      598  T|h|H|A|S|e|r|A|G|S|G|I|U|H|I|S|e|r|I|L|e|A|S|n|A|L|a|G|I|U|A|I|G|I|N|T|h|A|S|P|V|a|I|G|I|U|S|G|I|U|A|I  617
Db      1588  T|T|G|A|C|T|C|A|-----  1596
QY      618  V|A|L|A|G|Y|S|G|I|U|S|e|r|V|a|I|L|e|u|G|I|U|A|S|P|S|e|r|G|I|Y|T|Y|A|S|n|A|L|A|S|e|r|A|S|n|S|e|r|A|S|P|L|e|u  637
Db      1596  -----  1596

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QY      638  G|I|N|A|S|P|S|e|r|S|e|r|V|a|I|S|P|G|I|Y|S|A|P|L|e|u|S|e|r|S|e|r|H|I|S|A|S|P|G|I|U|C|Y|e|T|h|U|H|I|S  657
Db      1596  -----  1596
QY      658  A|G|Y|S|e|r|L|e|u|G|I|N|L|y|S|I|L|e|V|a|I|A|S|P|L|e|u|G|I|U|P|h|I|L|e|G|I|U|A|S|n|L|e|u|A|S|n|Y|S  677
Db      1596  -----  1596
QY      678  L|y|S|e|r|G|I|U|A|S|n|A|S|P|L|y|S|e|r|S|e|r|G|I|U|G|I|N|A|S|P|P|h|e|C|I|U|S|e|r|I|L|e|G|I|N|L|e|u  697
Db      1596  -----  1596
QY      698  C|Y|S|G|I|U|A|I|L|e|u|C|I|U|Y|S|A|L|A|S|n|A|L|e|u|G|I|U|L|e|u|A|L|e|u|S|e|r|A|S|P|A|S|e|r|P|  717
Db      1597  -----C|T|T|G|T|C|T  1605
QY      718  A|S|P|h|e|A|S|P|A|S|n|I|L|e|u|G|I|U|A|S|n|G|I|U|T|h|L|e|u|Y|S|A|G|Y|U|I|L|e|A|L|A|S|P|L|e|u|G|I|  737
Db      1606  G|A|C|T|A|T|G|A|T|A|T|C|T|G|T|T|A|G|A|C|T|A|T|A|C|A|C|A|C|A|G|A|A|A|A|A|A|A|A|A|T|G|A|  1665
QY      738  A|S|P|S|e|r|L|y|S|G|I|U|A|S|n|G|I|U|T|h|A|S|n|G|I|U|P|h|e|G|I|U|I|L|e|u|G|I|U|S|G|I|U|T|h|G|I|N  757
Db      1666  T|T|G|A|A|T|T|A|A|A|A|A|A|A|A|A|G|A|T|T|G|G|A|T|T|G|A|G|G|C|T|G|A|A|A|A|A|A|A|A|A|A|A|A|A|A|A|  1725
QY      758  L|y|S|G|I|U|H|I|G|I|U|A|G|I|N|L|e|u|I|L|e|H|I|S|G|I|U|I|L|e|G|I|S|e|r|L|e|u|Y|S|G|I|U|V|a|I|G|I|U|A|S|n  777
Db      1726  A|A|A|G|A|T|C|A|G|A|G|A|T|C|A|A|T|T|C|A|A|A|T|T|G|A|A|A|T|T|G|A|A|A|A|T|T|G|A|A|A|A|A|A|A|A|A|A|A|A|A|A|A|  1785
QY      778  A|L|a|G|I|U|S|e|r|T|Y|A|S|n|G|I|A|S|n|L|e|u|G|I|U|A|S|P|L|e|u|G|I|U|T|h|T|h|L|y|S|e|L|e|u|L|y|S  797
Db      1786  C|G|A|G|A|A|G|A|T|A|T|A|C|A|A|G|A|C|T|T|G|A|G|A|A|T|G|A|A|C|A|C|A|T|T|C|A|A|A|A|G|T|A|G|C|T|T|T|G|A  1845
QY      798  G|I|U|G|I|U|I|L|e|G|I|N|L|e|u|A|L|a|G|I|U|U|A|G|Y|S|A|G|A|L|A|S|P|A|S|n|L|e|u|G|I|U|Y|S|A|I  817
Db      1846  G|A|A|A|G|A|A|G|A|C|G|A|T|T|A|A|A|G|A|C|T|A|C|A|G|A|A|T|C|A|T|A|G|A|C|T|C|T|C|A|A|A|G|C|T|A|A|A|A|A|A|T  1905
QY      818  A|S|P|A|S|P|L|e|u|S|e|r|V|a|I|S|e|r|L|y|S|e|r|G|I|U|Y|S|e|r|G|I|U|Y|L|e|u|C|Y|G|I|U|I|L|e|P|h|e  837
Db      1906  A|T|A|A|A|A|T|G|A|C|T|G|T|C|T|A|C|A|T|G|-----G|A|A|G|A|C|T|T|G|A|A|A|C|C|A|A|A|A|  1953
QY      838  G|I|N|L|y|S|G|I|N|S|e|r|S|e|r|A|S|P|A|L|a|V|a|I|T|h|A|S|P|A|L|a|G|I|U|S|G|I|U|C|Y|S  857
Db      1954  C|A|A|T|G|A|G|A|C|A|C|C|T|T|G|A|T|G|C|T|G|A|A|C|T|G|A|G|C|C|T|T|G|A|G|C|C|A|A|G|A|G|A|A|T|C|A  2013
QY      858  S|e|r|P|h|e|L|e|u|A|G|S|e|r|G|I|U|A|S|n|L|e|u|G|I|U|L|e|u|Y|S|G|I|U|Y|S|e|r|G|I|U|A|S|P|T|h|S|e|r|A|S|n|T|P|r  877
Db      2014  G|C|C|T|T|C|T|T|A|G|A|G|A|A|A|T|C|T|G|A|G|T|T|G|A|A|G|G|A|A|A|T|G|A|A|A|A|A|C|T|T|G|A|A|C|T|A|C|A  2073
QY      878  T|Y|Z|A|S|n|G|I|U|S|G|I|U|Y|S|A|L|A|S|e|r|L|e|u|P|h|e|G|I|U|Y|S|G|I|N|L|e|u|G|I|U|T|h|G|I|U|S|e|r  897
Db      2074  T|A|C|A|G|C|A|A|A|T|G|A|A|A|T|G|A|T|T|C|A|G|T|T|A|T|A|C|A|A|C|C|A|A|T|T|G|G|A|G|C|A|A|A|-----  2127
QY      898  A|S|n|T|Y|L|y|S|L|y|S|e|r|G|I|U|A|I|A|S|P|L|e|u|G|I|N|Y|S|G|I|U|L|e|u|G|I|N|S|e|r|A|P|h|e|A|S|n|G|I|U|I|L|e  917
Db      2128  -----A|A|G|A|A|A|I|G|C|A|A|G|T|G|A|T|C|G|A|G|A|A|A|G|A|A|T|T|A|C|A|A|T|G|C|T|T|T|A|T|A|G|A|G|T|A  2181
QY      918  A|S|n|T|Y|L|e|u|A|S|n|G|I|U|A|I|A|S|P|L|e|u|G|I|N|Y|S|G|I|U|L|e|u|G|I|N|S|e|r|A|P|h|e|A|S|n|G|I|U|I|L|e  937
Db      2182  A|C|A|A|A|A|C|A|C|C|C|C|T|A|T|A|G|A|T|G|G|C|A|A|A|G|T|T|C|C|A|A|A|A|A|A|T|T|G|C|T|G|T|A|A|T|T|G|G|A|  2241
QY      938  L|e|u|G|I|U|Y|S|G|I|U|S|e|r|G|I|U|P|h|e|S|e|r|L|e|u|G|I|U|Y|S|A|L|A|S|e|r|G|I|U|G|I|U|L|y|S|A|S|n  957
Db      2242  T|T|G|A|A|G|A|A|A|G|A|T|T|A|C|G|A|T|T|C|C|A|A|A|A|C|T|T|A|T|A|A|A|A|G|A|A|T|T|G|A|A|A|A|A|A|T|G|A|  2301
QY      958  A|L|a|L|e|u|G|I|U|A|S|n|G|I|U|A|I|T|h|C|Y|e|L|e|u|S|e|r|G|I|U|Y|Y|S|P|h|e|L|e|u|P|r|o|A|S|n|G|I|U|A|I|G|I|U  977
Db      2302  G|C|T|T|G|G|G|G|A|A|A|G|A|G|A|T|T|T|G|C|T|T|C|A|G|A|T|T|G|A|A|T|T|T|A|C|T|T|T|C|T|T|G|A|A|T|G|A|A  2361
QY      978  C|Y|S|e|L|y|S|A|S|n|I|L|e|S|e|r|L|y|S|A|L|A|S|e|r|G|I|U|G|I|U|I|L|e|u|S|e|r|L|e|u|S|G|I|N|G|I|U|G|I|U|Y  997
Db      2362  A|G|C|T|G|A|G|A|A|A|G|A|T|C|A|G|A|C|A|A|A|T|C|T|G|A|A|G|G|C|C|C|A|T|A|T|A|T|A|A|C|T|C|A|G|A|A|A|A|  2421

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Qy 998 GluHisSerAlaSerIleIleSerIleGlnIleIleMetGlnGlnGlnSerGlnGln 1017
Db 2422 GATAAATTGTTTCTGAAGTACTGATAGAGAGACTAGAGCTTCAAGCTTACTGAGAA 2481
Qy 1018 IleLeuGlnLeuThrAspGluValThrIleSerGlnSerIleValGlnGlnThrGln 1037
Db 2482 ATTGGGAAAACAAAGATGACTTACCAACTACACGCTGAATTAATAAGACACTGATCA 2541
Qy 1038 GlnIleGlnLeuMetIleLysMetHisAspAspLeuPheGlnIleValIle 1053
Db 2542 GAATTCCAAAATTTCAAAACCTTCATATGAGCTTGAAGCAAAAGTATAGATGCTCT 2601
Qy 1054 -----IleArgAsnLysSerGlnValGlnAspLeuValGlnMetGlnVal 1070
Db 2602 GAGGAGATGAGAGATGATATCAGAAATTAATCTCTTAAAGAAAGCCCAAAATTT 2661
Qy 1071 LysGlnIleMetGlnSerValGlnValIleValIleAspThrLysIleGlnGln 1090
Db 2662 GATTGAGATTGGGCTTGAAGACGAGCTTCTTACAGACCCCAAGAACTTCAAGAG 2721
Qy 1091 ThrIleArgAspIleGlnGlnLeuIleGlnLysIleValIlePhePheGlnIleVal 1110
Db 2722 AAAACAGCTGAGCTTCAAGAAAGACTAATGAGATGAGACAGCTGAAGCAACATTA 2781
Qy 1111 ThrIlePheProIleThrProLeuSerAspSerIleProProSerIleValIleGln 1130
Db 2782 AAT-----AGAGATTCTCCCTGCAAACTGTAGCAAAAGGAGAAACACTGATTCTG 2835
Qy 1131 AsnSerGlnAspProIleGlnIleAsnAspIleIleAsnLeuIleValIleThrGln 1150
Db 2836 AAACTGACGAGAACTTATAGAA-----GAAGTAAAACTTAACTCAAGAAAGATGAT 2889
Qy 1151 ArgAsnAsnIleMetValCysLeuGlnIleThrGlnArgAsnSerIleLysGlnVal 1169
Db 2890 CTAAGAACACTCCAGAAAGCTTGCAATTTGAGAGGAGCAACACTCAAAAGTATATT 2949
Qy 1170 -----IleAspLeuAsnThrGlnLeuGln-----SerLeuGlnIleGln 1182
Db 2950 GATACTGTTAACTATGATATATGATATCTCAAGAACATTAAGAAATCTTGAAGCTC 3009
Qy 1183 SerIleGlnLysSerIleGlnLysIleValIleGlnAspLeuGlnIleGlnValIle 1202
Db 3010 AAAACAACATCAAAACAAATTAATACATAAAATTCGAAATTTCTGAG---GAAGTTC 3066
Qy 1203 LeuLeuLeuGlnIleMetGlnLeuLeuLysGlnIleThrAsp-----SerGln 1218
Db 3067 AGGAATTTGATATGAGAGAAATACAGAGAAACTAAAGATTAATTCAGCAAAAGATG 3126
Qy 1219 LeuSerIleGlnLysLeuGlnLeuGlnValIleThrGlnLysLeuGlnIleThr 1238
Db 3127 GTTGGCATATGATTAATAAGAG-----GATTTGAA---GCTAAATAATCCCAACACT 3177
Qy 1239 GlnGlnGlnMetLysAsnIleThrIle----- 1247
Db 3178 ACTGCAGATGTTAAGATATATGATATATGAGCAACAAAGAGATATTTCTTAAATA 3237
Qy 1248 -----GluArgAsnGlnLeuGlnIleThrAsnPheGlnValAspLeuValGln 1266
Db 3238 CAGAGAAATATGAACTCCAAATGTTAGAGAGCTTATATGCAAAAGAAACAAATTTG 3297
Qy 1267 LysGlnAspLeuSerGlnAsnIleGlnIleSerIleGlnIleAspGlnVal 1286
Db 3298 AAGACTGACTTAAGAAATTTGAAATGACATTTGAAACCAAGAGAAATTAAGACTT 3357
Qy 1287 AlaGlnGlnIleLeuArgGlnIleGlnIleValIleAspSerPheArgGlnIleLeu 1306
Db 3358 CTTGGGAGATGAATTAAGAAAGCAAGAGATAGTTGCAAGAAAGAAACCATGCACTA 3417
Qy 1307 AspCysSerValGlyIleSerSerProAsnHisAspAlaValAlaAsnGlnIleVal 1326
Db 3418 AAG---AAAGAGAGAGACTTCTTAGGACCTGTGACACACTGCGCAGAAAGTTGAAGAAA 3474
Qy 1327 SerLeuGlnIleValIleAsnSerLeuGlnSerGlnMet-----LeuArgGly 1341

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Db 3475 CTTAAAGAAAAGAGCCAGCACTCCAGAGAAAACGCAACAACTTAAATGATACAGAA 3534
Qy 1342 GluArgAspGlnLeuGlnIleThrSerCysLysAlaLeuValSerGlnLeuGlnLeu 1361
Db 3535 GAGATGAGTGAATGATCAGAAAAG-----ATTATGAAATGAGAAATTTAAG 3582
Qy 1362 AlaHisValLysSer-----ValGlnGlnGlnAsnLeuIle 1374
Db 3583 AATGAATTTAAAGAAACAAAGATTTGACATTGGAACATATGAGAAACAGAGAGCTTG 3642
Qy 1375 ThrLysLysLeuAsnGlnIleGlnLysGlnIleLeuGlnIleLysSerGlnGlnVal 1394
Db 3643 GCTCAAGAACTTAATGAAATTTATAGAGAGTGAATATTAACCAAGAAAGAAAGTT 3702
Qy 1395 LeuLysSerMetLeuGlnAsnLeuLysGlnAspAsnLeuLysGlnGlnAlaGln 1414
Db 3703 CTTAAAGAAATTAACAGAGTCAATTTGAAACAGAGAGACCACTTAGAGATAT----- 3756
Qy 1415 GluIleSerSerLysGlnAsnGlnPheSerLeuGlnIleValIlePheSerGlnLys 1434
Db 3757 -----ATTAAGAAATTAAGCTTACAGCCCTCA 3786
Qy 1435 LeuValAspGlnIleGlnValIleLysAlaGlnLeuLysAlaAlaGlnIleVal 1454
Db 3787 ACCAAAGAAAGAACTTAAATTTGCTCATATTCACCTTAAAGAACCAAGAAATTTGAT 3846
Qy 1455 IleLysAspArgAspIleValIleValIleGlnIleThrAlaAsnThrAsnLeuVal 1473
Db 3847 GAACTAAGAAAGAGCTTATCTGAGAGAGACAGCTCAATTAATAATCTCGAGACTTAG 3906
Qy 1474 GlyLysLeuGlnIleThrProLeuGlnAlaAsp-----HisGlnIleAsp 1487
Db 3907 ---AATCCCATACCAATTAACAAAGAGATCCCACTGCTTATGAGAAACAAGCTTA 3963
Qy 1488 -----SerIleAspArgArgSerGlnIleMet-----GlnIleValLeu 1501
Db 3964 CTGCTTAATGTGAAAAAGAGCTGAGACTCAGAGAAACAAATGATGAATGAGAGTATTA 4023
Qy 1502 GlyLysLys---LeuGlnArgAsnGlnIleThrLeuGlnIleValGlnGlnIleVal 1520
Db 4024 ACAGAACAGTCCACACCAAGAGACTCAACAACTGCAAGAAATGAAATGGAAGGCTC 4083
Qy 1521 GluLeuSerAsnLysLeuGlnIleLeuGlnLysGlnMetGlnIleThrSerValLeuLys 1540
Db 4084 AGGTTGATGAAAAATTTCAAGAAAGTCAAGAGAGATTAATCTTAACCAAGAAAGA 4143
Qy 1541 AspAspLeuGlnIleLysLeuGlnIleSerLeuLeuSerGlnAsnIleIleLysGln 1560
Db 4144 GACAACTTAAGACATTAAGAAAGAGCCCTTGAAGTTAAACATGACCAAGCTGAAGAACT 4203
Qy 1561 IleAspThrThrLeuLysHisHisSerAspThrGlnAlaGlnLeuGlnIleThrGln 1580
Db 4204 ATTAGAGAAACTTTG-----GCTAAATTCAGAGAGCTCAAGAC 4242
Qy 1581 GlnLeuGlnLeuAlaLysAsnLeuAlaIleAlaSerAspAsnCysProIleThrGln 1600
Db 4243 AAACAAGAACAGCTCTTAATATGAAAGAAAGAAACAAATGAACATCAAAATCTGAGT 4302
Qy 1601 GlnLysGln-----ThrSerAlaAspCysValHisProLeuGlnIleLysIle 1617
Db 4303 GAGATGAGCAATTCACAAACCAAGATTTAGACACTTATAGAGATGAATTAATAATGCTC 4362
Qy 1618 LeuLeuThrGlnGlnLeuIleGlnLysThrAsnGlnGlnIleLysLeuLysIle 1637
Db 4363 GGATTTGCTCAAAAGACTTCAAGAAAGTCAATGAAATGAATCTGTAGTACAGAGAA 4422
Qy 1638 AsnGlnLeuGlnGlnAlaGlnIleValIleLysCysGlnValGlnHisLeuMetLys 1657
Db 4423 GATGACTTACAGAGGCTGCAAGAACTTTCATATGAAAGTGAAGTGAAGCAAGCTC----- 4473
Qy 1658 MetIleGlnSerLysSerSerLeuGlnSerLeuGlnIleGlnIleValIleAspThrGln 1677

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Dd	4474	-----AAAGAAACCTTAAGAAATTTAGCTTAAACACCTGAAACCTGAGAC	4521
Oy	1678	GlnLeu-----LeuAlaLeuysgInglmetGlnValValThrGlnIuLyS	1693
Dd	4522	GAACCTTAAGTTGCTCATTTGTTGCTGAAAGAAACAAGAAACCTATTATGAGTTAGA	4581
Oy	1694	LyseGluLeuGlnGlnThrHisGlnHisLeuThrAlaGluValAspHisLeuLyseGluAsn	1713
Dd	4582	GTGAATCTTTGAGAGAAAGAA-----ACTGAAATATCAACATTCATCAAAAGACG	4629
Oy	1714	ILeglu-----LeuGlyLeuAsnPhelysAsnGluValagInglInLySThrThrLyseGluGln	1732
Dd	4630	TTAGAACCAATCAATGATTAATATTACAGAACCAAGATCCAAAGACATTATTAGCAAAAGAGAA	4689
Oy	1733	CysLeuLeuAsnGluAsnLyseGluLeuGlnGlnSerGlnHisArgLyseGluGlnCysGluIle	1752
Dd	4690	CAACTT-----AATATAAACAATATTAGTGAGCTTCAGGAAAAAGTGAAT---GAACTG	4740
Oy	1753	GlnGluLeuMetLySerLeuLyAspLyseGluSerAlaLeuGluThrLeuLyseGluSer	1772
Dd	4741	AAACATTTCAAGAGGACATCGCAAAAGCCAAAGATTCAGCATCAAAAGTAT-----	4791
Oy	1773	GlnGlnLySValIleAsnLeu-----AsnGlnGlnMetGlnMet	1785
Dd	4792	GAAAGTAAAGATGCTCGAGTTGACCAACACACTTCAAGAAAGTCAAGAAAGAAATTCAAATTT	4851
Oy	1786	ValMetLeuGlnMetGlnGluLeuLySAsnSerGlnArgThrValIleAlaGluArgAsp	1805
Dd	4852	ATGATTTAGGAAAAAAGAGAAATGAAAAAGATCAAGAGGCCCTTCACATAGAGAGAC	4911
Oy	1806	GlnLeuGlnAspAspLeuArgGluSerValGluMetSerIleGluThrGlnAspAspLeu	1825
Dd	4912	CAACTGAAAGAAACACACTTAAAGAAATTTGACTTAAATGAAAGAAATCTCAAGAA-----	4965
Oy	1826	ArgLySAlaGlnGluAlaLeuGlnGlnInLySAspLySValGlnGluLeuThrSerGln	1845
Dd	4966	AAAGAAATACGTTTCTTAAGATGACACCTGTCATGAGACTCAGGAGAAAAATGTGTA	5025
Oy	1846	IleSerValLeuGlnGlnIuLyIleSerLeu-----LeuGluAsn-----	1858
Dd	5026	ATAGAACCTTGAAGAGACCAATTGAGACCAGAAAGTTAAACCTTGAAAAACATGAAACG	5085
Oy	1859	-----GlnMetLeuTr--AsnValAlaThrValLyseGluThrLeu	1871
Dd	5086	GAGAAATATAAGTTGACTGACATGACTACATGATAAACTTGAAAGAAATGAGATCTGTAA	5145
Oy	1872	SerGluArgAspAspLeuAsnGlnSerLyseGlnHisLeuPheSerGluIleGluThrLeu	1891
Dd	5146	AAAGAAAGATGACCTTAGAGAGTGTGAGAGAGACTCCAAAGTAGAGAGAGACAGCTC	5205
Oy	1892	SerLeuSerLeuLySGLuLyS--GluPheAlaLeuGlnGlnAlaGluLyAspLyS--	1909
Dd	5206	AAAGAAACCTTAGAGAACTATTAATCTAGAGACTTGAAGAAACAAGAGAGACTTAAATTT	5255
Oy	1910	-----AlaAspAlaAlaArgLySThrIleAspIleThrGlnLySleSerAsn	1925
Dd	5266	GTTCAACATGATCGAAGAGAGACCAAGAAACTATTGAT-----AAACTAAGAGCG	5316
Oy	1926	IleGluGlnGlnLeuLeuGlnGlnAlaThrAsnLeuLySGLuThrLeu--TyrGluArg	1944
Dd	5317	ATTGTTTCAGAGAAAAACAATGAAATATCAATATGCAAAAGGACTTGAAACCTCAAAAT	5376
Oy	1945	GluSerLeu-----IleGlnLySGLuGlnLeuAlaLeuAsnThrGlnHis	1960
Dd	5377	GATGCTTAAAAAGCACAGGATCTGAAATATACAGAGGAACTTAGAGATTTGCTCACATGCAT	5436
Oy	1961	LeuArgGluThrLeuLySerLySAspLeuAlaLeuGlnLySmetGluGlnGluArgAsp	1980
Dd	5437	CTGAAGAGCAGCAGGAAATCATTCAGCAAACTCAGAGGAATTTGTTTCGAGAGACAGAT	5496
Oy	1981	GluAlaAlaAsnLySValIleAlaLeuThrGluLySmetSerSerLeuGlnGlnIle	2000
Dd	5497	AAACATTCAAATATGCAAAAGATTTGCAAAATTCCTTAAATTTCAAGAAAGATTT	5556

QY	2001	AenGluAenValThrThrLeuLysGluGlyGluGlyGluSerGluThrPheTyrluEnl	2020
Db	5557	CAGGA-----CTTAAGCAAAATACATCAACTTATTACCTTAAAAAAGAT	5604
OY	2021	ArgProSerLySGlnGlnSerSerSerGlnMetGluLeuArgGluSerLeuYthr	2040
Db	5605	GTCATGTAGCACACAGAAAAGTGCTGTGAATGGAGCACAATAAGAAAACAATTAAGAC	5664
OY	2041	LysAspLeuGlnLeuGluAlaGluLysGluIleSerGluAlaThrAsnGluIleLys	2060
Db	5665	CAAGGCTTAACCTGCAGTAATAA---GAAATAGAG	5697
OY	2061	AsnLeuThrAlaLysIleSerSerLeuGlnGluGlnIleLeuGlnAsnAlaSerIleLeu	2080
Db	5698	AATTTA-----AATTGGCTCAAGAACCTTCAGAAAACCTTGAAGAATG	5742
OY	2081	AsnGluAlaValSerGluArgLysAsnLeuArgHisSerLySGlnLeuValSerGlu	2100
Db	5743	AAATCTGTAAATGAAGAAGAGATATATCTAAGAGAGAGAGACACTCAACTGGAG	5802
OY	2101	LeuGluGlnLeuSerLeuThrLeu-----LysSerArgAspHisAlaPheAlaGln	2117
Db	5803	AGAGCCAACTCAAGAAAGAGCTCCAGAAACCAGAGCTAAGATCTGGAATACACAG	5862
OY	2118	-----SerLysArgGluLys-----AspGluAlaVal	2126
Db	5863	GAACTAAABAACTGCTCGATCTCATCAABAACACAAAGAACTGTTGATTAACCTTAG	5922
OY	2127	AsnLysIleAlaSerLeuAlaGluGluIleLysIleLeuThrLysGluMetAspGluPhe	2146
Db	5923	GAAAAAATTTCCAGAAAGACAACTCAAAATTTCAACACATCTCAAAAGGATTTTGATTA--	5979
OY	2147	ArgAspSerLysGluSerLeuGlnGlnGlnSerSerHisLeuSerGluLeuCysteHr	2166
Db	5980	-----TCAAAAGATGAATTCACAGAAAAGATCCAAGAACCTTCAG-----	6018
OY	2167	TyrlYThrGluLeuGlnMetLeuLysGlnIleLysGluAspIleAsnAsnLysLeuAla	2186
Db	6019	----AAAAGAAGAACTTCAACTCTTAGA--GTGAAGAAGATGTCATATATAGT---CAT	6069
OY	2187	GluLysValLysGluValAspGluLeu-----	2195
Db	6070	AAAAAAAAATTAAGAAATGGAAACATTTGAAGAACAAATTTGAGCCAACTATCTATGCAAG	6129
OY	2196	-----LeuGlnHisLeuSerSerLeuLysGluGlnLeuAspGlnIleGln	2210
Db	6130	TGTGAGATGGAATACTTCCAGTTGACTTAAGAATACTTCATGAAGCCTTGAAGAAATTAAGA	6189
OY	2211	MetGluLeuArg-----AsnGluLysLeuArgHisnTYrGluLeuCySgLuYMetAspIle	2229
Db	6190	ATTGAGCTTAAGAAAGAGATGAGACTTAAGGAGATTAAGAANAATCTCTCAAAATGGA--	6246
OY	2230	MetGluLysGluIleSerValLeuArgLeuMet-----Gln	2241
Db	6247	AGGAGCCAACTTCATAGCAACTTAAGGAAATGTAGCTAGAGACGCCAGAACCAACCA	6306
OY	2242	AsnGluProGlnGlnGlu-----GluAspAspValAlaGluArgMetAspIleLeuGlu	2259
Db	6307	GTAAAACTGAAAAAGAGTTACTTAAGGATGAGACACAGCACTTATGGAAGCTGAGA	6366
OY	2260	SerArgAsnGlnGluIleGlnGluLeuMetGluLysIleSerAlaValTYrSerGluGln	2279
Db	6367	GAAAAAGTCTCTAGAAATTAAGACCTTTTGAAGAGATCACTCAGAGAG--GATGATCAT	6423
OY	2280	HisThrLeuLeuSerSerLeuSerSerGluLeuGlnIleLysGluThrGluAlaHisLysHis	2299
Db	6424	TATGAGTCTTGATAGTATGTTCTCTCTTGACCTTGAGAGAAAGAAATTAATTCACAG--	6480
OY	2300	CysMetLeuAsnIleLysGluSerLeuSerSerThrLeuSerArgSerPheGlySerLeu	2319
Db	6480	-----	6480

QY 2320 GlnThrGlnHisValLysLeuAsnThrGlnLeuGlnThrLeuLeuAsnLysPheLysVal 2339
 Db 6481 -----ATCATGAAGAAAGTGAAGAT 6501
 QY 2340 Val-----TyrArgThrAlaAlaValLysGluAspHisSerLeuIleLysAspTyrGlu 2357
 Db 6502 GTGTTAAGCTATGTTACAAATAATAAGAAACAACATGAATCCATCATATAATTTGAA 6561
 QY 2358 LysAspLeuAlaAlaGluGlnLysArgHisAspGluLeuArgLysGlnLeuGlnCysLeu 2377
 Db 6562 ATGATTTTATGATGAAAGTGAAGAAAGAAAGAAATGCTTAATTTAAATACACACCTT 6621
 QY 2378 GlnGlnHisGlyArgLysTyrSerAspSerAlaSerGlnLysLeuLysPheCysGluIle 2397
 Db 6622 CAACAAGAT-----TGTCATCTACCATCCAGAAATTAAGGATCTCAAAATG 6669
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 QY 2438 HisLysLysGlyPheMetGlnTyrLeuGlnGluPheGlyAspLeuHisValAspAlaLys 2457
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 QY 2535 LeuLeuGlyIleLeuLysThrValGlnAspGlu-----SerLysLys 2548
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 Db 7102 ACACAGTTAACACACAGAGAAATTCGAGAGCTGGAATTCATCTCATGAAGCTAAAGAA 7161
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 Db 7162 AGTGCATTCATAGGAAGAAAGCAAGATTAAGAGTCAGAAAGAACTTGAGTGCTAAT 7221
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 QY 2645 LysTyrSerLysAlaThrAspGlnGluIleAlaTyrLeuLysSerCysLeuGlnLysLys 2664
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 QY 2665 GluGlnGlyLeuArgArgLeuLysGlnLysLeuArgAlaGlnAlaAspAsnAspThr 2684

Db 7453 AAGGAAGTATTAAGGCTATTGAGAGAAATTCACAGAAAGTCAACAGGCCAAGATACC 7512
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 QY 2725 GluArgGluLeuSerHisTyrLysLysLysTyrHisIleLeuSerArgThrMetSerSer 2744
 Db 7633 GAAAAAGAAATTTCTAAGTTAAAGCAAAATGAACGCTA----- 7674
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 Db 7846 -----TCTCA 7851
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 QY 2900 AspValLysSerLysSerMetProTyr---CysProSerGlnPhePheAspAsnSerLys 2918
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 QY 2919 LeuGlyAspPheSerGlnLeuLeuAsnThrAlaGluSerAsnAspLysSerGlnAlaGluAsn 2938
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 QY 2939 TyrTyrTyrGluAlaLysLysGlnThrAlaProGluCysLysThr 2953
 Db 8032 CTTTGGCAGCGCTCTCCAGCAAGATGTGCTGTGAGTCAAAACT 8076
 RESULT 3
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 Sequence 2, Application US/08353700
 Patent No. 559919
 GENERAL INFORMATION:
 APPLICANT: YEN, TIMOTHY J.
 APPLICANT: RATNER, JEROME B.
 TITLE OF INVENTION: NUCLEIC ACID ENCODING A
 TITLE OF INVENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN,
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DANN, DOREMAN, HERRELL AND SKILLMAN
 STREET: 1601 MARKET STREET, SUITE 720

QY 571 uLeuValGlnSerPheGluLeuLysLeialGluLeuGluGluInuSerValLysAl 591
Db 1754 GAAGAAATACCTCTCAGAAACCATGTAAAGATCTTCAAGAAAAATA 1802
QY 591 aLysasnLeuGluMetValThrAsnSerArgLuhIserIle 605
Db 1803 -----AATCAGCAAGAAAACTCTTGACTTTAGAAAACTGAA 1840
QY 606 -----AsnAlaGluValGlnThrAspValGluLysGluValValArgLysGlu 621
Db 1841 GCTTGCTGTGCTGCTATCGAAAAAGCAGATGTTCTCAACACCTTTGAAAGAAAG 1900
QY 621 uMetSerValLeuGluAspSerGlyTyrAsnAlaSerAsnSerAspLeuGluAspSerSe 641
Db 1901 A-----GAACATCACCATTGAAACAACTTAATGATGATTAAGTTAAGCAAGACAGA 1945
QY 641 rValAspGlyLysArgLeuSerSerSerHisAspGluCysIleGluHisArgLysMetIle 661
Db 1946 GAAGAGATCCAAACCTTGCTGAGTGCCT-----TT 1975
QY 661 uGluGluLysIleValAspLeuGluGluPheIleGluAsnLeuAsnLys 677
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QY 678 -LysSerGluAsnAspLys-----GlnLysSerSerGluGluAspPheMetGluSe 694
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QY 694 r-----IleGluLeuLys 698
Db 2096 TAAATTAATACATGCGAAACCTGTCTGAGACACAGCAAAATAAAAAGTCATGATACAA 2155
QY 699 -----GluAlaIleMetAlaGluLysAlaAsnAlaLeuGluGluLeuAlaLeuMe 715
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QY 735 pleuGluArgSer----- 739
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QY 740 -LeuLysGluAsnGluGluThrAsnGluPheGluIleLeuGluLysGluThrGluLysGlu 759
Db 2336 TTGTAAGACTCTCTCAGCTTAAGCGCAAGTTGAAAGATCTA-----GA 2377
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QY 804 -----AlaGluLeuAspGlyLysArgAlaAspAsn-----LeuGluLys 815
Db 2600 GAGGAGTGAATGCTCTTTAGAAAGCAGACAAAGTCCGAAAAATCTGCCATCTTAACAAA 2659
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QY 830 uLysLeuLysGluGluIlePheGluLeuLysGlnSerLeuSerAspAlaGluAlaValThr 850

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Db 2774 GAAGACAGAAACAGATGATCAAAAGTTTGTGGCTGAAACAAAGTCAGCCCATTTAGAACTT 2833
QY 870 sMetGluAspThrSerAsnIlePylTrAsn----- 880
Db 2834 ACAGAGACACTTGTGCTCAACAGAAATGTTGTGCTGAAACCTTAAGTCCCTTGAGAA 2893
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QY 912 -----SerAl 913
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Db 3314 AAAGAAATCTTAATTAAGATGCTTGCTTAATGATGACACATGCTTTGTGCAAAATAGG-- 3371
QY 971 eLeuProAsnGluValGluCysLeuLysAsnGlnIleSerLysAlaSerGluGluLeu 991
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QY 1017 -----GlnIleLeuGluLeuThrAspGluValThrHisThrGlnSerLysVal 1032
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QY 1048 -----AspLeuPheGluLysTyrIleArgAsnLysSerGluAlaGluAspLeuLeuArgGlu 1066
Db 3668 TCAAATCTTAAGATCAAGCAACATTTAGAACTCTGTGAAAGAAAGAGAGAGAGAGAAA 3727
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Db 3728 TCAATGATTTTAAACCTCAGATGATCTTGAAGTTAAAGAAATTTCTAGATATGTTA 3787
QY 1076 -----SerValGluValLysIleLeuAspThrLysHisGluLeuGluGlu 1090

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 Qy 1090 uThrl1eargAspIysGluGlnLeuLeuHisGluIysIysTyrPhePheGlnIalaMetG1 1110
 Db 3848 AAGTGAGAGAGAGAGAGAGTGCCTGCACATGAA-----TTACA 3886
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 Qy 1142 -----HisnLeuIleAlaLeuAlaThrGluArgAsnAnIleMetValCysLe 1158
 Db 3989 TTCAGGCGCTCATGAGTGTGCACAAACAGTCAAAACACATGACACCTTCAGTGTCTCT 4048
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 Qy 1178 rLeuGlnIalaGlnSerIleGlu-----LysSerAspLeuG1 1190
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 Qy 1212 ----- 1212
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 Qy 1230 uValThrGluIysLeuGlnInthrLeuGlnGluIleMetLysAsnIleThrIleGluArgAs 1250
 Db 4388 ATTCCAAGAGAAATTTATCTTATCTTACAAAGTGAACAAATTTTACATGATGACACACTG 4447
 Qy 1250 nGluLeuGlnInthrAsnPheGluAspLeuIysAlaGlnHisAspSerLeuIysGlnAspLe 1270
 Db 4448 TCAGATGAGCTCTAATAATGTCAGAGCTGCAGACCTATGACTCATTTAAAG----- 4499
 Qy 1270 uSerGluAsnIleGluGlnSerIleGluThrGlnAspGluLeuArgAlaIleGlnGluG1 1290
 Db 4500 -GCCGAAATTTGCTCTGTCA-----ACGAATCTGAGAAATCTTCAAGGTGA 4546
 Qy 1290 uLeuArgGluGlnIysGlnLeuValAspSerPheArgGlnGlnLeuLeuAspCysSerVa 1310
 Db 4547 CTGTGTGAAGAGATGACAGT-----GCCCTTGAGAGAGGGCTGCTTCATCCCTGTGC 4600
 Qy 1310 lGlyIleSerSerProAsnHisAspAlaValAlaAsnGlnIysValSerLeuGlyG1 1330
 Db 4601 ATCTCTTTGTGCTGCTGACAGCTCAAGCTTATGAC-----AGTTGGAGGA 4645
 Qy 1330 uValAsnSerLeuGlnSerGluMetLeuArgGlyGluArgAspGluLeuGlnInthrSerCy 1350
 Db 4646 C--TCTCTTTTACAGAGCTCTTTAGAA-----CAGACAGGAGA 4684
 Qy 1350 sLysAlaLeuValSerGluLeuGlu----- 1358
 Db 4685 TATGTCTCTTTTGAATAATTAGAGGGGCTGTTTCAACAAACAGTCACTAGTATGATGA 4744
 Qy 1359 -----LeuLeuArgAlaHisValIysSerValGluGluGluAsnLeuGluG1 1374
 Db 4745 AGTATTTTGCAGACGCTGCAGACCTATGTGACTCATTAAGGCCGAAATTTTGTCTT 4804

Qy 1374 eThrLysIysLeuAsnGlnLeuGluIysGluIleLeuGlnLysSerGlu-----G1 1391
 Db 4805 GTCACGCAATCTGCAAACTTTCAAGGTGACTGTGTGAAGAGATGACGCTGGCTTGA 4864
 Qy 1391 uSerGluValLeuIysSerMetLeuGluAsnLeuIysGluAspAsnAnIleLysLeu-- 1410
 Db 4865 GGAGGGCTGCTTCATCTCCGTATCTCTTGTGTGCTGACAGCTCTAGCTTTAGAG 4924
 Qy 1411 -----GluGlnIalaGluIlyrSer----- 1417
 Db 4925 TTTGGAGACTCTCTTTTACAGAGCTCTTTAGAACAGCAGGAGATATCTCTTTT 4984
 Qy 1418 -----SerLysGluAsnGlnPheSerGluGluValIlePhe----- 1429
 Db 4985 GAGTATTTAGAGGGGTGTTTTCAGCAAAACAGTGCAGTGTAGATGAATTTTTCAG 5044
 Qy 1430 -----SerGlySerGlnLysLeuVa 1436
 Db 5045 CAGTCTGCAGAGAGAACTGACCCAGAAAGAAACCCCTTCGCCGCCAGGAAAGCTGT 5104
 Qy 1436 lAspGluIle-----GluValLeuLysAlaGlnLeuLysAlaIleGluLys 1452
 Db 5105 TGAAGAGCTGAGTCCCTGTGTGAGGTGTACCGGAGTCCCTCGAAGACTAGAGAGA 5164
 Qy 1452 gLeuGlu-----IleLysAspArgAspTyrPheGluLeuValGlnThrAlaAs 1468
 Db 5165 AATGGAAGTCAAGGAGTATGAAATAATGAGAAATTCAAGAGCTCGACAGATTATTAAG 5224
 Qy 1468 nThrAsnLeuValGlu--GlyLysLeuGluThrProLeuGlnIalaPheIleGlu---- 1485
 Db 5225 TTTCAAGGCAAGCTTGAAGTCTGCTAGGAGAGAGATTTTTCAGAAATGAAACAGTG 5284
 Qy 1486 -GluAspSerIleAspArgArgSerGluGluMetGluIleLysValLeuGlyGluLysLe 1505
 Db 5285 GCAACAGAGCTGCACAGCTGACTGTGAGATGATGAGTCCAAAGTTGGCGGCAAGAAAGAA 5344
 Qy 1505 uGluArgAsnGlnIlyrLeuLeuGlu-----ArgLeuGlnGluGluLysLeuG1 1521
 Db 1521 uLeuSerAsnLysLeuGluIleLeuGlnLysGluIleMetGluThrSerValLeuLeuLysAs 1541
 Qy 5405 CTTAAGTCTCGG-----TCTTGTCTTCGCAT 5431
 Db 1541 pAspLeuGlnIlyrLeuLeuGlnSerLeuLeuSerGluAsnIleIleLeuLysGluAsnI1 1561
 Qy 5432 CGACACAGAGATGCTATTCAAGC-----CGAAATGAGAGCTG 5470
 Db 1561 eAspThrThrLeuLysHisHisSerAspThrGlnAlaGlnLeuGlnLys----- 1577
 Qy 5471 TGACATATCAAAAGAACTACTTCAGAACTTACAGAAAGAACACCAACCAAGCATGATGTTCA 5530
 Db 1578 -----ThrnGlnGluLeuGlnLeu-----AlaLys 1586
 Qy 5531 TCAGATTTTGATAAAGATGCTCAGCAGAGACTCAATTTAGACATTTGAGAAATTAAGTGA 5590
 Db 1586 sAsnLeuAlaIleAlaAspAspAsnCyProIleThrGlnGluLysGluThr----- 1604
 Qy 5591 GACGTGTCACTGAACCAACCAAGAGAGTGTCTGGGCAACAGTCCCAAGATTAACAAATTA 5650
 Db 1605 -----SerLysAspCysValHisProLeu----- 1612
 Qy 5651 TGAAGCTCCAGGAGAGATTAACCAAGGCTTTTCAAAATGCAATTTTGAATTTGTCAAT 5710
 Db 1613 -----GluGluLysIleLeuLe 1618
 Qy 5711 TTTGCTCTAATGCTTTGTGTAAGTATTTCTGGGGAATCAGAAATATTCATTA 5770
 Db 1618 uLeuThrGluIleuHisGlnIlyrThrAsnGluGlnGluIysLeuLeuHisGluLysAs 1638
 Qy 5771 TCTTCAACTGGGGTAAAGAGACATCAATGAGAAATTTAGATTAATTGATGTGATGA 5830

Db 7794 -----CAATTAAAGAGCTCATATGAGAGTGGACGCTGCTAATATGACCAAGAAC 7846
 Qy 2281 rleuLeuser-----SerLeuSerSerGluLeuGlnGlyGluThrGlnAlaHisIle 2298
 Db 7847 CTGTAAGGCCCAAGAGCAGAAATCTTAGTCAAGTAGAG----- 7886
 Qy 2288 sHisCysMetLeuAsnIleGlySerLeuSerSerThrLeuSerArgSerPheGlyse 2318
 Db 7887 -----TGCTT-----GAACTTGAGAAAGCTCAGTTGCTCAACAAAGCCTTGAGCA 7930
 Qy 2318 rLeuGlnThrGlnHisValGlyLeuAsnThrGlnLeuGlnThrLeuLeuAsnGlyPhe 2338
 Db 7921 GGCCTAAATATATATTATGTTTTCATCTTCAGTGAAGAGCCTCATTCAGAA----- 7985
 Qy 2338 sValValIlyrArgThrAlaAlaValGlyGluAspHisSerLeuIleGlyAspTyrGly 2358
 Db 7986 -----CTAGCAAGATGGCAACA 8002
 Qy 2358 sAspLeuAlaAlaGluGlnIlyrArgHisAspGluLeuArgLeuGlnLeuGlnCysLeuG 2378
 Db 8003 GAAATGGAGAAAGATGTAAGAAATCATGATGTAATAATCAAAATTCAGACCAAGA 8062
 Qy 2378 uGlnHisGlyArgIlyrSerSerSerAlaSerGluGluLeuIlyrPhe----- 2394
 Db 8063 GCAGCTTCTCTAACTGCTCCAGGTGGAAGAGAGACCAACTTGGAAAGAGCAAAA 8122
 Qy 2395 -CysGluIleGluPheLeuAsnGlnLeuLeuPheIlyrGlyAlaAsnIleIleGlnSerVa 2414
 Db 8123 CTTAGAACTGAAATCTGACGCTGGAATTTGGACAGCAAGATCCCAAGCTCAATCCAA 8182
 Qy 2414 IGlAspAspPheSerGluValGlnValPheLeuAsnGlnValGlySerThrLeuGlnG 2434
 Db 8183 AAATGCTCTTTCAGACACATTAAGTCTGAGAGTCTTAACAAGATCTTAGAGA 8242
 Qy 2434 uGlnLeuGlnIlyrHisIlyrGlyPheMetGlnIlyrLeuGlnGluPheGly----- 2450
 Db 8243 TGAGCTTGAATTTGACAAATAATGACAAATATGCTTGTGTAAGAAAGTAACAAATGAC 8302
 Qy 2451 -----AspLeuHisValAspAlaIlyrIlyr-----Le 2459
 Db 8303 TGCAAGAGAACTGAGCTGACAGAGGAAATGCATGATGACAGCAAGAAACAGCAGACT 8362
 Qy 2459 uSerGlnGluMetGlnGlnGlnIlyrAsnArgIleAlaSerThrIleGlnLeuLeuThrIly 2479
 Db 8363 GCAGAAAGAACTGACAGTGAAGAAATAATGAGTACCTGAGAGTTCAGTTCTTGA 8422
 Qy 2479 sArgLeuIlyrAlaValIleGlnSerIlyrIleGlnArgGluIleThrValIlyrLeuAsnG 2499
 Db 8423 AGAAATTAAGAGC-----AGCAAGATCA----- 8447
 Qy 2499 nPheGlnAlaIlyrLeuGlnGlnIlyrGlyGlnIlyrAsnIlyrGluLeuMetArgArgMetG 2519
 Db 8448 -----TTGAAGAGAGCTCACACTAGAAATATGTAATGTAAGAG----- 8486
 Qy 2519 uHisHisGlyProSerAlaSerValMetGlnGlnIlyrAsnAlaArgLeuLeuGlyIlyle 2539
 Db 8487 -----AGCCTAGATTGCATGACCAAAACAGAGTGAAGAAAGAGG----- 8528
 Qy 2539 uIlyrThrValGlnAspGluSerIlyrGlyLeuGlnIlyrSerArgIleGlyMetLeuGlnAla 2559
 Db 8529 -----AAAGTGAGAGAGAAATGCTGAATATCAGTACG----- 8564
 Qy 2559 uLeuAsnLeuValIlyrAspAspAlaMetHisIlyrGlyIlyr-----ValAlaIlele 2577
 Db 8565 -----CTTCATGAACTGAAAGAAACCCAGGCTTGTCT 8599
 Qy 2577 uGlnAspIlyrLeuLeuSerArgAlaAlaGlnAlaGlnIlyrLeuAsnAlaMetGlnValIlyle 2597
 Db 8600 TTGTGAC-----ACAAACAAACAGATATGAAGTAATAATCCAGACATCCAGAGAAAT 8653
 Qy 2597 uThrIlyrGlyGlnAspAsnLeuGlnAlaAlaMetIlyrGlnIleGlnAsnLeuGlnIlyrMe 2617
 Db 8654 GACTTCTTAAGAAGATGCTCTCAGTTCACAGAGCTGAGATGACCTTTTAACTCAG 8713

Qy 2617 cValAlaIlyrGlyAlaValProTyrIlyrGlnGluIlyrLeuAspAsn----- 2631
 Db 8714 T-----AAAGAAAGCTCAATATTTATTTGAAAGCTACTAC 8749
 Qy 2632 -----LeuIlyrThrIlyrValIlyrIleGlnMetGluIlyrIleGlyIlyr----- 2646
 Db 8750 TCAGATTTTGGAGATTTGAAGAAACCAAGATGACATCAATCAAAATATGTAATCAGTT 8809
 Qy 2647 -----SerIlyrAlaThrAspGlnGluIleAlaTyrLeuIlyrSerCys----- 2660
 Db 8810 GAAGAGGAAATATGAACCTGCCAGGCGGAAATGAAGTTGTTGATCAAAATCCTGTAACA 8869
 Qy 2661 -LeuGlnAspIlyrGlnGlnIlyrLeuArgArgLeuIlyrGlnIlyrLeuArgAlaGlnAla 2680
 Db 8870 CTTGGAAGAGGAAAGAGATCTGACAAAGAACTCTCAACTTCAAGCTGCACAGA 8929
 Qy 2680 sAspAsnAspThrThrValCysValProIlyrAspTyrGlnIlyrAlaSerThrPheProVa 2700
 Db 8930 GAAGCAGAAACA----- 8942
 Qy 2700 IThrCysGlyGlyGlySerGlyIleValGlnSerThrAlaMetLeuValLeuGlnSerG 2720
 Db 8943 -----GGTACTGTTATGATGATCAAGGTCGATGAATTAACAATGA 8983
 Qy 2720 u-----IlyrAlaAlaLeuGln-----ArgGluLeuSerHisTyrIlyrIly 2733
 Db 8984 GATCAAGAACTGAAAGAACTTTGAAGAAACCAAGAGCGACGATGAATACTTGA 9043
 Qy 2733 sIlyrTyrHisIleLeuSerArgThrMetSerSerSerGluAspArgIlyrIlyrThrIlyrAl 2753
 Db 9044 TAAGTACTGCTCTTG-----CTTATAAGCATTAATAAGTTAGAGAAAGCTAAAGA 9094
 Qy 2753 sIlyrSerAspAlaHisSerSerHisIlyrGlySerSerHis-----ArgG 2768
 Db 9095 GATGTAGAGACACAAAGTGCCTATCTGTTCACAGCAATCTAAACAAGATTCGCCGAG 9154
 Qy 2768 ySerProHisIlyrThrGlnIlyrThrTyrArgHisGlyProValIlyrProGlnIlyrSerG 2788
 Db 9155 GTCTCTCT-----TTGCTAGGTCGCAATGTTTCCAGAGCACTTCCAT 9196
 Qy 2788 cProSerLeu-----HisLeuGlnIlyrSerProIlyrIlyrLe 2799
 Db 9197 CCTTTCTTACTGAAAGAGCTTATCATCTGCGCCAAATTAAGCTTACAGCAGAGCA 9256
 Qy 2799 rGlnIlyrSer-----ThrIlyrArgValIlyrSerProAsnArgSerGluIlyrI 2815
 Db 9257 AAGATCCAGTGAATATGAGAAATGTAAGAGACCAACACTGCTACCCAGAGAGCTT 9316
 Qy 2815 rSer-----GlnLeuValMetSer-----ProGly-IlyrThrGlyMet 2828
 Db 9317 TTCTTAATAAAAGCAAGAAAGATCATGATGATTCACCTGCGAGAAACA----- 9369
 Qy 2828 sIlyrHisIleLeuSerProSerIlyrValGlyLeuHisIlyr-----IlyrAspAlaLeu 2846
 Db 9370 -----CGAAGGTACTAGTTGAGCCAGAGGACTTCCAGAAAGTTGTAAGAAAGGTTTGC 9427
 Qy 2846 eProAsnArg-----SerGluMetProThrGlnHisIly 2857
 Db 9428 TGACATCCCGACAGAAAGACTAGCCCATATATCTCGGAGAAACAAACATGAGCA----- 9483
 Qy 2857 aIleSerProGlyIlyrThrIlyrLeuHisIlyrAsn-----LeuThrG 2871
 Db 9484 -----CTCGAGCCAGCCCGCTGCGTGCACAAAGTTAGCGGTATCCCACTGAGTCTCG 9541
 Qy 2871 IuserThrLeuPheAspAsnLeuSerSerProCysIlyrGlnGlnIlyrValGlnIlyrAsn 2891
 Db 9542 CAAGAAATC-----TTGCAGAGTCTTCCAAACCAACAGCTGTGTGCA-----G 9586
 Qy 2891 euAsnSerProIlyrGlyIlyrLeuPheAsp-----ValIlyrSer 2904
 Db 9587 CAGATCACAAAAGTCAAAGTTGCTCAGCGGAGCCAGTATTCAGGACCACTCTCTCG 9646

QY 2904 ysserMetProTyrcysProserGln-----PhepheAspAsnSerLysLeuGlyA 2921
 Db 9647 AGAACCCACGACGAAATCCGTCGCAATTAATCTTCGAGAGAACTCCAGCTGACAG 9706
 QY 2921 sPheSerGluLeuAsnThrAlaGluSerAsnAspLysSerGlnAlaGluAsnTrp 2939
 Db 9707 CCCAGAGAGGCGCTGAGGCTCAAGCAGGCGGACTTGTCCAGCCCCCAAGGCTGG 9762
 RESULT 4
 PCT-US95-16216-2
 ; Sequence 2, Application PC/TUS9516216
 ; GENERAL INFORMATION:
 ; APPLICANT: Yen, Timothy J.
 ; APPLICANT: Ratner, Jerome B.
 ; TITLE OF INVENTION: Nucleic Acid Encoding a Transiently
 ; TITLE OF INVENTION: Expressed Kinetochores Protein, and Methods of Use
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
 ; STREET: 1601 Market Street Suite 720
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19103-2307
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; FILING DATE:
 ; APPLICATION NUMBER: PCT/US95/16216
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/353,700
 ; FILING DATE: 09-DEC-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Reed, Janet E.
 ; REGISTRATION NUMBER: 36,252
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 563-4100
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 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10136 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; PCT-US95-16216-2
 Alignment Scores:
 Pred. No.: 5,46e-83 Length: 10136
 Score: 1153.00 Matches: 736
 Percent Similarity: 37.84% Conservatve: 581
 Best Local Similarity: 21.15% Mismatches: 1163
 Query Match: 7.81% Indels: 1001
 DB: 5 Gaps: 144
 US-09-724-584-1 (1-2954) x PCT-US95-16216-2 (1-10136)
 QY 81 PheAlaTyrglnThrSerSerGlyLysThrTrpThrMetMetGlyThrProAsnSer 100
 Db 465 TTCGAGAGAGCACTGAAATTCAGGCAA----- 494
 QY 101 LeuGlyIleIleProGlnAlaIleGlnGluValPheLysIleIleGlnGluIleProAsn 120
 Db 495 -----AAACAATAGAAAAAAGCTGAGAGCAAGAACTTAAAGG 530
 QY 121 ArgGluPheLeuLeuArgValSerTrpMetGluIleTrpAsnGluThrValLysAspLeu 140
 Db ----- 140

Db 531 TGTAAATCTGAGCTTGAAAGAACCAAGAGCTGGCAGTCTGCAATGCTCTCTGAT 590
 QY 141 LeuCyAspAspArgArgLys-----LysProLeuGluIleArgGluAspPheAsn 157
 Db 591 CCATCAATATACCAACAAAAATTTTCAACTCCATCAACCAACCAAGTCAATATATAGT 650
 QY 158 ArgAsnValIleValAlaAspLeuThrGluGluLeuValMetValProGlnIleValIle 177
 Db 651 GGTTCCAGTAT---GAAGATCTTAAAGAAAAATTAATAAGAGCTTGA----- 698
 QY 178 GlnTrpIleLysGlyGlyGlyLysAsnArgHisTrpGlyGluThrLysMetAsnAspHis 197
 Db 699 -----GAACGAAAAAGATTAGAGCAGAGGTTAAAGCTTCAGAGCT 740
 QY 198 SerSerArgSerHisThrIlePheArgMetIleValGluSerArgAsp-----ArgAsn 215
 Db 741 AAAAAAGCAAGCGAGACTTCTCCACAGCCACCAATGATATCCAGCATTCGCCGCGCAT 800
 QY 216 AspProThrAsnSerGlu---AsnCysAspGlyAlaValMetValSerHisLeuAsnLeu 234
 Db 801 CAGGCTTCATCATCTGTCTCTCATGGCAGCAAGAAAGCCCAAGTCACTTTCA--- 857
 QY 235 ValAspLeuAlaGlySerGluArgAlaSerGlnThrGlyAlaGlyValArgLeuLys 254
 Db 858 -----TCTAATTCCAAGAACT----- 875
 QY 255 GluGlyCysAsnIleAsnArgSerLeuPheIleLeuGlyGlnValIleLysLysLeuSer 274
 Db 876 -----CCAAATAGAGAGATTCTCT 896
 QY 275 AspGlyGlnAlaGlyGlyPheIleAsnTrpArgAspSerLysLeuThr 290
 Db 897 GCATCTTACTTTCTGCGGAAGTACAGTGATCCAGTCGATCAATTCGAAATAGGG 956
 QY 291 ---ArgIleLeuGlnAsnSerLeuGlyGlyAsnAlaLysThrValIleIleCysThrIle 309
 Db 957 AAAAGAGATGCTAATACAGATTTCTTGCAATTCAGC----- 995
 QY 310 ThrProValSerPheAspGluThrLeuSerThrLeuGlnPheAlaSerThrAlaLysHis 329
 Db 996 AGTCCTCATCTTTGGAT-----CAATTAAGGCGCAATCAAGAG 1037
 QY 330 ValArgAsnThrProHisValAsnGluValLeuAspAspGluAlaLeuLeuLysArgTyr 349
 Db 1038 CTAGAGAAAC-----AAGATTATGAGTTG-----GAATCAGCCCTGCAAGACAT 1082
 QY 350 ArgLysGluIle-----LeuAspLeuLysGlnLeuGlu--- 361
 Db 1083 GAAAAAGAAATGAAAGCCCAAGTGAATTAAGTTCAAGAACTCCAACTCCAACTGAGAGAA 1142
 QY 362 ---AsnLeuGluSerSerSerGluThrLysAlaGlnAlaMetAlaLysGluGluHisThr 380
 Db 1143 GCAAAAGTGGAATTAATGAAAAAGAAAGATTGAAACAAATGTGGGATGAACTAGAG 1202
 QY 381 GlnLeuLeuAlaGluIleLysGlnLeu-----HisLysGluArgGluAspArgIle 397
 Db 1203 AGAACAACAGCAAAATACGACGCGGTCAACCAAGTATATGTCATTGGAACAAAACTG 1262
 QY 398 TrpHisLeuThrAsnIleValAlaLysSerGlnGluSerGlnGln----- 413
 Db 1263 AAAAAATTGACGGAATTTGAGTTGTCAGCCGCAAAATGCAAGAAAGTCCAGATCTTCT 1322
 QY 414 ---AspGlnArgValLysArgLysArgValThrTrpAlaPro---GlyLysIleGln 431
 Db 1323 CTGGAACAGAAATTAAGAAAAAGAAAGAGATTCAAGAGAGCTCCGCTCAACAG 1382
 QY 432 AsnSerLeuHisLysSerGlyValSerAspPheAspMetLeuSerArgLeu---ProGlyAs 451
 Db 1383 CGTTCTTTCCAAACACTGAGCAAGAGTCAATCCAGATTAAGGCACTTCAACAGAGG 1442
 QY 451 nPheSerLysLysAlaLysPheSerAspMetProSerPheProGluIleAspAspSerVa 471
 Db 1443 TTACAGCAAG-----CCAAGAT 1460

QY 471 lcystrglupheserAspPheaspapalaleusermetcAspSerAsnGlyLeas 491
 DB 1461 ATGCACAAAGCTCTGCAGCGCTGAACTGATTAACATCATCTAGTAAAGCAACGCTAGAA 1520
 QY 491 palaglutPheAsnLeuAlaserLyserValThrHisArgGluLeuTherSerLeuHisGlnSe 511
 DB 1521 AACAAATTTGGAGAGTTTAAGCAAAAGTTGTGC-AAGCTGAACAGCGCTTCCAGCGGAG 1579
 QY 511 rwcilLeapPheGlyGlnIleSerAspSerValGlnPheHisAspSerSerLyseGluAs 531
 DB 1580 TCAGATCAAGAGAAAGAGACTGAGAGAGAGATGAGAG-----GAATGAGAGAGAGAAA 1633
 QY 531 nglnleuglnTyrlLeuProLyasPserGlyAspMetAlaGluCyArgLyAlaserPh 551
 DB 1634 CAACCTCTTAAGAGCTCACTGTGAGCAAAAGCCAGAGAAAGTCTGCACCTGAGAGGAGA 1693
 QY 551 egluLyseGluIleTherSerLeuGlnGlnLeuGlnSerLyseGluGluGluLyseGlu 571
 DB 1694 ACTCAAGACATCAAAACAGTGTTTAAATCAGACCCAGAAATTTTGCAGAAAGAAATGAAAGC 1753
 QY 571 uLeuValGlnSerPheGluLeuLyseIleAlaGluLeuGlnGlnLeuSerValIysAl 591
 DB 1754 GAAGATACCTCTCAGAGAAACCATGTTAAGATCTTCAAGAAAAATA----- 1802
 QY 591 alyAsnLeuGluMetValThrAsnSerArgLysHisSerIle----- 605
 DB 1803 -----AATCAGCAAGAAAACTCTTGACTTGTAGAAAAACTGAA 1840
 QY 606 -----AsnAlaGluValGlnThrAspValGluLyseGluValAlaArgLyseGlu 621
 DB 1841 GCTTGCTGCTGCTGATCTGAAAAGCAGAGATTTCTTCAAGACCTTTTGAAGAAAAG 1900
 QY 621 uMetSerValLeuGlyAspSerGlyTyrlAsnAlaserAsnSerAspLeuGlnAspSerSe 641
 DB 1901 A-----GAACATCACATTAACCACTTAATGATTAAGTAAAGACAGACAGA 1945
 QY 641 rValAspGlyLyseArgLeuSerSerSerHisAspGlyCyseIleGluHisArgLyseMetLe 661
 DB 1946 GAAAGAGTCCAAAGCCTTGCTGAGTGT-----TT 1975
 QY 661 uGlnGlnLyseIleValAspLeuGlnGlnPheIleGluAsnLeuAsnLyse----- 677
 DB 1976 AAGAGTTAAAGAAAGAAATATGAGAAATTTGAAAGAGAAAACTCTTTTCTTTGTTG 2035
 QY 678 -LyseArgLysAsnAspLyse-----GlnLyseSerGlnGlnAspPheMetGluSe 694
 DB 2036 GAAAAGTGAAGAAAGAAAGCTTTTAAGTCAAGTGAATGCAAGAAAGAAAGAACTTGAGAGG 2095
 QY 694 r-----IleGlnLeuCyse----- 698
 DB 2096 TAAAAATTAATCACTTGAAAGAACTTGCTGAAAGACACAGCAAAATAAAGTCAATGAATACAA 2155
 QY 699 -----GluAlaIleMetAlaGluLyseValAlaAsnAlaLeuGlnGluLeuAlaLeuMe 715
 DB 2156 CGAGAGAGTAAAGACGCTGAGATGACAGAGAAAGCTTAAGTGTGAGATCAAGAAAGCT 2215
 QY 715 rArgAspAsnPheAspAsnIleIleLeuGlnAsnGlnThrLeuLyseArgGluIleAlaAs 735
 DB 2216 TCACAAAGCTTAAAGACATTAAGTCAAGTGAAGAGACCCAGAAAGCTTAATATGGA 2275
 QY 735 pLeuGlnArgSer----- 739
 DB 2276 GCTTAAGCAGCAAGCTGAGTCTCAGATCAGAAACATCAGAAAGAAATGAATATGTG 2335
 QY 740 -LeuLyseGlnAsnGlnGlnThrAsnGlnPheGlnIleLeuGlnLyseGluThrGlnLyseGlu 759
 DB 2336 TTGGAAGACTTCTCAAGCTTACCTGCGCAAGCTTAAGATCTA-----GA 2377
 QY 759 uHisGlnAlaGlnLeuIleHisGlnIleGlySerLeuLyseValGluAsnAlaGlu 779
 DB 2378 ACACAAAGCTTCAAGTACTGTCA-----AATGAATTAATGCAAGAAAGACCG 2422

QY 779 uMetTyrlAsnGlnAsnLeuGlnGluAspLeuGlnThrTyrlSerThyLeuLeuLyseGluGlu 799
 DB 2423 GGTTCAC-----CAAGACTTGACATGCCGAATATAGAGCTTCAGAGGATCTGTAAATCCAA 2479
 QY 799 nglnIleGlnLeu----- 803
 DB 2480 AAGATGCTCTGTGAGCAAAATGAAGATCATCAGAGAAAGTCTTTGGCTTTGATCAGCA 2539
 QY 803 ----- 803
 DB 2540 GCCTCGCATGATCATCTCTTGTCAAAATATATGAGAAACAAGAGAGCATGCTTCAGCA 2599
 QY 804 -----AlaGluLeuAspGlyLyseArgAlaAspAsn-----LeuGlnLy 815
 DB 2600 GAGGAGTGATGTCTGTTAAGAACAGACCAAGTCCGAAAAATTTCTGCCATCTTACAAAA 2659
 QY 815 rArgValAlaArgAsnPheAspLeuSerValSerMet-----GlyAspSerGlu 830
 DB 2660 TAGAGTTGATTCACCTGAATTTTCAATTGAGTCTCAAAAACAGATGAATCAGACCTGCA 2719
 QY 830 uLyseLeuCyseGlnGlnIlePheGlnLeuLyseGlnSerLeuSerAspAlaGluAlaValTh 850
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 QY 850 rArgAspAlaGlnLyseGluCyseSerPheLeuArgSerGluAsnLeuGlnLeuLyseGluLy 870
 DB 2774 GAAGCAGAACAGATGATCAATCAAAAGTTTGTGCTGAACAAACATCAGCCGATTAAGTAA 2833
 QY 870 sMetGlnAspThrSerAsnIlePheAsn-----Gln 880
 DB 2834 ACAGAGAGACATTTGTGCTGCACAGATGTTGTGCTGAACCTTAAGTCCCTTGAGAA 2893
 QY 880 nLyseGluLyseAlaAlaserLeuPheGlnLyseGlnLeuGlnThrGluLyseSerAsnTyrl 900
 DB 2894 CAAGGAAAAAGAGCTGCAACTTTTAATGATTAAGTAAAGTGAAGAACTGAGCAGAGATTTCA 2953
 QY 900 sLyseMetGlu-----AlaAspLeuGlnLyseGlnLeuGln----- 911
 DB 2954 AGAATTAATAAAGAGCAACCATCTACTGAAGACCTCTTAAGAGAGCTTAACAACTTTATC 3013
 QY 912 -----SerAl 913
 DB 3014 CGAAACCTTAAGCTTGAGAGAAAGAAAGAAATGAGTTCATCTTTTAAATAAAGGGA 3073
 QY 913 aPheAsnGlnIleAsnTyrlLeuAsnGlyLeuLeu-----AlaGlyLy 927
 DB 3074 AATTGAAGAGCTGACCCCAAGAGAAATGGAGACTTTAAGAAATTAATGATCTTAAATCA 3133
 QY 927 sValProArgAspLeuLeuSerArgVal-----GluLeuGlu 939
 DB 3134 AGAGAAAGATGAACCTTAATCCAGAAAAAGTGAAGTTTGCAAAACCTATATAGATGAAGGGA 3193
 QY 939 uLyseLyseValSerGluPheSerLyseGlnLeuGln----- 950
 DB 3194 GAAAGACATTTCAAGTATCTGATCAAGTCAAGCAAGAAAGAACTTATTACTTCAAG 3253
 QY 951 -----LyseAlaLeuGluGlu 955
 DB 3254 ATGTGAAGAAACCGAAATGATATGAGATCTTATGCTCAAAAATCAAGAGCAGACAGA 3313
 QY 955 uLyseAsnAla-----LeuGlnAsnGlnValThrCyseLeuSerGluTyrlLysePh 971
 DB 3314 AAAGAAATCTTAATTAAGATGCTTGCTTAATGAAGTGAAGTCTGCTTGTGAAATAGG-- 3371
 QY 971 eLeuProAsnGlnValGluCyseLeuLyseAsnGlnIleSerLyseValAspSerGlnGluIleMe 991
 DB 3372 -----AAAAATGATTTGAACACGCTTAAGAGAGCATTTGCAAGAGAACCAAGATTTCTT 3427
 QY 991 eLeu-----LeuLyseGlnGlnGlnIlePheHisSerAlaserIleSerLyseGlnGlnIleI 1010
 DB 3428 AACAAATTAAGATTTGCTGTAAGAAAGAAATCAGAAATCTGATGCTTAAGTGTGAGAGACAGT 3487
 QY 1010 eMetGln-----GluGlnSerGlu----- 1016

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Db      3488 GCACCAAGCTGTGAGATCTGAGATGACAGATACCAAAACAAATTCCTAGAGCGAGCTGG 3547
QY      1017 -----GlnIleuGlnIleuThrAspGluValThrHisThrGlnSerIysVa 1032
Db      3548 TGGTTTAAGCAAAATCATGACTTTAAAGAAACAAACAAATTCGAAAAGAGT 3607
QY      1032 1-----GlnGlnThrGluGlnIleuThrIleuGluMetIleuLysMetHisAsp-- 1047
Db      3608 TAATGACTTATTAACAAGATGAACAGCTGATGAAGATGAAGTAACTAAACCTGATG 3667
QY      1048 ----AspLeuPheGlnIleuThrIleuArgAsnIleuSerGluAlaGluAspLeuIleuArg 1066
Db      3668 TCAAAATCTGAATCAAGAACCAATTAAGAACTCTGTGAAGAAAGAGAGAGTGAAGAAA 3727
QY      1066 uMetGluAsnLeuLysGlnIleuThrMetGlu----- 1075
Db      3728 TCAATGTAAATTTTAAACCTCAGATGATCTTGAAGTAAAGAAATTTCTTACATAGTTA 3787
QY      1076 -----SerValGluValIleuLysIleuAlaAspThrLysHisGluLeuGlu 1090
Db      3788 TAATGCCAGCTGTGTGCAATTAAGAGCTATGCTAAGAAATTAAGAAATTAATTAACCTCAG 3847
QY      1090 uThrIleuArgAspLysGlnIleuLeuHisGluIleuLysIleuThrPhePheGlnIleuMetG 1110
Db      3848 AAGTGAGAGAGAGAGAGAGAGTGCCTGCAGCATGAA-----TTACA 3886
QY      1110 nThrIleuPheProIleuThrProLeuSerAspSerLeuProSerLysLeuValGlu 1130
Db      3887 GAGCAAT-----AGAGAGATCTTGAACCAAGCAATTTGCAACACAT 3928
QY      1130 yaSerGlnAspProIleuIleuLysnAspTyr----- 1141
Db      3929 GCAGTCACAGAAATTAAGTGCCTTAAAGACTGTGAATAGATGCCGAAAGAAAGTATAT 3988
QY      1142 -----HisAsnLeuIleAlaLeuAlaThrGluArgAsnAlaMetValCysIle 1158
Db      3989 TTCAGGCGCTCATGATTTGCACAACTCAAAACCAATGCACACCTTCAGTCTCTCT 4048
QY      1158 uGlnThrGluArgAsnSerLeuLysGlnIleuValIleuAspLeuThrGlnLeuGlnSe 1178
Db      4049 GCAAACAAACATGAACACAGCTGAATGAG-----CTAGAGAAATATGTGAAT 4096
QY      1178 rIeuGlnAlaGlnSerIleGlu-----LysSerAspLeu 1190
Db      4097 ACTGCGAGCTGAAAGATATGAATCTGTAAGCTGAATGATTAAGGTCTGAAGTATAT 4156
QY      1190 nLysProLysGlnAspLeuGlnIleuValIleuLysLeuLeuGluMetGluLeu 1210
Db      4157 CACAGCACTAGGAAATAGCAGAGAGAGTAGGAAATTAATTAAGTAAATATAT 4216
QY      1210 uLysGlu----- 1212
Db      4217 AAATGATGACAGTGTCTTCTCCATGTGATGATTAAGTGAAGACATACAGAGAGTGAAT 4276
QY      1212 ----- 1212
Db      4277 TGGTGAACAACAATGAACACACCTGTCTTGGCTCCATTGGACGAGAGTAAATTC 4336
QY      1213 -----HisLeuThrAspSerGlnLeuSerIleuLysLeuGlnIleuGluAsnLeu 1230
Db      4337 CTACAGACACTTGACA-----TTGTCAACAACAAGAGTTCAATGCACTTGCCGA 4387
QY      1230 uValThrGluLysLeuGlnThrLeuGlnIleuGluMetLysAsnIleuThrIleuGluArg 1250
Db      4388 ATTGCAAGAGAAATCTTATCTTACAAAGTGAACAACAATTTTACATGATGATGCACCTG 4447
QY      1250 nGluLeuGlnThrAsnPheGluAspLeuLysAlaGluHisAspSerLeuLysGlnAspLe 1270
Db      4448 TCAGATGAGCTTAATATGTCTGAGAGCTGACAGACCTATGTGACTCATTAAG----- 4499
QY      1270 uSerGluAsnIleuGlnIleuGlnIleuThrGlnAspGluLeuArgAlaGlnIleu 1290
Db      1290 ----- 1290

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Db      4500 -GCCGAAATTTGCTTGTCA-----ACGAATCTGAGAAATTTCAAGTCA 4546
QY      1290 uLeuArgGluGlnLysGlnLeuValAspSerPheArgGlnIleuLeuAspCysSerVa 1310
Db      4547 CTGTGTAAGAGAGATGCACCTG-----GGCTTGAGAGAGGGGCTGTTCCATCCCTGTC 4600
QY      1310 1GlyIleuSerProAsnHisAspAlaValAlaAsnGlnIleuLysValSerLeuGlu 1330
Db      4601 ATCCCTCTGTGCTGACAGCTGACAGCTTATGAC-----AGTTGGAGGA 4645
QY      1330 uValAsnSerLeuGlnSerGlnMetLeuArgGluValArgAspGluLeuGlnIleuSerCy 1350
Db      4646 C---TCCTCTTTTACAGAGCTCTTTTGA-----CAGACGAGGA 4684
QY      1350 sLysAlaLeuValSerGluLeu----- 1358
Db      4685 TATGCTCTTTTGAAGTAAATTAAGAGGGCTTTACACAAACAGTGCAGTATAGTGA 4744
QY      1359 -----LeuLeuArgAlaHisValLysSerValGluGluAsnLeuGlu 1374
Db      4745 AGTATTTTGACAGAGCTGACAGACCTATGACTCATTAAGCCGAAATTTGCTT 4804
QY      1374 eThrLysLysLeuGlnGlnIleuGluLysGluIleuGlnLysSerGlu-----G 1391
Db      4805 GTCAACGAATCTGAGAACTTTCAAGAGTGTGTGAGAGATGACAGCTGGCTTGA 4864
QY      1391 uSerGluValLeuLysSerMetLeuGluAsnLeuLysGluAspAsnLysLeuLys-- 1410
Db      4865 GGAGGGCTCGTTCATCCCTGATCTCTGATCTTGTGTGCTGACAGCTTACTGCTTACAG 4924
QY      1411 -----GlnGlnAlaGluIleuLysSer----- 1417
Db      4925 TTTGGAGACTCTCTTTTACAGAGCTTTTGAACAGACAGAGATATGCTCTTT 4984
QY      1418 -----SerLysGluAsnGlnPheSerLeuGlnIleuValPhe----- 1429
Db      4985 GAGTAAATTTAGAGGGCTTTTTCAGCAACAGTGCAGTGAATGAATATTTTTCAG 5044
QY      1430 -----SerGlySerGlnLysLeuVa 1436
Db      5045 CAGTCTGACAGAGAGATCTGACACGAGAAAGAACCCCTTCCGCCACGAGAGGGTGT 5104
QY      1436 lAspGluLe-----GluValLeuLysAlaGlnLeuLysAlaAlaGluIleuArg 1452
Db      5105 TGAAGAGCTTGAATCCCTCTGTGAGGTGACCGGCACTCCCTGAGAGCTTGAAGAGAA 5164
QY      1452 gLeuGlu-----IleLysAspArgAspTyrPheGlnLeuValGlnThrAlaAs 1468
Db      5165 AATGGAAGTCAGAGGATTTGAAAAATTAAGAAATTCAGAGCTGAGCACTTATTAAG 5224
QY      1468 nThrAsnLeuValGlu--GlyLysLeuGlnThrProLeuGlnAlaAspHisGlu----- 1485
Db      5225 TTTGAAAGGCAAGAGCTTGAAGCTTGAAGAGCAGTATTTGTCAAGAAATGAACAGTG 5284
QY      1486 -GluAspSerIleAspArgArgSerGlnIleuMetGluIleuValLeuGlnLysLe 1505
Db      5285 GCAACAGACCTGACCAAGCGTGACTGTGAGATGAGTCCCAAGTGCAGCGGCAAAAAAGAA 5344
QY      1505 uGluArgAsnGlnIleuLeuGlu-----ArgLeuGlnGluLysLeuGlu 1521
Db      5345 ACAAGCGAACAACACTGCACTTGAAGTGAAGAGCAACAGCTCCACACTACAAAGTTCGA 5404
QY      1521 uLeuSerAsnLysLeuGlnIleuGlnLysGluMetGluThrSerValLeuLysAs 1541
Db      5405 CTTAAGTTCGCG-----TCTTGTGCTTGCAAT 5431
QY      1541 pAspLeuGlnIleuLysLeuGlnSerLeuSerGluAsnIleuIleuLysGluAsn 1561
Db      5432 CGACACAGAAAGATCTATTAAGC-----CGAATGAGAGCTG 5470
QY      1561 eaAspThrThrLeuLysHisSerAspThrGlnAlaGlnIleuGlnLys----- 1577
Db      5471 TGACATATCAAAAGACATTAATTCAGAACTACAGAAAGAACCCAAACATGATGTTCGA 5530

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Db      7589  CCAAAGCTCGAGAGCTCGAATTTAGATTGTTCTTCTTAAAGTCAGAGAAAAAGAAATCT 7648
Qy      2181  eAsmenlyslEuaAlaGluValylLysGluValAspGluLeuLeuGlnHisLeuSerSe 2201
Db      7649  GCAAAATGATTTACAAAAAGACAGACGGAATCTCGAATTA----- 7691
Qy      2201  rleuylsegluInleuAspGlnlleGlnMeGluLeuArgAspGluLysLeuArgAsnTy 2221
Db      7692  -----GAAATATAAATTTCATCTTTGAAAT-- 7718
Qy      2221  rGluLeuCysGluLysMetAspIleMeGluLysGluIleSerValLeuArgLeuMeG1 2241
Db      7719  -----ATTTCGAAAAAAGA 7735
Qy      2241  nAsnGluProGlnGlnGlnGluAspAspValAlaGluArgMetAspIleLeuGlnSerAr 2261
Db      7736  GCAAGAGAAAGTGAAGTGAAGAAAAATCAAGACCTGCCATGGAGATCTTCAACA-- 7793
Qy      2261  gAsnGlnGluIleGlnGluLeuMetGluLysLysIleSerAlaValTyrSerGluGlnHisTh 2281
Db      7794  -----CAATTAAGAAGCTCAATGAGAGAGTGGAGCCCTGCATATATGACCAAGAAC 7846
Qy      2281  rleuLeuSer-----SerLeuSerSerGluLeuGlnLysGluThrGluAlaHisLys 2298
Db      7847  CTGTAAAGCCAAAGACAGATCTTAGTCAAGTACAG----- 7886
Qy      2298  sHisCysMetLeuAsnIleLysGluSerLeuSerSerThrLeuSerArgSerPheGlySe 2318
Db      7887  -----TGTCTT-----GAACTTGAGAAAGCTCAGTTGCTTACAGCCCTTGATGA 7930
Qy      2318  rleuGlnThrGlnHisValLysLeuAsnThrGlnGlnGlnThrLeuLeuAsnLysPheLys 2338
Db      7931  GCCCAAAATATATTTATTTGTTTTCATCTTCAAGTGAAGCCCTCAATCAAGAA----- 7985
Qy      2338  sValValTyrArgThrAlaAlaValLysGluAspHisSerLeuIleLysAspTyrGluLys 2358
Db      7986  -----GTAGAGATGGCAAGCA 8002
Qy      2358  sAspLeuAlaAlaGluGlnLysArgHisAspGluLeuArgLeuGlnLysGlnCysLeuG1 2378
Db      8003  GAAATCTGAGAGAGAGATGAAAGAAATCAGTACGTAAGTGAAGAAATTCAAATTCAGACCA 8062
Qy      2378  uGlnHisGluLysArgLysTrpSerAspSerAlaSerGluGluLeuLysPhe----- 2394
Db      8063  GCAGCTTGCTCTTAACTGTCCAGCTGGAAGAGACCACAACTTTGAGAGACCAAA 8122
Qy      2395  -CysGluIleGluPheLeuAsnGluLeuLeuPheLysLysAlaAsnIleIleGlnSerVa 2414
Db      8123  CTTAGAACTGAGAAATCTGACGGTGAATTGGAGCAAGATCCCAAGTCTACATCCAA 8182
Qy      2414  lGlnAspAspPheSerGluValGlnValPheLeuGlnGlnValGlySerThrLeuGlnG1 2434
Db      8183  AAATGCTCTTTGACAGACACATTTAGAGTCTGACAGATTCTTAACAAGATCTAGAGAA 8242
Qy      2434  uGluLeuGlu-----HisLysLysGlyPheMetGlnThrLeuGlnGluPheGly----- 2450
Db      8243  TGAAGCTTGAATTGACAAAATGACAAAATGCTTTGTGAAAAGAAATGAACAAATGAC 8302
Qy      2451  -----AspLeuHisValAspAlaLysLys-----Le 2459
Db      8303  TCCAAAGCAAACTGAGCTGACAGAGGAAATGATGATGACAGAAACACAGAGCT 8362
Qy      2459  uSerGluGluMetGlnGlnGlnGlnAsnArgAlaIleAsnSerThrIleGlnLeuLeuThrLy 2479
Db      8363  GCAAGAGAAAGCTGAGAGAGAAATAGGCTGAGAGAGTGGAGAGTGGAGTCTTGGCA 8422
Qy      2479  sArgLeuLysAlaValAlaGlnSerLysIleGlnArgGluIleThrValTyrLeuAsnG1 2499
Db      8423  AGAATTAAGAGC-----AGCAAAAGATCAA----- 8447
Qy      2499  nPheGluAlaLysLeuGlnGlnLysLysGluGlnAsnLysGluLeuMetArgArgMetG1 2519
Db      8448  -----TTGAAGAGCTCACACTAGAAAAATAGTGAATTTGAAGAG----- 8486
Qy      2519  uHisHisGlyProSerAlaSerValMetGluGlnGlnGlnAsnAlaArgLeuGlnGlyLe 2539
Db      8487  -----AGCTTGATTTGCATGCAACAAGACCAAGCTGAGAAAGAGAGG----- 8528
Qy      2539  uLysThrValGlnAspGluSerLysLysLeuGlnSerArgIleLysMetLeuGlnGlnG1 2559
Db      8529  -----AAAGTGAGAGAGAAATAGCTGAATATCATCGTCAAG----- 8564
Qy      2559  uLeuAsnLeuValLysAspAspAlaMetHisLysGlyLysLys-----ValAlaIleLe 2577
Db      8565  -----CTTCATGAAGCTGAAGAAAGAACACAGCGCTTTGCT 8599
Qy      2577  uGlnAspLysLeuLeuSerArgAsnAlaGlnAlaGlnLeuAsnAlaMetGlnValLysLe 2597
Db      8600  TTTGGAC-----ACAAACCAACAGTATGAAGTGAATCCAGACATACCGAGAGAAAT 8653
Qy      2597  uThrLysLysGlnAspAsnLeuGlnAlaAlaMetLysGluIleGlnAsnLeuGlnLysMe 2617
Db      8654  GACTTCTAAGAGAGATGCTCAGTTCACAGAAAGCTGGAGATGACCTTTTAAAGCTAG 8713
Qy      2617  tValAlaLysGluAlaValProTyrLysGluGlnIleAspAsn----- 2631
Db      8714  T-----AAAGAAAGCTCAATAATTCATTTGAAGCTACTAC 8749
Qy      2632  -LeuLysThrLysValValLysIleGlnMetGluLysIleLysTyr----- 2646
Db      8750  TCAGATTTTGAAGAAATGAAAGAAACCAAGATGACCAATCTTAAATATGTAAATCAGTT 8809
Qy      2647  -----SerLysAlaThrAspGlnGlnIleAlaTyrLeuLysSerCys----- 2660
Db      8810  GAAGAGAAAGAAATGAACGTGCCAGGCAAAATGAAGTTGTTGATCAAAATCTGTAAACA 8869
Qy      2661  -LeuGluAspLysGluGlnGluLysLeuArgArgLeuLysGlnGlnLeuArgAlaGlnAl 2680
Db      8870  GCTGGAAGAGAGAAAGAGATGCTGCAGAAAGAACTCTTCAACTTCAGCTGCACAGCA 8929
Qy      2680  sAspAsnAspThrThrValCysValProLysAspTyrGlnLysAlaSerThrPheProVa 2700
Db      8930  GAAGCAAGAAACA----- 8942
Qy      2700  lThrCysGlyGlyGlySerGlyIleValGlnSerThrAlaMetLeuValLeuGlnSerG1 2720
Db      8943  -----GGACTGTTATGATACCAAGCTGATGAATTAACAATCA 8983
Qy      2720  u-----LysAlaAlaLeuGlu-----ArgGluLeuSerHisTyrLysLys 2733
Db      8984  GATCAAAAGAACTGAAGAACTCTTGAAGAAAAACCAAGAGAGCAGATGAATACTTGA 9043
Qy      2733  sLysTyrHisHisLeuSerArgThrMetSerSerSerGluAspArgLysLysThrLysAl 2753
Db      9044  TAAAGTACGTTCCCTG-----CTTATACCCATGAAGAAATTTAGAGAAAGCTTAAAGA 9094
Qy      2753  sLysSerAspAlaHisSerSerHisThrGlySerSerHis-----ArgG1 2768
Db      9095  GATTTAGACACACAAAGTCCATCTGTTCACAGCAATTAACAAGATTTCCGAGG 9154
Qy      2768  ySerProHisLysThrGluThrTyrArgHisGlyProValThrProGluArgSerGluMe 2788
Db      9155  GTCTCCCT-----TTGCTAGTCAAGTTGTTCCAGAGCAATCTCCAAAT 9196
Qy      2788  tProSerLeu-----HisLeuGlySerProLysLysSe 2799
Db      9197  CCTTCTGTTACTGAAAAAGGTTTATCATCTGGCCAAATTAACCTTCAGCAAGAGAGCA 9256
Qy      2799  rGluSerSer-----ThrLysArgValAlaSerProAsnArgSerGluLety 2815
Db      9257  AAGATCACTGGAATATGAGAGAAATGAGAGACCAACACTCTTACCCAGAGAGCTT 9316
Qy      2815  rSer-----GlnLeuValMetSer-----ProGly-LysThrGlyMetH 2828
Db      9317  TTTCAAAAAAGCAAGAAAGATGATGATGATTACCTTGACAGAGACA----- 9369

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QY	786	GlulGluAspLeuGlnThrIlysrThrIlysrLeuLeuIyrgLgInGlnIuIleGlnLeuAlaGlu	805
Db	1279	GTC-----GCTGAACCAAGTACGCCATTAGATTACAGGAAGAACACTTCGCTCAC	1332
QY	806	LeuIArgIyAsrAlaAspAsn-----LeuGlnIyIyValArgAsnPhesLeu	822
Db	1333	CAGAAAGTTGTTGTCCTGAACCTTAAGTCCCTTGAAGAACAGAAAGAACCTGCACCTT	1392
QY	823	SerValSerMetCylAspSerGluIyIySerCysGluGlnIlePheGlnLeuIyGlnSer	842
Db	1393	TTAAATGATPAAGTAAACCTAGACG-----GCAGGATTCAAGAAATTTAAAGAGGC	1446
QY	843	LeuSerAspAlaGlnAlaValThrArgAspAlaGlnIySgIyCysSerPheLeuArgSer	862
Db	1447	-----AACCATCTACTGAAGCTCTCTAAAGACCTCAACACTTTA---TCC	1491
QY	863	GluAsnLeuGlnLeuIySgIySerMetGluAspThrSerAsnTPyrAsnGlnIySgIu	882
Db	1492	GAACCCCTAAGCTTAGAGAGAAAGAAATGAGTTCATCTTCTCTAAATTAAGGAGAA	1551
QY	883	IySAlaAlaSerLeuPheGlnIySgInLeuGlnIuThrGluIySerAsnTPyrIyValyMet	902
Db	1552	-----ATTGAAGCTGACCCCAAGAAATGGGACTCTTAAGGAATTT	1593
QY	903	GluAlaAspLeuGlnIySgIu-----LeuGlnSerAlaPheAsnGlnIleAsn	918
Db	1594	ATGATCCTCTTAATCAAGAGAAATGAACTTAATCCAGAAAGTAGAGTTTGCAAC	1653
QY	919	TyrLeuAsnGlyLeuLeuAlaGlyIyValProArgAspLeuLeuSerArgValGluLeu	938
Db	1654	TTATATAGAT-----GAAAGG	1668
QY	939	GluIyIyValSerGluPheSerIySgInLeuGlu-----	950
Db	1669	GAGAAAGCATTTGACAGTTATCTGATCAGTACAAGAGAAACCTATTTTACTACA	1728
QY	951	-----IySAlaLeuGlu	954
Db	1729	AGATGTGAAGAAACCGGAATGCATATGAGATCTTAGTCMAAAATACAAAGACGACAG	1788
QY	955	GluIyAsnAla-----LeuGlnAsnGlnValThrCysLeuSerGluIyIyIy	970
Db	1789	GAAAGATTCCTAAATTAGAAATGCTTGCTAAATGAATGACACTAGCTTGTGAAATAG	1848
QY	971	PheLeuProArgGlnValGluCysLeuIyAsnGlnIleSerIySAlaSerGluIuIle	990
Db	1849	-----AAAAATGAGTTGGAACACTTAAAGAACACTTTCAAGAGAACCTCAAGATTC	1902
QY	991	MetLeu-----LeuIySgInGlnIyGlnHisSerAlaSerIleIleSerIySgInIuIle	1009
Db	1903	TTAACAAATTTAGCATTTGCTGAAGAAAGAAATCAGAAATGATGATGCTAGAGTTGGAGACA	1962
QY	1010	IleMetGln-----GluGlnSerGlu-----	1016
Db	1963	GTGACAGAACTCTGAGATCTGAGATACAGATTAACCAAAACAATCTTAAGACCGAGGCT	2022
QY	1017	-----GlnIleLeuGlnLeuThrAspGlnValIhrHisThrGlnSerIyS	1031
Db	2023	GGTGCTTTAAAGCAAGAAATCATACTTTAAAGGAGAAACAAATATGCAAAAGGAA	2082
QY	1032	Val-----GlnIuThrGlnGluGlnTPyrIleuGlnMetIySylMetHisAsp	1047
Db	2083	GTTAATGACTTATTACAGAGAAATGAAACACTGATGATGAAGTAAAGACTAAACATGAA	2142
QY	1048	-----AspLeuPheGlnIyIyIleArgAsnIySerGluAlaGluAspLeuLeuArg	1065
Db	2143	TGTCAAAATCTAGACATAGAACCAATTAAGGAACCTGTGTGAAGAAAGAGAGGTGAGACA	2202
QY	1066	GluMetGluAsnLeuIySgIyThrMetGlu-----	1075
Db	2203	AATCAATGTATATTTAAACCTCAGATGATCTTGAAGTTAAAGAAATTTCTCTAGATAGT	2262
QY	1076	-----SerValGluValIyIleAlaAspThrIyHisGluLeuGln	1089

Db	2263	TATATGCGGAGTTGGTGCATATTGAAAGCTATGCTAAAGAAATTAAAGAAATTAAACTTTCG	232
Qy	1090	GIuThrIleArgAspIysGIuGlnLeuHisGIuLysIleTyrPhePheGlnAlaMet	110
Db	2323	GAAGGTAGAGAGAGAAAGAGTCCCTGCAGCATGAA-----TTA	236
Qy	1110	GIuThrIlePheProIleThrProLeuSerAspSerLeuProProSerLysLeuValGlu	112
Db	2362	CAGACAAATT-----AGAGCAGATCTTGAAACCAAGCAATTTGGCAAGC	240
Qy	1130	GIYAsnSerGlnAspProIleGluIleAsnAspTyr-----	114
Db	2404	ATGCAGTCACAAAGAAATTAGTGCCCTTTAAAGACTGTGAATATGATCGGAGAGAAAGTAT	246
Qy	1142	-----HisAsnLeuIleAlaLeuAlaThrGluArgAsnAsnIleMetValCys	115
Db	2464	ATTTCAGGGCCTCATATAGTTGCTCAACAACTCAAAACGAAATGACACACCTTCAGTCTCT	252
Qy	1158	LeuGluThrGluArgAsnSerLeuLysGIuGlnValIleAspLeuAsnThrGlnLeuGln	117
Db	2524	CTCGAAACCAACATGAAACAGCTGATGAG-----CTAGAGAAATATGTGAA	257
Qy	1178	SetLeuGlnAlaGlnSerIleGlu-----LysSerAspLeu	118
Db	2572	ATACTCAGGCTGAAAGATGATGATCACTGTAAGCTGATGATGATGATTCAGAGCTCAAGATGT	263
Qy	1190	GlnLysProLysGlnAspLeuGluGluGluValLysLeuLeuLeuGluMetGluLeu	120
Db	2632	ATACACGCAACTAGAGAAATGGCAGAGAGAGGTAGGAAACTACTAAATGAAATGTAATA	269
Qy	1210	LeuLysGly-----	121
Db	2692	TTAAATGATGAGAGATGCTCTTCATGATGATGATTAGTGAAGACATACACAGAGGTGA	275
Qy	1212	-----	121
Db	2752	TTTGTGGAAACAACCAATGACAGACACCTGTCTTTGGCTCCATTGAGACAGAGTAAT	281
Qy	1213	-----HisLeuThrAspSerGlnLeuSerIleGluLysLeuGlnLeuGlnAsnLeu	122
Db	2812	TCCTACGACACTTGACA-----TTGTACAGCAAAAGAACTTCAATGACACTTGGCC	286
Qy	1230	GluValThrGluLysLeuGlnThrLeuGlnGluMetLysAsnIleThrIleGluArg	124
Db	2863	GAATTGCAAGAGAAATCTTATCTTTCAAAAGTGAACAACAATTTTCATGATCAGCAC	292
Qy	1250	AsnGluLeuGlnThrAsnPheGlnAspLeuLysAlaGluHisAspSerLeuLysGlnAsp	126
Db	2923	TGTCAAGATGAGCTCTTAATATGTCAGAGCTGCAGACCTATGTTGACTCTTTAAAG-----	297
Qy	1270	LeuSerGlnAsnIleGluGlnSerIleGluThrGlnAspGluLeuArgAlaIleGlnGlu	128
Db	2977	---GCCGAAATTTGGCTCTTGCA-----ACGAATCTGAGAAACTTTCAAAGGT	302
Qy	1290	GluLeuArgGluGlnLysGlnLeuValAspSerPheArgGlnGlnLeuAspCysSer	130
Db	3022	GACTTGGTGAAAGAGATCAGCTG-----GCCTTGAGAGGGGCTGTGTTCCATCCCTG	307
Qy	1310	ValGlyIleSerSerProAsnHisAspAlaValAlaAsnGlnGluLysValSerLeuGly	132
Db	3076	TCATCTCTTGTGCTGCAGACAGCTTATGCTTAGC-----AGTTTGGGA	312
Qy	1330	GluValAsnSerLeuGlnSerGlnMetLeuArgGluArgAspGluLeuGlnThrSer	134
Db	3121	GAC---TCCTCTTTTACAGACTCTTTTGA-----CACACAGCA	315
Qy	1350	CysLysAlaLeuValSerGluLeuGlu---LeuLeuArgAlaHisValLysSerValGlu	136
Db	3160	GATATGCTCTTTTGAGTAATTTGAAGGGGCTCTTCAGCAAAACCAAGTCAGGTATGAT	321
Qy	1369	GlyLeuLeuLeuGluIleThrLysLysLeuAsnGlyLeuGluLysGluIleLeuGlyLys	138

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Db      3220 -----GAACTATTT-----TCACAGCTCTGCAGAGAGAACTGACCAG 3261
QY      1389 SerGluGluSer-----GluValLeuLysSerMetLeuGluAan 1401
Db      3262 AAGAAACCCCTTCGGCCCGAGGAGGTGTTGAAGAGCTTGAGTCCCTGTGTGGGTG 3321
QY      1402 LeuLysGluAspAsnLysLeuLysGluGlnAlaGluLutYrSerSerLysGluAan 1421
Db      3322 TACCGGCACTCCCTCGAAGAGCTGAGAAGAAAATGAAAAGTCAAGGATTTAGAAAAT 3381
QY      1422 GlnPheSerLeuGluGluValPheSerGlySerGlnLysLeuValAspGluLeuVal 1441
Db      3382 AAG-----GAAATTCAAAG 3396
QY      1442 LeuLysAlaGlnLeuLysAlaAlaGluGluValArgLeuGluLutLysAspArgPhe 1461
Db      3397 CTCGAGCACTTTATTAAGTTCTGAAGCAAGAGCTTGACTGCTTAGAGACGATTTTG 3456
QY      1462 GluLeuValGlnThrAlaSerThrAsnLeuValGluGlyLysLeuGluThrProLeuGln 1481
Db      3457 TCA-----GAA 3462
QY      1482 AlaAspHisGluGluAspSerLysAspArgSerGluGluMetGluLutLysValLeu 1501
Db      3463 AATGAACAGTGGCAACAGAACTGACACAGCTGACTCTGAGATGAGTCCAAAGTTGGCG 3522
QY      1502 GlyGluLysLeuGluArgAsnGlnTyrLeuLeuGlu-----ArgLeuGlnGlu 1517
Db      3523 GCAGAAAGAAACAGACGAGAACACTGTCATTTGAGCTGAAAGTAGACAGACTCCAGCTA 3582
QY      1518 GluLysLeuGluLysSerAsnLysLeuGluLutLeuGlnLysGluMetLutThrSerVal 1537
Db      3583 CAAGCTCTGGACTTAAGTTCTCG-----TCT 3609
QY      1538 LeuLeuLysAspAspLeuGlnGlnLutLysLeuGluSerLeuLeuSerGluAsnLutLeu 1557
Db      3610 TTGCTGGCATCGACACAGAAAGTGTATTCAAGC-----CGA 3648
QY      1558 LysGluAsnLutLeuAspThrThrLeuLysHisLysAspThrGlnAlaGlnLeuGlnLys 1577
Db      3649 AATGAGAGCTGACATATCAAAAGAACACTTCTGAAACTACAGAAACACCAACCAAG 3708
QY      1578 -----ThrGlnGluLeuGlnLeu----- 1584
Db      3709 CATGATGTTCACTCAATTTGTGATTAAGATGCTCAGAGAGCTTCATTAACATTTAG 3768
QY      1585 -----AlaLysAsnLeuAlaIleAlaLysAspAsnLysProLutThrGlnGluLys 1602
Db      3769 AAAAATACTGAGACTGTGCTATTGAAGCCACAGAGAGTCTCTGGGAAACAGTCCCA 3828
QY      1603 GluThr-----SerAlaAspCysValHis 1610
Db      3829 GATACCAATTATGAGCTTCAGAGGAGATATAAACCCAGAGGCTTTCAAGATGACTTCT 3888
QY      1611 ProLeu-----GluGlu 1614
Db      3889 GAATTCATATTTCTGGTCTTAATGCTTTGTACTTATGATTTCTCGGGAATAGAGA 3948
QY      1615 LysIleLeuLeuLeuThrGluLutLysHisGlnLutLysAsnGluGlnLutLysLeu 1634
Db      3949 GATATCCATTAATCTTCAACTGCGGGAAGAAAGACATCAATGAGAAATTTGAGATTACTT 4008
QY      1635 HisGluLysAsnGluLeuGlnAlaGlnValGluLeuLysCysGluValGluHisLeu 1654
Db      4009 CATGTATAGAGGACCGTACAG-----AAAGTTGAAAGTTTG 4047
QY      1655 MetLysSerMetIleGluSerLysSerSerLeuGluSerLeuGlnHisGluLysHisAsp 1674
Db      4048 CTAAATGAATGAATGAATTAAGCTCAAAATC-----CATTTA 4086
QY      1675 ThrGlnGlnGlnLeuLeuAla-----LeuLysGlnGlnMetGln 1687
Db      4087 CAGGAGGTAACTAATGACCAAAATGAGACATGATGAATTTGAAAAAATTAAGTTGGG 4146

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QY      1688 ValValThrGlnGluLysGluLeuGlnGlnIleThrHisGluHisLeuThrAlaGluVal 1707
Db      4147 GAACCTTAAGAAAGAAAACCTCAGATTTTAAGTGAATAATGGAATATTTTCTGTGTAC 4206
QY      1708 AspHisLeuLysGluAsnLutLeu-----GlyLeuAsnPheLysAsnGluAlaGln 1725
Db      4207 CAGGAGTTACTCAGAGAGTAGAATCTTGAAGGCTCAATTCGATTTAGAAATGCAAT 4266
QY      1726 ---GlnLysThrThrLysGluGlnCysLeuLeuAsnGluAsnLys----- 1739
Db      4267 GCAGATTAATCATCACTGAGATATTTGAGATTAATGTCGCCAAGGTGAATGACAGCTCG 4326
QY      1740 -----GluLeuGluGlnSerGlnHisArgLeuGlnCysGlu----- 1751
Db      4327 AAGAGAGATTTCTTGATGTGAAAAATGACCTGAGATGAGATGATCGGAGAAAGCTTAC 4386
QY      1752 -----IleGluGluMetLysSerLeuLysAspLysGluSer 1764
Db      4387 ATTGACATGAAGCCCTTACTGAGAGGCTGACTTAGAGTACTTCAACAGAGAACTTA 4446
QY      1765 AlaLeuGluThrLeuLysGluSerGluGlnLysValIle--AsnLeuAsnGlnMet 1783
Db      4447 TGTTAGAAAAAAGACAATGAATAAAGCAGAGATTATGTCTGCTTGAAAGAACTC 4506
QY      1784 GluMetValMetLeuGluMetGluGluLutLutLysAsnSerGlnArgThrValIleAlaGlu 1803
Db      4507 TCAGTGGTCACAAAGTGAAGAAACAGCTTCTTGAGAAATTGATATGCTTCAAAAAA 4566
QY      1804 Arg-----AspGlnLeuGlnAspLeuArgLysLeuValGluMetSerIleGlu 1820
Db      4567 ACCAGGCACTGATCAAGTTGTCTGAAAAATGAAGAGAAAACAA--GAGCTTGG 4623
QY      1821 Thr-----GlnAspAspLeuArgLysVal 1828
Db      4624 TCTCAATCAAGTGAAGTCTCCATTCATTCAGTGGCAGAGCAGAGGAGTGAAGGAAAG 4683
QY      1823 GlnGluValAlaGlnGlnGlnLutLysAspLysValGlnGluLeuThrSerGlnLutSerVal 1848
Db      4684 ACGGAATCTCTTCAACTTTGTCTGTGATGAGTGAAGCTGTAAACACAAATCAT 4743
QY      1849 LeuGlnGluLysIleSerLeuLeuGlnAsnGlnMetLeuThrAsnValAlaThrValLys 1868
Db      4744 CTCGAGAAAGCTCAGAGTTGGAAGAAAGCTCAGAGGCTGTCTTGAACAAATGT 4803
QY      1869 GluThrLeuSerGluArgAspAspLeuAsnGlnSerLysGlnHisLeuPheSerGluIle 1888
Db      4804 GAGCTGAAACCAATGCACTGAATGAATAAGAAAGAAATTCCTGTCAAGGATCT 4863
QY      1889 GluThrLeuSerLeuSerLeuLysGluLysGluPhe-----Ala 1901
Db      4864 GAAAGCTTCGAGCGCAGACTGATGAAATCAGATTTTGAAGAAAGCTGAATCTTCAAGGCC 4923
QY      1902 LeuGluGlnAlaGluLysAspLysAlaAspAlaIleArgLysThrIleAspLutThrGlu 1921
Db      4924 TTGGAGCGGCACTGTGTGAAGAGTGAAGTTCGATTGAGGCTGAGCTCAACACAGAG 4983
QY      1922 LysIleSerAsnIle-----Glu 1927
Db      4984 GAAGTCATCACTGATGAGAAAGGCATCGAGAAATCGAGATTTGCGATTGAGGCGCATGA 5043
QY      1928 GlnGlnLeuLeuGlnAlaIleThrAsnLeuLysGluThrLutLutLutLutLutLutLut 1947
Db      5044 AAGAAAGCACTGCACATGCGAGAGAACTGAAGAAACCGAGCGGGAATGATGATCATT 5103
QY      1948 IleGlnCysLysGluGlnLeuAlaLeuAsnThrGlnHisLeuArgGluThrLeuLysSer 1967
Db      5104 -----AAGGATTAAGTTGAGAACTTGAAGGGAATTTGAGATGCGAGAAAGAAC 5154
QY      1968 LysAspLeuAlaLeuGlyLysMetGlnGlnLutArgAspArgLutAlaAsnLysValIle 1987
Db      5155 CAGGAGCTAAGGATTT-----CTTGATGCCGAGATTCCAAGAC----- 5193

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QY	1998	AlaLeuThrGlnIuLysMetSerSerLeuGlnGlnIleAsnGluAsnValThrThreLeu	2007
Db	5194	-----GAAGTAGAGACTCTAAACACACAAATGAGAGATGCCAGAACCTG	5241
QY	2008	LysGlnGlu-----GlyIuLysGluThrPheTyLeuGln	2020
Db	5242	AAAGTTTGGAAATTGACCTTGTCACTTAAGTCTGAAAAAGAAAATCTGCACAAAAC	5301
QY	2021	ArgProSerLysGlnGlnSerSerGergInMetGluLeuArgGluSerLeuLysThr	2040
Db	5302	ATACAGAAAAACAGAGTCAGTTGTCAGAACTACAGACAGATTACTCTTCATTAAAAAGT	5361
QY	2041	LysAspLeuGlnLeuGlnGluAlaIleLysGluLieserGluAlaThr-----	2056
Db	5362	CTGTTAGAGAAAGAGACCAAGACCAAGATACAGATCAAAAGAAATCTMAAACCTGCAGTG	5421
QY	2057	-----AsnGluIleLysAsnLeuThrAlaLysIleSerSerLeu-----Glu	2070
Db	5422	GAGATGCTTCAGAAATCAGTTAAAGAGCTAAATGAGCAGTAGACCTTGTGTGTGCAC	5481
QY	2071	GlnGluIleLeuGln-----AsnAlaSerIleLeuAsnGluAlaValSerGluArgLysAsn	2089
Db	5482	CAAGAAATTATGAAGCCACACAGAAACAGAGTCTAGACCCACCAATATGAGAGAGACATCAG	5541
QY	2090	LeuArgHisSerLysGlnGlnLeuValSerGluLeuGlu-----GlnLeu	2104
Db	5542	CTGAAATAATAGCATTTGAAAGAGCTGAGACCCGCTTGAGAGCTGATGAAAGAGACAGCTC	5601
QY	2105	SerLeuThrLeuLysSerArgAspHisAlaPheAlaGlnSerLysArgGluLysAspGlu	2124
Db	5602	TGTGCTTACACAACTGAG-----GAAAGTGACATCATGCAGATTTA	5646
QY	2125	AlaValAsnLysIleAlaSerLeuAlaGlnGluIleLysIleLeuThrLysGluMetAsp	2144
Db	5647	CTTAAGGAGAGGTGAGACCTTGAAAGAGAGCTAGAGATAGCAGAGACAAACCAAGAG	5706
QY	2145	-----GluPheArgAspSerLys-----GluSerLeuGlnGlnSer	2157
Db	5707	CATGCAGCTCTTGAGCAGAGAAATCCAAAGAGAGCTAGAGACCTTAAAGCAAATA	5766
QY	2158	SerHisLeuSerGlnGluLeuGlySerThrLysThrGlnLeuGlnMetLeuLysGlnGln	2177
Db	5767	GAAAGGATGACCCCAAGCTGTGAGAGCTGTGAAATTAGTGTGTTACTATAGGTCAGAA	5826
QY	2178	LysGlnAspIleAsnAsnLysLeuAlaGluLysValLysGluValAspGluLeuLeuGln	2197
Db	5827	AAAGAAATCTGCACAAATGAATTCACAAAAAGCAGACGCAATATCTGAATT-----	5880
QY	2198	HisLeuSerSerLeuLysGlnGlnLeuAspGlnIleGlnMetGluLeuArgAsnGluLys	2217
Db	5881	-----GAAATATATAATTCATCA	5898
QY	2218	LeuArgAsnLysGlnLeuLysGlnLysMetAspIleMetGluLysGluLieserValLeu	2237
Db	5899	TTTGAAAT-----ATTGTG	5913
QY	2238	ArgLeuMetGlnAsnGluProGlnGlnGlnGluAspArgValAlaGluArgMetAspIle	2257
Db	5914	CAAGAAAAAGCAGAAAGATACAGATGAAAGAAAAATCAAGCATGCCATGAGATG	5973
QY	2258	LeuGlnSerArgAsnGlnGluIleGlnGlnLeuMetGluLysIleSerAlaValLysSer	2277
Db	5974	CTTCAACA-----CAATTMAAAGCTCAATGAGAGATGGACCCCTCATATAT	6024
QY	2278	GluGlnHisThrLeuLeuSerSerLeuSerSerGluLeuGlnLysGluThrGluAlaHis	2297
Db	6025	GACCAA-----GAAGCCTGT	6039
QY	2298	LysHisCysMetLeuAsnIleLysGlnSerLeuSerSerThrLeuSerArgSerPheGly	2317
Db	6040	AAG-----GCCAAAGCAGGAATCTTAGTAGCAAGTAGAG	6075
QY	2318	SerLeuGlnThrGlnHisValLysLeuAsnThrGlnLeuGlnThrLeuLeuAsnLysPhe	2337

Db	6076	TGCTTTGAACCTTGAAGGCTCAGTCTGCTCAAGGCTTGAATGAGCCAAAAATTAATAT	6133
Qy	2338	LysValValTyrArgThrAlaAlaValIsgLusPniSerLeuIleLysAspTyrGlu	2357
Db	6136	ATTGTTTTCACATCTTCAGTG-----AATGGCCTATTCAAGAGTAGAA	6180
Qy	2358	LysAspLeuAlaAlaGluGlnLysArgHisAspGlu-----LeuArgGluGlnLeu	2374
Db	6181	GATGCAACAGCAAACTAGAGAGAGATGATACAGAAATCAGTAGACTGAAAAATTCMAATT	6244
Qy	2375	GlnCysLeuGlnGlnHisGlyArgGlyTrpSerAspSerAlaSerGluGlnLeuLysPhe	2394
Db	6241	CAAGACCAAGAGGAGCTTGTCTCTTAACCTGTCTCCAGGTGAAAGAGACCAACTTTGG	6300
Qy	2395	-----CysGluIleGluPheLeuAsnGlnLeuLeuPheLysAlaAsnIle	2410
Db	6301	AAGAGCAAAACTTAGACTGAGAAATGTGACAGTGGAAATTGGACAGAAATGCCAAGTGG	6366
Qy	2411	IleGlnSerValGlnAspAspPheSerGluValGlnValPheLeuAsnGlnValGlySer	2431
Db	6361	CTACACTCCAAAAATGCTCTTTGCGAGGACACATTGAAAGTGTGCGACAGTCTTCAACAG	6422
Qy	2431	ThrLeuGlnGluGlnLeuGlu-----HisLysGlySerPheMetGlnTrpLeuGlnGluPhe	2445
Db	6421	AATCTAGAGATGAGCTGTAATTGACAAAAATGCAAAAAATGCTCTTGTGAAAAAGTGA	6480
Qy	2450	Gly-----AspLeuHisValAspAlaLysLys	2458
Db	6481	AACAAATAGACTGCAGAAAGAAATGAGCTGCAGAGGAGAAATGCATGAGATGGACAGAA	6540
Qy	2459	-----LeuSerGluGlyMetGlnGlnGlnLysAsnArgArgIleAlaSerThrIleGln	2475
Db	6541	ACAGCAGACCTGCAGAAAGAACTCAGTGGAGAAAAATAGCTAGCTGAGAGATTTGACAG	6600
Qy	2476	LeuLeuThrLysArgLeuLysAlaValValGlnSerLysIleGlnArgGluIleThrVal	2499
Db	6601	TTACTGTTGGAAAGATTAAGAGC-----AGCAAAAGATCA-----	6638
Qy	2496	TyrLeuAsnGlnPheGluAlaLysLeuGlnGlnLysLysGlnGlnAsnLysGluLeuMet	2515
Db	6637	-----TTGAGAGAGCTCCACACTAGAAAAATAGCAATTGAAAG	6672
Qy	2516	ArgArgMetGluHisHisGlyProSerAlaSerValMetGluGlnGlnAsnAlaArgLeu	2535
Db	6673	AAG-----AGCCTAGATTGCATGCACAAAGACCAAGTGGAAAA	6711
Qy	2536	LeuGlyIleLeuLysThrValGlnAspGlnSerLysLysLeuGlnSerArgIleLysMet	2555
Db	6712	GAAAGG-----AAAGTAGAGAGGAAATAGCTGAATTCAGCTACGG-----	6753
Qy	2556	LeuGluAsnGlnLeuAsnLeuValLysAspAspAlaMetHisLysGlyGluLys-----	2572
Db	6754	-----CTTCATGAAGCTGAAAAAGAAAC	6777
Qy	2574	ValAlaIleLeuGlnAspLysLeuLeuSerArgAsnAlaGluValGluLeuAsnAlaMet	2593
Db	6778	CAGGCTTTCCTTTGGAC-----ACAAACAAACAGATGAGAGTAAGTAATCCAGCATAC	6831
Qy	2594	GlnValLysLeuThrLysLysGlnAspAsnLeuGlnAlaAlaMetLysGluIleGluAsn	2613
Db	6832	CGAGAGAAATGACTCTTAAAGAAAGAAATGCTCAGTTACAGAAAGCTGGAATATGACCTT	6891
Qy	2614	LeuGlnLysMetValAlaLysGlyAlaValProTyrLysGluGluIleAspAsn-----	2631
Db	6892	TTTAAAGTCTAGT-----AAAGAAAGCTCAATTAATTCATTG	6922
Qy	2632	-----LeuLysThrLysValValLysIleGluMetGluLysIleLysTyr	2646
Db	6928	AAAGTACTACTCAGATTTTGGAGAAATGAAAGAAACCAAGATGAGCAACTTAATAATAT	6987
Qy	2647	-----SerLysAlaThrAspGlnGluIleAlaTyrLeuLys	2655

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Db      6988 GTAATCAGTTGAGAGAGAAATGAACTGCCAGGGGAAATGAAAGTTGTTGATCAAA 7047
Qy      2655 SerCys-----LeuGlnAspIysGlnGlnGlyLeuArgLeuLysGlnGlnLeuArg 2676
Db      7048 TCCTGTAAACAGCTGGAGAGAGAAAGAGATATCTGCAGAAAGAACTCTCTCAACTTCAA 7107
Qy      2677 ArgAlaGlnAlaAspAsnAspThrThrValCysValProLysAspTyrGlnLysAlaSer 2696
Db      7108 GCTGCACAGAGAGAGAGAGAAACA----- 7131
Qy      2697 ThrPheProValThrCysGlnGlyGlySerGlyIleValGlnSerThrAlaMetLeuVal 2716
Db      7132 -----GGTACTGTTATGGATATCAAGGTCATGAA 7161
Qy      2717 LeuGlnSerGlu-----LysAlaAlaLeuGln-----ArgLysLeuSer 2729
Db      7162 TTAAACAATGAGATCAAGAACTGAAAGAACTTTGAAAGAAACCAAGGAGGAGAT 7221
Qy      2730 HisTyrLysLysLysTyrHisHisLysSerArgThrMetSerSerSerGlnAspArgLys 2749
Db      7222 GAATTACTTGATTAAGTACTGTTCTTG-----CTTATTAAGCCATGAAAGTTAGAG 7272
Qy      2750 LysThrLysAlaLysSerAspAlaHisSerSerHisThrGlySerSerHis----- 2766
Db      7273 AAAGCTAAAGAGATGTTAGACACAAAGTCCCATCTGTTCACAGCAATCTTAACA 7332
Qy      2767 -----ArgGlySerProHisLysThrGlnThrTyrArgHisGlyProValThrProGlu 2784
Db      7333 GATCCCGAGGCTCTCT-----TTGCTAGTCCAGTTGTTCCAGAG 7374
Qy      2785 ArgSerGlnMetProSerLeu-----HisLeuGlySerProLysLysSerGlnSer 2801
Db      7375 CCATCTCCCACTCTCTGTTACTGAAAGAGTTATCATCTGCCAAATAAAGCTTCA 7434
Qy      2802 SerThrLysArgValLysSer-----ProAsnArg 2811
Db      7435 GGCAAGAGGCAAGATCCAGTGAATATGGAGAAATGGAGAGACCAACACTGCTTACC 7494
Qy      2812 SerGlnLysTyrSer-----GlnLeuValMetSer-----ProGlyLys 2824
Db      7495 CCAGAGAGCTTTTCTTAAAAAAGCAAGAAAGCATGATGATGATTCACCTCGAGAA 7554
Qy      2824 ----- 2824
Db      7555 GACACGAGAGTACTGATTTGAGCCAGAGGACTTCAGAAAGTTGTAAGAAAGGTTT 7614
Qy      2825 -----ThrGlyMetHisLys-HisIle-----Le 2832
Db      7615 GGTGACATCCCAAGAGAAAGATAGCCATATATCTCGAAGAAACCAATGGCACT 7674
Qy      2832 uSerProSerLysValGlyLeuHisLysLysArgAlaLeuSerPro----- 2847
Db      7675 CGGACACAGCCCCCGCTGCTGCACAG-AAAGTTAGGGCTATCCCACTGAGTCTGGCAA 7733
Qy      2848 -----AsnArgSerGlnMetProTh 2854
Db      7734 AGAAATCTTGAGAGTCTCTCAAAACCAACAGCTGTGCAGACAGATCAAAAGGTCAA 7793
Qy      2854 rGlnHisValIleSerProGlyLysThrGly-----LeuHisLysAsnLeuThrLysLe 2872
Db      7794 AGTTGCTACGGGAGGAGCCAGTATTCAGGACACATCTTCGAGAAACCAACAGAAATC 7853
Qy      2872 rThrLeuPheAspAsnLeuSerSerProCysLysGlnGlnLysValGlnGlnAsnLeuAs 2892
Db      7854 GCTCCAGACATTAATCTTCCTGAGAGAGTCCGAGTGAAGCCCAAGAGAGGCGCTGAG 7913
Qy      2892 nSerProLysGlyLysLeuPhe-----AspValLysSerLysSerMetCys 2907
Db      7914 GGTCAAGCAGGCGCAGCTTGCTCCCAAGCCCAAAAGCTGAGTGAATCCAAAGGCGAGTGA 7973
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Db      7974 GAACCTGTAAGTCCAG 7989

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RESULT 6
US-09-572-191-1
; Sequence 1, Application US/09572191
; Patent No. 6355466
; GENERAL INFORMATION:
; APPLICANT: Berard, Christophe
; APPLICANT: Sakowicz, Roman
; APPLICANT: Wood, Kenneth
; TITLE OF INVENTION: No. 6355466el motor proteins and methods for
; FILE REFERENCE: 1017
; CURRENT APPLICATION NUMBER: US/09/572,191
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4757
; TYPE: DNA
; ORGANISM: Human
US-09-572-191-1

Alignment Scores:
Pred. No.: 3,34e-75 Length: 4757
Score: 1051.00 Matches: 417
Percent Similarity: 42.34% Conservative: 304
Best Local Similarity: 24.49% Mismatches: 548
Query Match: 7.12% Indels: 434
DB: 4 Gaps: 60

US-09-724-584-1 (1-2954) x US-09-572-191-1 (1-4757)
Qy      2 SerGlnGlyAspAlaLysValLysValArgValArgProLeuIleGlnArgGlu--- 20
Db      64 NATGAAGGTGATGCATCAAGTTTGTGGCAATTCCTCTCGACAGAAAGATCTGGG 123
Qy      21 -----GlnGlyAspGlnAlaAsnLeuGlnTyrLysAlaGlnAsnThrLysSerGln 38
Db      124 TCAGCTGATGAGAGACAG--AACTTATGCTTATCTGTGCTGCTCTCCACGAGTCCGG 180
Qy      39 ValAspGlyThr-----LysSerPheAsnPheAspArgValPheAsnSerHisGlu 55
Db      181 CTGCACTCCAAACCCGAGCCCAAGACCTTCACGTTGATCATGTTGCAGATGTGATACC 240
Qy      56 SerThrSerGlnLysTyrGlnGlnLysAlaValProIleLysArgSerAlaLeuGlnGly 75
Db      241 ACTCAGAAATCTGATTCGCAACTGTGCTAAAGCAATTTGAGATGATTCGATGAGCGGT 300
Qy      76 TyrAsnGlyThrIlePheAlaTyrGlnThrSerSerGlyLysThrTyrThrMetCys 95
Db      301 TATAATGGTACCATTTTGCATATGAGACAGATGCTGAGGAGAAACATTAATTAATGATG 360
Qy      96 Gly-----ThrProAsnSerLeuGlnGlnLysIleIleProGlnAlaIle 108
Db      361 GGACCATCTGAATCTGATTAATTTTCTCATTAACCTGAGAGAGATATCCCAAGAGTTT 420
Qy      361 GGTGACATCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Qy      109 GlnGlnValPheLysIleIleGlnGlnLys-----ProAsnArgGlnLys 123
Db      421 GAATATTTGTTTCTTATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Qy      124 LeuLeuArgValSerTyrMetGlnLysTyrAsnGlnThrValLysAspLeuLeuLysAsp 143
Db      481 CTTTGTAAAGTCTCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 534
Qy      144 AspArgGlyLysLysProLeuGlnLysLeuArgLysAspPheAsnArgAsnValTyrValAla 163
Db      535 GACTCTGATCGGCTGAGCTGATCTTAAGAGAGCATATCAACAGAGAGGAGTCTTTGTTGT 594
Qy      164 AspLeuThrGlnGlnLeuValMetValProGlnHisValIleGlnTyrIleLysLysGly 183
Db      595 GGTGCGGTGAGACAGAGTGTAACTCAGCTGCTGAAGCCTTACAGTGTGCTGAGAGA 654
Qy      184 GlnLysAsnArgHisTyrGlnGlnLysThrLysMetAsnAspHisSerSerArgSerHisThr 203

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Db      655 TGAAGATAGACGTGTGGCATCAACATCAATGAAACAGAAATCGTCTAGCTCTCATGCC 714
      204 ILePheArgMetIleValGluSerArgAspArg---AsnAspProThrAsnSerGluAsn 222
      715 GCTTTACATTAACATTAAGAGTCAATGAGAAAGTAATAGATTGGAAAT----- 765
Qy      223 CysAspGlyAlaValMetValSerHisLeuAsnLeuValAspLeuAlaGlySerGluArg 242
      766 -----ATACGACCTCCCTACTCAACCTGGTGATTACAGAGATCTGAAAG 813
Qy      243 AlaserGlnThrGlyAlaGluGlyValArgLeuLeuGluGlyCysAsnIleAsnArgSer 262
      814 CAAAAAGATACCATGACAGAAAGGATGAGATTGAGAGACAGCTTAACATAATTCATCA 873
Db      263 LeuPheIleLeuGlyGlnValIleLysLysLeuSerAspGlyGlnAlaGly-----Gly 280
      874 TTGAGCTGCTGGCCAGATGATTACAGCACTTGTCGACGTGGTAAATGGAACACAGAGA 933
Qy      281 PheIleAsnTyrArgAspSerLysLeuThrArgIleLeuGlnAsnSerLeuGlyGln 300
      934 CATGTTGTACAGAGACTCCAAACTTACCTTCTTACCGGATTCCCTTGAGAGTAAAT 993
Qy      301 AlaLysThrValIleIleLysThrIleThrProValSer-----PheAspGluThrLeu 318
      994 GCCAAACACCCCTAATTTGCAAAATGTTTCATCTGATCCAGGCTGTTTGGGAAACCTTA 1053
Qy      319 SerThrLeuGlnPheAlaSerThrAlaLysHisValArgAsnThrProHisValaGln 338
      1054 TCACACCTTAACCTTCTCAAGAGCCAAAGCTGATTAAAAACAAAGCAGATTAATGAA 1113
Db      339 ValLeuAspAspGluAlaLeuLeuLysArgTyrArgLysGluIleLeuAspLeuLys 358
      1114 -----GACACCCAAAGAAATGAGCCACGCTCCAACTGAAGTGAAGGCTCAAGAA 1167
Qy      359 GlnLeuGluAsnLeuGluSerSerGluThrLysAlaGlnAlaMetAlaLysGln 378
      1168 CAACCTGGCGAGTCTCTCAGAGACAGACACCAAGAAAGCTCTCTGACACAGACAAA 1227
Qy      379 HisThrGlnLeuLeuAlaGluIleLysGlnLeuHisLysGluArgGluAspArgIleTyr 398
      1228 AAGAACTACTATATGAGATATTTCCAG-----GAAACAATGTTATTC 1272
Db      399 HisLeuThrAsnIleValValAlaSerSerGlnGluSerGlnAspGlnArgValLys 418
      1273 TTT-----AAGAAATCTGAACAGGAAAGAG----- 1299
Qy      419 ArgLysArgArgValThrTyrAlaProGlyLysIleGlnAsnSerLeuHisAlaSerGly 438
      1299 ----- 1299
Db      439 ValSerAspPheAspMetLeuSerArgLeuProGlyAsnPheSerLysLysAlaLysPhe 458
      1300 ---TCTCTGATAGAAAAAGTTACCCCAATTAGAAGACCTCACCCCTCAAAAAAGAAAAATTT 1356
Qy      459 SerAspMetProSerPheProGluIleAspAspSerValCysThrGluPheSerAspPhe 478
      1356 ----- 1356
Db      479 AspAspAlaLeuSerMetSerMetAspSerArgLysIleAspAlaGluTyrAsnLeuAlaSer 498
      1357 ---ATTCAATCTAATAAATGAATGATGTAATTCGGA---GAGAT 1395
Qy      499 LysValIleThrHisArgGluLysThrSerLeuHisGlnSerMetIleAspPheGlyGlnIle 518
      1396 CAAATTAATACGCTTGAAAAAG---CTCCAC----- 1422
Db      519 SerAspSerValGlnPheHisAspSerSerLysGluAsnGlnLeuGlnTyrLeuProLys 538
      1423 -----AAGGAATCCCGGAGGCTTTCTTGCTGAG 1452
Qy      539 AspSerGlyAspMetAlaGluCysArgLysAlaSerPheGluLysGluIleThrSerLeu 558
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Db      1453 GAGCAGATCGTTTGCTC-----TCAGATTAAAGGAATGAGATTCAACTCTG 1500
Qy      559 GlnGlnGlnLeuGlnSerLysGlyGluGluGluLysGluLeuValGlnSerPheGluLeu 578
      1501 CAGAAACAAATAGACACCAACCCAGAGTTGCAAAAGTATGCTTAAGAAATATTTCCCTC 1560
Qy      579 LysIleAlaGluLeuGluGlnGluLeuSerValLysAlaLysAsnLeuGluMetValThr 598
      1561 AGG-----GAGGAGAAATAGAGACTGAGATTAA-----TTAGAGCTGTGAAA 1602
Db      599 AsnSerArgGluHisSerIleAsnAlaGluValGlnThrAspValGluLysGluValVal 618
      1603 AGAGCTCAAGAA----- 1614
Qy      619 ArgLysGluMetSerValLeuGlyAspSerGlyTyrAsnAlaSerAsnSerAspLeuGln 638
      1614 ----- 1614
Db      639 AspSerSerValAspGlyLysArgLeuSerSerSerHisAspGluCysIleGluHisArg 658
      1614 ----- 1614
Qy      659 LysMetLeuGluGlnLysIleValAspLeuGluGluPheIleGluAsnLeuAsnLysLys 678
      1615 ---ATGATGCCACAGACCATGCAAAACTAGAAAAAGCTTCTCTGAAATAGTGGCATG 1671
Qy      679 SerGluAsnAspLysGlnLysSerSerGluGlnAspPheMetGluSerIleGlnLysCys 698
      1672 GAGAAAGTGAACAA-----AATCAGCAAGAGATTTCACCTTAAGCTCAGAAAGAG 1722
Db      699 GluAlaIleMetAlaGluLysAlaAsnAlaLeuGluGluLeuAlaLeuMetArgAspAsn 718
      1723 CCATGTTGTTTGA----- 1737
Qy      719 PheAspAsnIleIleLeuGluAsnGluThrLeuLysArgGluIleAlaAspLeuGluArg 738
      1738 -----AACCTGAGAAAGTTAAAGACAACTCTGCAAAATTCAGAGCA 1779
Qy      739 SerLeuLysGluAsn---GlnGluThrAsnGluPheGluIleLeuGluLysGluThrGln 757
      1780 GAGCTGAATTAATTCAAAGCAAGATATGAAGATTTC-----AAGAACTTAAT 1827
Db      758 LysGlnHisGluAlaGlnLeuIleHisGluIleGluSerLeuLysLeuValGluAsn 777
      1828 AGAAAAAGCCAGTGAATGGAATCAAGCTTCAAGCTTGGCAAAAAAGCC----- 1878
Qy      778 AlaGluMetTyrAsnGlnAsnLeuGluLysAspLeuGluThrLysThrLysLeuLys 797
      1879 -----AACCTTAATCTTGAAGAACTTTGAGAGCA---ACAAAAGCCTGCAG 1923
Qy      798 GlnGlnGluIleGlnLeuAlaGluLeuArgLys---ArgAlaAspAsnLeuGln----- 814
      1924 CGGCAAGAAAGTT---TTCAGCTGAATAAATTCATGCTGAAACATTAAGATTATA 1977
Qy      815 -----LysLysValArgAsnPhe-----AspLeuSerValSer 825
      1978 ACTACACCAACCAAGGCTTACCAACTTCATTCGCCAGCACTACCAAAATTAAGCCCTGAA 2037
Qy      826 MetGlyAspSerGluLysLeuCysGluGluIlePheGlnLeuLysGlnSerLeuSerAsp 845
      2038 ATGGGAAGCTTTGGCTCTTA-----TACACTCAGAAATTCATGACATATTGAT 2085
Qy      846 AlaGluAlaValIleThrArgAspAlaGlnLysGluCysSerPheLeuArgSerGluAsnLeu 865
      2086 AATGATATATTAAATGAGCAAGTTCCTCAG----- 2118
Db      866 GluLeuLysGluLysMetGluAspThrSerAsnTyrAsnGlnLysGluLysAlaAla 885
      2119 -----ATGAATGAACAACTTTT 2136
Qy      886 SerLeuPheGluLysGlnLeuGluThrGluLysSerAsnTyrLysLysMetGluAlaAsp 905
      2137 GAGGCCATTTCTGAAGAGCTTAGAACAGTGCAGAAACAAATGAGTCTTCAAGCCAA 2196

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Db      4048 -----CATGAGAAATTGCTGATGCTGAGTAAAGAGAAATGTCAGG 4095
QY      1584 LeuAlaLysAsnLeuAlaIleAlaSerAspAspCysProIleThrGlnGlu 1603
Db      4096 CTTCCTGAGAGACAGAAAAGTTCGCGCCGAAATGTAATTTTAAAGAAAAGAA 4155
QY      1604 ThrSerAla 1606
Db      4156 AGTGAATCT 4164

RESULT 7
US-09-723-262-1
/ Sequence 1, Application US/09723262
/ Patent No. 6379912
/ GENERAL INFORMATION:
/ APPLICANT: Beraud, Christophe
/ APPLICANT: Sakowicz, Roman
/ APPLICANT: Wood, Kenneth
/ TITLE OF INVENTION: No. 6379912el motor proteins and methods for
/ TITLE OF INVENTION: their use
/ FILE REFERENCE: 1017
/ CURRENT APPLICATION NUMBER: US/09/723,262
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: US 09/572,191
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 4757
/ TYPE: DNA
/ ORGANISM: Human
US-09-723-262-1

Alignment Scores:
Pred. No.: 3,34e-75 Length: 4757
Score: 1051.00 Matches: 417
Percent Similarity: 42.34% Conservative: 304
Best Local Similarity: 24.49% Mismatches: 548
Query Match: 7.12% Indels: 434
DB: 4 Gaps: 60

US-09-724-584-1 (1-2954) x US-09-723-262-1 (1-4757)
QY      2 SerGlnGlyAspAlaValLysValCysValArgValArgProLeuIleGlnArgGlu--- 20
Db      64 AATGAAGGATGATGCATCAAGCTTTTGTTCGCAATTCGCTCCGCAAGAAAGATCTGGG 123
QY      21 -----GlnGlyAspGlnAlaAsnLeuGlnTrpLysAlaGlyAsnAsnThrIleSerGln 38
Db      124 TCAGCTGATGAGAGACAG---AACTTATGCTTATCTGCTGCTCCCTCCACGAGTCTCCGG 180
QY      39 ValAspGlyThr-----LysSerPheAsnPheAspArgValPheAsnSerHisGlu 55
Db      181 CTGCACTCCCAACCTGAGCCCAAGACCTTCACGTTGATCATGTTGCGAGATGTGATACC 240
QY      56 SerThrSerGlnIleTyrlGlnIleAlaValProIleIleArgSerAlaLeuGlnGly 75
Db      241 ACTCGAATCTGTAATCGCAACTGTGCTAAAGCATTTGTGACATGACGCGT 300
QY      76 TyrAsnGlyThrIlePheAlaTyrlGlnThrSerSerGlyLysThrThrThrMetMet 95
Db      301 TATATGATGATCCATCTTTCATATGACACGACTGCTCAGGAAACATTTATCTATGATG 360
QY      96 Gly-----ThrProAsnSerLeuGlyIleIleProGlnAlaIle 108
Db      361 GCACCATCTGAATCTGATATATTTTCTCATACCTGAGAGAGATATCCAGAGATTTC 420
QY      109 GlnGluValPheLysIleIleGlnGluIle-----ProAsnArgGluPhe 123
Db      421 GAATATTTTCTTCTTATATGATGCTGAAAAAGAGCTGAGCTGAAAGAGTTTC 480
QY      124 LeuLeuArgValSerTyrMetGlnIleTyrlAsnGlnIleThrValLysAspLeuLeuGln 143

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Db      481 CTTTGAATGTTCTTTATGAAATCTAACACGAGCAGATATGATGATCTGCTG----- 534
QY      144 AspArgGlyLysProLeuGlnIleArgValAspPheAsnArgValTyrValAla 163
Db      535 GACTCTGCATCGGCTGAGCTGACTGACTTAAAGGAGCATATCAAGACAGAGAGCTTTGTGTT 594
QY      164 AspLeuThrGlnGluLeuValMetValProGlnHisValIleGlnTrpIleLysLysGly 183
Db      595 GGTGGCGTGGAGCAGAGTGTAACTCAGCTGCTGAAGCTTACAGTGTGTTGCTGAGAGA 654
QY      184 GlnLysAsnArgHisTyrlGlyLysThrLysMetAsnAspHisSerSerArgSerHisThr 203
Db      655 TGGAGAAATAGACGTGTGCATCAACATCAATGAAACAGAGAATCTCTTAGGCTTCATCC 714
QY      204 IlePheArgMetIleValGlnSerArgAspArg---AsnAspProThrAsnSerGlnAsn 222
Db      715 GTCTTTACAATTACATGATGATGATGAGAAAAGTAAATGAGATTGTAAT----- 765
QY      223 CysAspGlyAlaValMetValSerHisLeuAsnLeuValAspLeuAlaGlySerGlnArg 242
Db      766 -----ATACGAGCTCCCTACTCAACCTGCTGATTTAGCAGGATCTGAAAGG 813
QY      243 AlaSerGlnThrGlyAlaGlnGlyValArgLeuLysGlnGlyCysAsnIleAsnArgSer 262
Db      814 CAAAAAGATACCATGACGAAAGGATGATGAAAGAGCAGGATCAATTAATCGATCA 873
QY      263 LeuPheIleLeuGlyGlnValIleLysLysLeuSerAspGlyGlnAlaGly-----Gly 280
Db      874 TTGAGCTGCTGGCGCAAGTATTAACAGACACTTGTCCACGTGGGTAATGAAAAACAGAGA 933
QY      281 PheIleAsnTyrlArgAspSerLysLeuThrArgIleLeuGlnAsnSerLeuGlyLysn 300
Db      934 CATGTTCTACAGAGACTCCAAACTTACCTTACTTACAGGATTCCTTGAGAGATAT 993
QY      301 AlaLysThrValIleIleCysThrIleThrProValSer-----PheAspGlnThrLeu 318
Db      994 GCCAAAAGACCATTAATGCAATGTTCAATCTGATCTGATCCAGCTGTTTGGGAAACCTTA 1053
QY      319 SerThrLeuGlnPheAlaSerThrAlaLysHisValArgAsnThrProHisValAsnGlu 338
Db      1054 TCACACTTAATCTTGTCCCAAGAGCCAGCTGATTAACAAAGCAGCTGTAATGAA 1113
QY      339 ValLeuAspAspGlnAlaLeuLeuLysArgTyrlArgLysGlnIleLeuAspLeuLysLys 358
Db      1114 -----GACACCCAAGAAATGTGAGCCAGCTCCAACTGAAAGTGAAGAGCTCAAGAA 1167
QY      359 GlnLeuGlnAsnLeuGlnLysSerSerSerGlnThrLysAlaGlnAlaMetAlaLysGlnGlu 378
Db      1168 CACTGGCGGAGCTTGCTTCGACACACACACACACCAAGACCTTCGACCAAGAGACAAA 1227
QY      379 HisThrGlnLeuLeuAlaGlnIleLysGlnLeuHisLysGlnArgGluAspArgIleTrp 398
Db      1228 AAGAAGACTAATCTATATGAGATATTCAG-----GAAGCAATGTTATTC 1272
QY      399 HisLeuThrAsnIleValAlaSerSerGlnLysGlnGlnAspGlnAspGlnValLys 418
Db      1273 TTT-----AGAAATCTGAACGAGAAAGAG----- 1299
QY      419 ArgLysArgArgValThrTrpAlaProGlyLysIleGlnAsnSerLeuHisAlaSerGly 438
Db      1299 ----- 1299
QY      439 ValSerAspPheAspMetLeuSerArgLeuProGlyAsnPheSerLysAlaLysPhe 458
Db      1300 ---TCTGTGATAGAAAAAGTTAACCAATTGAAGACTCAACCCCAAAAAAGAAATTT 1356
QY      459 SerAspMetProSerPheProGlnIleAspAspSerValCysThrGlnPheSerAspPhe 478
Db      1356 ----- 1356
QY      479 AspAspAlaLeuSerMetMetAspSerAsnGlyIleAspAlaGlnTrpAsnLeuAlaSer 498

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Db 1357 -----ATTCAATCTAATAAATGATTGTAATTCGGA---GAGCAT 1395
 Qy LysValThrHisArgGluYsthrSerLeuHisGlnSerMetLeuAspHeGluGlnIle 518
 Db 1396 CAATAATATACGCTTGAAAAAG-----CTCCAC----- 1422
 Qy SerAspSerValGlnPheHisAspSerSerLysGlnAsnGlnLeuGlnIleuPheProLys 538
 Db 1423 -----AAGGAATCCCGGAGGCTTTCTGCTGTG 1452
 Qy AspSerGlyAspMetAlaGluCysArgLysAlaSerPheGlnLysGlnIleThrSerLeu 558
 Db 1453 GAGCAGATCGTTTGCTC-----TCAGAAATTAAGAAATGAGATTCAAACTCTG 1500
 Qy GlnGlnGlnLeuGlnSerLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 578
 Db 1501 CGAAGAACAAATAGACACACCCAGAGTTGCAAAAGTATGTAAGAAATCATTTCCCTC 1560
 Qy LysIleAlaGluLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 598
 Db 1561 AGG-----GAGAGAAATAGACACTGAGTTA-----TTAGAGCTGTGAAA 1602
 Qy AsnSerArgGlnHisSerIleAsnAlaGluValGlnThrAspValGlnLysGlnValVal 618
 Db 1603 AGAGCTCAAGAA----- 1614
 Qy ArgLysGluMetSerValLeuGlnLysAspSerGlyTyrAsnAlaSerAsnSerAspLeuGln 638
 Db 1614 ----- 1614
 Qy AspSerSerValAspGlyLysArgLeuSerSerSerHisAspGluCysIleGlnHisArg 658
 Db 1614 ----- 1614
 Qy LysMetLeuGlnGlnLysIleValAspLeuGlnGlnPheIleGlnAsnLeuAsnLysLys 678
 Db 1615 ---ATGGAATGCCAGACCATTCGCAAAAGTAAAGAAAGCTTCTCGAATAATAGTGGCATG 1671
 Qy SerGluAsnAspLysGlnLysSerSerGlnGlnAspPheMetGlnSerIleGlnLeuCys 698
 Db 1672 GAGAAAGTGACAAA-----AATCAGCAAGGATTTTCACTTAAGCTCAGAAAGAG 1722
 Qy GluAlaIleMetAlaGluLysAlaAsnAlaLeuGlnGlnLeuAlaLeuMetArgAspAsn 718
 Db 1723 CCATGTTGTTTGA----- 1737
 Qy PheAspAsnIleIleLeuGlnAsnGlnIleThrLeuLysArgGlnIleAlaAspLeuGlnArg 738
 Db 1738 -----AACACTGAGAAAGTTAAAGCACAACCTCTCGAATTCAGACA 1779
 Qy SerLeuLysGluAsn---GlnGluThrAsnGlnIlePheGlnIleLeuGlnLysGlnThrGln 757
 Db 1780 GAGCTGAATTAATTCAGCAAGCAAGAAATATGAAAGATTC-----AAGAACTTACT 1827
 Qy LysGlnHisGlnAlaGlnLeuIleHisGlnIleGlySerLeuLysLysLeuValGlnAsn 777
 Db 1828 AGGAAAGGACGACTGAATGGAATCAGAGCTTCAGTCTTTCAGAAAGCG----- 1878
 Qy AlaGluMetTyrAsnGlnAsnLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 797
 Db 1879 -----AACCTTAATCTTGAAAACTTTTGAAAGCA---ACAAAACTCTGCAAG 1923
 Qy GlnGlnGlnIleGlnLeuAlaGluLeuArgLys---ArgAlaAspAsnLeuGln----- 814
 Db 1924 CGGCAAGAGATT-----TCTCAGCTGAATAAATTAATTCAGTGAACAACCTTAAGATTATA 1977
 Qy LysLysValArgAsnPhe-----AspLeuSerValSer 825
 Db 1978 ACTACACCAACCAAGCCTTACCAACTTATCCCAACAGTACCAAAATTAAGCCCTGAA 2037
 Qy MetGlyAspSerGlnLysLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 845
 Db 2038 ATGGGAAGCTTTGGCTCTCTA-----TACACTCAGAAATTTAGCATATTATGAT 2085

Qy AlaGluAlaValThrArgAspAlaGlnLysGluCysSerPheLeuArgSerGluAsnLeu 865
 Db 2086 AATGATATATTAATATGACCACTTCTCTGAG----- 2118
 Qy GluLeuLysGluLysMetGluAspThrSerAsnTyrIleAsnGlnLysGlnLysAlaAla 885
 Db 2119 -----ATGATGAAACCACTTTT 2136
 Qy SerLeuPheGlnLysGlnLeuGlnIleThrGlnLysSerAsnTyrLysLysMetGlnAlaAsp 905
 Db 2137 GAGGCCATTCTTGAGAGACTTGAACAGTGCAGGAACAAATGAGTCTTTCACACCAAA 2196
 Qy LeuGlnLysGlu-----LeuGlnSerAlaPheAsnGlnIleAsnTyr 919
 Db 2197 CTGATGAAGAGACGATTAACAACTTAACGACGACATGTTGACAACTGAAACAT 2256
 Qy LeuAsnGlyLeuLeuAlaGlyLysValProArgAspLeuLeuSerArgValGluLeuGln 939
 Db 2257 CATCTACCCCAATG-----CAGGAGCTTTCTCATCAGAAAGAAAT--- 2298
 Qy LysLysValSerGluPheSerLysGlnLeuGlnLysAlaLeuGlnLysLysAsnAlaLeu 959
 Db 2299 -----GATTGACCAACACGACGAGAGAGCTTCTCTCACAGTTGATGTCCTT 2346
 Qy GluAsnGluVal---ThrCysLeuSerGlnTyrLysPheLeuProAsnGluValGluCys 978
 Db 2347 GAAAGACGCTTCAAGACATCAAACTTAATAATGACTTTTGAAGAGTAGAGTACATGAC 2406
 Qy LeuLysAsnGlnIleSerLysAlaSerGlnGlnIleMetLeuLysGlnGln----- 996
 Db 2407 CTGCGAGTAGTCCTTCATTCGTCGACAGAGGCTTCTTCAGTGAATTTGGAATATAGT 2466
 Qy 997 -----GlyGlnHisSerAlaSerIleIleSerLysGlnGlnIleMet 1011
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 Qy ValGlnGlnThrGlnGlnGlnIleThrLysLeuMetLysLysMetHisAspAspLeuPheGlu 1051
 Db 2587 CTACGAGATTCCTATGACAACTTACAGAAATATGAATTTGAGATTGACCACTTCA 2646
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 Qy LysGlnThrMetGlnSerValGluValLys-----IleAla 1082
 Db 2707 ATGAGCTTCTTGAGCGCAAGAAAGCAATTAACAAATATATACCTTGAACAA 2766
 Qy AspThrLysHisGlnLeuGlnGlnIleThrIleArgAspLysGlnGlnLeuHisGlnLys 1102
 Db 2767 GATTAAGAAAACAGTCTTAAGAAATCTTAAGATCTTGAAGCTTGAAGCTTACAGAGAAA 2826
 Qy LysTyrPhePheGlnAlaMetGlnIleThrIlePheProIleThrProLeuSerAspSer 1121
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 Qy LeuProProSerLysLeuValGlnGlnLysAsnSerGlnAspProIleGlnIleAsnAspTyr 1141
 Db 2887 TTG----- 2889
 Qy HisAsnLeuIleAlaLeuAlaThrGlnArgAsnAsnIleMetValCysLeuGlnThrGln 1161
 Db 2890 -----CTTGCTACTGAAAA-----GTGATCAGTCCCTGAAAAAGCT 2928
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QY 1182 GlnSer11eGluYsSerAsp---LeuGlnLysProLySGlnAspLeuGlnGluGlu 1200
Db 2989 TCGGTCTGTGAGAAAACAGAACTATAGACACCTGAAACAAAGACTGAGACATTAAT 3048
QY 1201 ValIys-----LeuLeuGlnMetGluLeuLeuGlyHisLeuThrAspSer 1217
Db 3049 TCGAAATATACACTCTCTCTTGGTTGACAGAGAA-----GAGAGC 3087
QY 1218 GlnLeuSer11eGluYsLeuGlnLeuGlnLeuGlnValThrGluYsLeuGlnThr 1237
Db 3088 AAGAGTGTGATCAGAGAACAGAGATGATTCGATCTGAAAGAAACCTTAGC--- 3144
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Db 3163 GACATA-----GAGAGGATATGCTCTGTAGAGACCTGGCTCATGCCACTGAGACAGCTG 3216
QY 1277 -----Ser11eGluThrGlnAspGluLeuArgAlaAlaGlnGluGlu 1290
Db 3217 AACATGCTCAGACAGAGCCTCAAAAAACACTCGGGGCTGCTGAGCTGCCCGAGAGAA 3276
QY 1291 LeuArgGlnGlnYsGlnLeuValAspSerPheArgGlnGlnLeuLeuAspCysSerVal 1310
Db 3277 CTGACCAAGAAAGAAAGCCCTGATTCAGAACTTACAGACAAAGCTA----- 3321
QY 1311 Gly11eSerSerProAsnHisAspAlaValAlaAsnGlnGluYsValSerLeuGlyGlu 1330
Db 3322 -----AACCAAAAGAA----- 3333
QY 1331 ValAsnSerLeuGlnSerGlnMetLeuArgGlyGluArgAspGluLeuGlnThrSerCys 1350
Db 3334 -----GAGGAAGTAGAAACAGAGAAAGATGATTAATCACTCAAAATG 3375
QY 1351 LysAlaLeuValSerGluLeuGluLeuLeuArgAlaHisValYsSerValGluGluGlu 1370
Db 3376 AGGCACATA-----GAACATGTGATGATTCGTGCTGTAG 3411
QY 1371 Asn-----LeuGln11eThrLysLysLeuAsn 1379
Db 3412 GATGCCCAAGAGCTCTAGACACCACTCACTTCAAAACATTTGGCAAAACCTCGGAA 3471
QY 1380 GlyLeuGlnYsGlu11eLeuGlyYsSerGlnYsSerGluValLeuYsSerMetLeu 1399
Db 3472 ACACAGAACACAGAGTA-----GAGATGAGAAAGAGCTCTAAGACTCTCTTGG 3519
QY 1400 GluAsnLeuYsGluAspAsnAsnLysLeuYsGlu-----GlnAlaGlnGluYrSer 1417
Db 3520 GAACACCTTGTAACAAAGCTTAATGAAGACAGAGAGTCAAAATGCTGAATCCTCAGA 3579
QY 1418 SerLeuGlnAsnGlnPheSerLeuGlnGluValPheSerGlySerGlnYsLeuValAsp 1437
Db 3580 ATGAAAGACACAGTGGTGAATGGAAACCTACCGCTGGAAAGTCACACAGTTAATAGAG 3639
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QY 1458 ArgAspYrPheGlnLeuValGlnThrAlaAsn----- 1468
Db 3700 CAGAAATCATCCAGATATCAACAGCTGAAGATGAACAGAAAGATATCAAGAAAGA 3759
QY 1469 -----ThrAsnLeuValGlnGluYsLeuGlnThrProLeuGlnAlaAspHisGlu 1485
Db 3760 CTTCGAAAAAGTAATATGTTGAGAAATGCTGAAA-----ATGAAAGACAGACTGAA 3813
QY 1486 GluAspSer11eAspArgSerGlnGluMetGlu11eYsValLeuGlnGluYsLeu 1505
Db 3814 GAAAGTCAAAGTCCCTTTACAAAGAGATGATGATCCCTAGATGATGATGAGATC 3873
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QY 1526 LeuGln11eLeuGlnYsGlnMetGluThrSerVal11eLeuYsAspLeuGlnGln 1545
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QY 1546 LysLeuGlnSerLeuLeuSerGluAsn-----11e11eLeuYsGluAsn11eAspThr 1563
Db 3994 CAGGTGAGATGCTTGTCTGAGGAAATGAAAGTTGTGATGACCAAAATTTG----- 4047
QY 1564 ThrLeuYsHisSerAspThrGlnAlaGlnLeuGlnYsThrGlnGlnGluGln 1583
Db 4048 -----CATCAGAAAGATTGATGATGAGTGTGACATTAAGAAAGAAATGTCAGG 4095
QY 1584 LeuAlaYsAsnLeuAla11eAla11eAspAsnYsPro11eThrGlnGluYsGlu 1603
Db 4096 CTTCGTGAGAGACAGAAAGATGTCGCGCCGAAATGATTTTAAAGAAAGAAAGAA 4155
QY 1604 ThrSerAla 1606
Db 4156 AGTGAATCT 4164

RESULT 8
US-09-723-219-1
/ Sequence 1, Application US/09723219
/ Patent No. 6391613
/ GENERAL INFORMATION:
/ APPLICANT: Beraud, Christophe
/ APPLICANT: Sakowicz, Roman
/ APPLICANT: Wood, Kenneth
/ TITLE OF INVENTION: No. 6391613el motor proteins and methods for
/ FILE REFERENCE: 1017
/ CURRENT APPLICATION NUMBER: US/09/723,219
/ CURRENT FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: US 09/572,191
/ PRIOR FILING DATE: 2000-05-17
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 4757
/ TYPE: DNA
/ ORGANISM: Human
US-09-723-219-1

Alignment Scores:
Pred. No.: 3,34e-75 Length: 4757
Score: 1051.00 Matches: 417
Percent Similarity: 42.34% Conservative: 304
Best Local Similarity: 24.49% Mismatches: 548
Query Match: 7.12% Indels: 434
DB: 4 Gaps: 60

US-09-724-584-1 (1-2954) x US-09-723-219-1 (1-4757)
QY 2 SerGlnGlyAspAlaValYsValCysValArgValArgProLeu11eGlnArgGlu--- 20
Db 64 AATGAAGGTGATGATCCATCAAAAGTTTGTGGCAATTCCTCCCTCGCAAGAAAGATCTGG 123
QY 21 -----GlnGlyAspGlnAlaAsnLeuGlnThrPlyAlaGlyAsnAsnThr11eSerGln 38
Db 124 TCAGCTGATGAGAGACAG--AACTTAAGCTTATCTGTGCTGCTCCACAGAGTCTCGG 180
QY 39 ValAspGlyThr-----LysSerPheAsnPheAspArgValPheAsnSerHisGlu 55
Db 181 CTGCACTCCAAACCTGAGCCCAAGACCTTCACGTTTATCATGTTGCAAGATGGAATACC 240
QY 56 SerThrSerGln11eYrGlnGln11eAlaValPro11e11eArgSerAlaLeuGlnGly 75
Db 241 ACTCAGAAATCTGATTTGCAAACTGTGCTTAAAGCATTTGGAGAGTCTTCGATGAGCGGT 300
QY 76 TyrAsnGlyThr11ePheAlaTyrGlyGlnThrSerSerGlyLysThrTyrThrMetMet 95

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Db 301 TATAATGGACATCTTTTCATATGACAGACTGGCTCAGGGAAGCATTTACTATGATG 360
Qy 96 Gty-----ThrProAsnSerLeuGlyTleIleProAlaIle 108
Db 361 GGACCATCTGAATCTGATTAATTTTCTTAACCTGAGAGAGTAAATCCACGAAGTTT 420
Qy 109 GInGluValPheIleIleIleGInGluIle-----ProAsnArgIlePhe 123
Db 421 GAATATTTGTTTCTTAATGATGCTGAAAAAGAAAGCTGGAGCTGGAAAGCTTTC 480
Qy 124 LeuLeuArgValSerTyrMetGluIleTyrAsnGluThrValIleAspLeuLeuCysAsp 143
Db 481 CTTTGTAGTGTTCTCTTATTAATCTTAACAGAGACAGATATATGATGATCTG----- 534
Qy 144 AspArgGlyValPheProLeuGluIleArgGluAspPheAsnArgAsnValTyrValAla 163
Db 535 GACTCTGCATCGGCTGAGCTGTACTTAAGGAGACATATCAAGAAAGGAGCTTTGTTGT 594
Qy 164 AspLeuThrGluGluLeuValMetValProGluHisValIleGlnThrIleIleValysGly 183
Db 595 GGTGGCGGTGGAGCAGGTGTAACCTCAGCTGTAAGCCTATCAGGTGTGCTGGAGGA 654
Qy 184 GlnIysAsnArgHisTyrGlyIleThrIleMetAsnAspHisSerSerArgSerHisThr 203
Db 655 TGGAGGATATAGCCTGTGSCATCAACATCAATGAACAGAGATCGCTAGCTCATGCC 714
Qy 204 IlePheArgMetIleValGluSerArgAspArg---AsnAspProThrAsnSerGluAsn 222
Db 715 GCTTTTACCAATTACATAGAGTCAATGAGAAAAAGTAATGATGATGCTGAAAT----- 765
Qy 223 CysAspGlyAlaValMetValSerHisLeuAsnLeuValAspLeuAlaGlySerGluArg 242
Db 766 -----ATACGAGCCTCCCTACTCAACCTGGTGATTTAGCAGAGATCTGAAGG 813
Qy 243 AlaSerGlnThrGlyAlaGluGlyValArgLeuIleGluGlyCysAsnIleAsnArgSer 262
Db 814 CAAAAAGATATCCCATATGACAGAGGATGAGATTGAAAGAGACAGCTAACTAAATGATGA 873
Qy 263 LeuPheIleLeuGlyGlnValIleIleValysLeuSerAspGlyGlnAlaGly-----Gly 280
Db 874 TTGAGCTGCTGGCCCAAGTGAATTAACAGCATTTGACGCTGGATATGAAAGACAGAGA 933
Qy 281 PheIleAsnTyrArgAspSerIleLeuThrArgIleLeuGlnAsnSerIleuGlyGluAsn 300
Db 934 CATGTTGCTACAGAGACTCCAAACTTACTTACTAAGGAGATTCCCTTGAGGTAAAT 993
Qy 301 AlaIleThrValIleIleCysThrIleThrProValSer-----PheAspGluThrLeu 318
Db 994 GCCAAACAGCCATTAATTCGAAATGTTCTCCTGATCCAGGTGTTTGGGAAACCTTA 1053
Qy 319 SerThrLeuGlnPheAlaSerThrAlaIleValAsnHisValArgAsnThrProHisValAsnGlu 338
Db 1054 TCAACACTTAACCTTCTCAAGAGCCAGCATGATTAATAACAGAGCATAGTAAATGAA 1113
Qy 339 ValLeuAspArgGluAlaLeuLeuValysArgTyrArgGlyValysGluIleLeuAspLeuIleValys 358
Db 1114 -----GACACCCCAAGAAATGTGAGCCAGCTCCAAAGTGAAGTGAAGGCTCAAGAA 1167
Qy 359 GlnLeuGluAsnLeuGluSerSerSerGluThrIleValAlaIleMetAlaIleValysGlu 378
Db 1168 CAATGGGGGAGCTTGTCTCAGAGACAGACACCAAGAAAGCTTCTGACCCAGAGACAA 1227
Qy 379 HisThrGlnLeuLeuAlaGluIleIleValysGlnLeuHisIleValysGluAspArgIleTyr 398
Db 1228 AAGAGAGCTAACTATATGAGATATTTCAG-----GAAACATATGTTATTTC 1272
Qy 399 HisLeuThrAsnIleValAlaIleAspSerGlnGluSerGlnGluAspGlnArgValIle 418
Db 1273 TTT-----AAGAAATCTGAACAGAGAAAGAG----- 1299
Qy 419 ArgIleValArgValThrTyrAlaProGluIleGlnAsnSerLeuHisAlaSerGly 438

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Db 1299 ----- 1299
Qy 439 ValSerAspPheAspMetLeuSerArgLeuProGluIleAsnPheSerTyrAlaIleAspPhe 458
Db 1300 ---TCTTGATGAGAAAGTTTACCAATTAAGAGACCTCACCTTCAAAAAGAAATTT 1356
Qy 459 SerAspMetProSerPheProGluIleAspAspSerValCysThrGluPheSerAspPhe 478
Db 1356 ----- 1356
Qy 479 AspAspAlaLeuSerMetMetAspSerAsnGlyIleAspAlaGluTyrAsnLeuAlaSer 498
Db 1357 -----ATTCAATCTAATTAATAAGATTGCAAAATTCGGA---GAGAT 1395
Qy 499 LysValIleThrHisArgGluIleThrSerLeuHisGlnIleAsnSerMetIleAspPheGlyGlnIle 518
Db 1396 CAATAATTAACGCTTGAAAG---TCCAC----- 1422
Qy 519 SerAspSerValGlnPheHisAspSerSerIleValysGluAsnGlnLeuGlnTyrLeuProIle 538
Db 1423 -----AAGAAATCCCGGAGGCTTTCTGCTGAG 1452
Qy 539 AspSerGlyAspMetAlaGluCysArgIleValAspSerPheGluIleThrSerLeu 558
Db 1453 GAGCAGATCGCTTCTC-----TCAGATTAAGGAATGAGATTCAAACTCTG 1500
Qy 559 GInGlnGlnLeuGlnSerIleValysGluGluValysGluLeuValGlnSerPheGluLeu 578
Db 1501 CGAGAAACAATAGACACACCACCCAGAGTTGCCAAAGTATGTAAGAAATCATTTCCCTC 1560
Qy 579 LysIleAlaGluLeuGluGlnLeuSerValIleValAlaIleAsnLeuGluMetValThr 598
Db 1561 AGC-----GAGGAGATTAAGAGACTGAGATTA-----TTAGAGCTGTGAAA 1602
Qy 599 AsnSerArgGluHisSerIleAsnAlaGluValGlnThrAspValGluIleValysGluVal 618
Db 1603 AGAGCTCAAGAA----- 1614
Qy 619 ArgIleValMetSerValLeuGluIleAspSerGlyTyrAsnAlaSerAsnSerAspLeuGln 638
Db 1614 ----- 1614
Qy 639 AspSerSerValAspGlyIleArgIleuSerSerSerHisAspGluCysIleGluHisArg 658
Db 1614 ----- 1614
Qy 659 LysMetLeuGlnGlnIleValAlaAspLeuGlnGluPheIleGluAsnLeuAsnIleValys 678
Db 1615 ---ATGATGCCACACCATTCGAAATAAGAAAGCTTCTGAAATTAAGTGCATG 1671
Qy 679 SerGluAsnAspIleValysSerSerGluIleAspPheMetGluSerIleGlnLeuCys 698
Db 1672 GAGAAAGAGTGAACAA-----AATCAGCAAGAGATTTTCACTTAAGCTCAGAAAGAG 1722
Qy 699 GluAlaIleMetAlaGluIleValAlaAsnAlaLeuGluGluLeuAlaLeuMetArgAspAsn 718
Db 1723 CCATGTTGTTGCA----- 1737
Qy 719 PheAspAsnIleIleLeuGluAsnGluThrIleValysArgIleValAlaAspLeuGluArg 738
Db 1738 -----AACCTGAGAAATTTTAAAGCAACAACTCTGCAAAATCAGACA 1779
Qy 739 SerLeuIleValysGluAsn---GlnGluThrAsnGluPheGluIleLeuGlnIleValysGluThrGln 757
Db 1780 GAGCTGAATTAATTCACAAAGAAATATGAAAGATTC-----AAGAACTTACT 1827
Qy 758 LysGlnHisGluAlaGlnLeuIleHisGluIleGlnSerLeuValysLeuValGluAsn 777
Db 1828 AAGAAAGAGCGCTAGAAATGGAATCAGAGCTTCACTTGTGCAAAAAGCG----- 1878
Qy 778 AlaGluMetTyrAsnGlnAsnLeuGluIleAspLeuGluThrIleValysLeuLeuValys 797
Db 1879 -----AACCTTAATCTGAAACCTTTGGAAGCA---ACAAAGCCTGCAAG 1923

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QY 798 GluGlnGluIleGlnIleuAlaGluLeuArgLys---ArgAlaAspSerLeuGln----- 814
DB 1924 CGCGAAGAGAGTT-----TCTCAGCTGAATAAATTATCATCTGAACACTTAAGATTATA 1977
QY 815 -----LysLysValArgAsnPhe-----AspLeuSerValSer 825
DB 1978 ACTACACCAACCAAGGCTTACCAACTTCATTCCTCCGACAGCTACCAAAATTAAACCTCTGAA 2037
QY 826 MetGlyAspSerGluLysLeuCySGluGluIlePheGlnLeuLysGlnSerLeuSerAsp 845
DB 2038 ATGGGAAGCTTTGGCTCTCTA-----TACCTGAGAATTCTACATATTAGAT 2085
QY 846 AlaGluAlaValThrArgAspAlaGlnLysGluCysSerPheLeuArgSerGluAsnLeu 865
DB 2086 AATGATATATTAATGAGCCAGTTCCTCTGAG----- 2118
QY 866 GluLeuLysGluLysMetGluAspThrSerAsnTrpTyrAsnGlnLysGluLysAlaAla 885
DB 2119 -----ATGAAATGAAACAACCTTTT 2136
QY 886 SerLeuPheGluLysGlnLeuGluIleThrGluLysSerAsnTyrLysLysMetGluAlaAsp 905
DB 2137 GAGCCATTCTCGAAGAGCTTAGAACAAGTCAGAGAACAAATGAGTCTCTTCAAGCCAA 2196
QY 906 LeuGlnLysGlu-----LeuGlnSerAlaPheAsnGluIleAsnTyr 919
DB 2197 CTGGATGAAGAAAGCATAAACCTAAAGCTTCACAGAGTGTGACAACTGGAACAT 2256
QY 920 LeuAsnGlyLeuLeuAlaGlyLysValProArgAspLeuLeuSerArgValGluLeuGlu 939
DB 2257 CATTCACCCCAATG-----CAGAGCTTTTCTTCATCAAGAAAGAAAT--- 2298
QY 940 LysLysValSerLeuPheSerLysGlnLeuGluLysAlaLeuGlnLysAsnAlaLeu 959
DB 2299 -----GATTGACCAAAACAGAGAAAGAGCTTCTCTCAAGTGAATGTCCT 2346
QY 960 GluAsnGluVal---ThrCysLeuSerGluTyrLysPheLeuProAsnGluValGluCys 978
DB 2347 GAAAGACAGCTTCAGAGACTCAACAACTAAATGACTTTTGAAGAAAGTACGATGAC 2406
QY 979 LeuLysAsnGlnIleSerLysAlaSerGluGluIleMetLeuLeuLysGlnGlu----- 996
DB 2407 CTGCGAGTAGTCTCTCATCTCTGTCGACAGAGACTTCTTCAAGTGAATGGAATTAAT 2466
QY 997 -----GlyGlnHisSerAlaSerIleIleSerLysGlnGluIleMet 1011
DB 2467 TCATTCAAAACGAATCAGAGAAAGAAATTCACAAACTTTCCGAAAGACATGATGTA 2526
QY 1012 GlnGlnLysSerGluGlnIleLeuGlnLeuThrArgGluValThrHisThrGlnSerLys 1031
DB 2527 CAGCTTCAAATTGATATCTCAGGTTAGAAAAGAAAGCTCTTGAGAGCAAAACCTGCG 2586
QY 1032 ValGlnGlnThrGluGlnIleThrLeuGlnMetLysLysMetHisAspAspLeuPheGlu 1051
DB 2587 CTACAGGATTCCTTAATCTCAGGTTAGAAAAGAAAGTGAATTTGAGATTGACCACTTCA 2646
QY 1052 LysTyrIleArgAsn---LysSerGluAlaGluAspLeuLeuArgGlnMetGlnAsnLeu 1070
DB 2647 AGAAACCTTCCAAACTTCAAAAGAAATGAATGAATCTGAAATCTGAATTAATTGG 2706
QY 1071 LysGlyThrMetGluSerValGluValLys-----IleAla 1082
DB 2707 ATGGAGCTTCTTGAGGCAAAAAGACCAATTAACAATTATCTTACAGTTGAGAA 2766
QY 1083 AspThrLysHisGluLeuGlnGluIleThrIleArgAspLysGlnGlnLeuHisGluLys 1102
DB 2767 GATAAAGAAAACAGTTCTAAAGAAATCTTAAAGTTCTTGAGGCTGTAAGTCAGAGAGAA 2826
QY 1103 ---LysTyrPhePheGlnAlaMetGlnThrIlePheProIleThrProLeuSerAspSer 1121
DB 2827 CAGAAAGAGACGGCAGAGTGTGAGCAGATGGCAAAAGTAACAGAAACTGAGAGAGGC 2886

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QY 1122 LeuProPheSerLysLeuValGluGlnLysSerGlnAspProIleGluIleAsnAspTyr 1141
DB 2887 TTG----- 2889
QY 1142 HisAsnLeuIleAlaLeuAlaThrGluArgAsnAsnIleMetValCysLeuGluThrGlu 1161
DB 2890 -----CTTGCTACTGAAATAA-----GTGATCAGTTCTCCGAAAAAGTCT 2928
QY 1162 ArgAsnSerLeuLysGluGlnValIleAspLeuAsnThrGlnLeuGlnSerLeuGlnAla 1181
DB 2929 AGAGATTCTGATAGAAAAGTTGTAAGTCTCATGAAACCGATCCAGATCCAGAGCTAAGATCA 2988
QY 1182 GlnSerIleGluLysSerAsp---LeuGlnLysProLysGlnAspLeuGluGluGlu 1200
DB 2989 TCGGTCTGAGAAAAGAAACATATAGAACCCCTGAAACAAAGAACTGAGAGACTTAAT 3048
QY 1201 ValLys-----LeuLeuLeuGlnMetGluLeuLeuLysGlyHisLeuThrAspSer 1217
DB 3049 TGCAAATACAACTCGCTTGTGTTGACAGAGAA-----GAGAGC 3087
QY 1218 GlnLeuSerIleGluLysLeuGlnLeuGlnLysAsnGluValThrGluLysLeuGlnThr 1237
DB 3088 AGAGTGTGATCAGAGACAGAGAGTGAATTTCTGATCTGAAAGAAACCTTAGC--- 3144
QY 1238 LeuGlnGlnLysMetLysAsnIleThrIleGluArgAsnGlnLeuGlnThrAsnPheGlu 1257
DB 3145 -----CTGAGAAATCTTCTGAG 3162
QY 1258 AspLeuLysAlaGlnHisAspSerLeuLysGlnAspLeuSerGluAsnIleGluGln--- 1276
DB 3163 GACATA-----GAGAGGATATGCTCTGTAGGACCTGGCTCATGCGCATGACCTGACCTG 3216
QY 1277 -----SerIleGluThrGlnAspGluLeuArgAlaAlaGlnGlu 1290
DB 3217 AACATGCTCACAGAGGCTCTAAAAAACACTCGGGGCTGCTGCACTGCTGCCAGAGAA 3276
QY 1291 LeuArgGlnGlnLysGlnLeuValAspSerPheArgGlnGlnLeuLeuAspCysSerVal 1310
DB 3277 CTGACCAAGAAAGAAAGCCCTGATTCAGGAACCTTGACGACAAAGTA----- 3321
QY 1311 GlyLysSerSerProAsnHisAspAlaValAlaAsnGlnGlnLysValSerLeuGlu 1330
DB 3322 -----AACCAAAAGAA----- 3333
QY 1331 ValAsnSerLeuGlnSerGluMetLeuArgGlyGluArgAspGluLeuGlnThrSerCys 1350
DB 3334 -----GAGGAAGTGAACAGAAAGAAATGAATTAATTAATCAAAATG 3375
QY 1351 LysAlaLeuValSerGluLeuGlnLeuLeuArgAlaHisValLysSerValGluGlyGlu 1370
DB 3376 AGGCAACTA-----GMAATGTGATGATTTGCTGCTGAG 3411
QY 1371 Asn-----LeuGlnIleThrLysLysLeuAsn 1379
DB 3412 GATCCCAAGAGTCTCTAAGACACCACTCTTCAAAACATTTGGGAAAACCTCTGAA 3471
QY 1380 GlyLeuGlnLysGlnIleLeuGlnLysSerGlnGlnSerGluValLeuLysSerMetLeu 1399
DB 3472 ACACAAAGAACAGAGATA-----GAAGATGAGAGAGCCCTTAAGACTTCTTG 3519
QY 1400 GluAsnLeuLysGluAspAsnAsnLysLysLeuGlu-----GlnAlaGluGluTyrSer 1417
DB 3520 GAACACCTTGTAAACAAAGCTTAATTAAGAGACAGAGAGTCAAAAATGCTGAATCTTCAGA 3579
QY 1418 SerLysGlnAsnGlnPheSerLeuGlnValAlaPheSerGlySerGlnLysLeuValAsp 1437
DB 3580 ATGAGAGAGAGATGGGTGAATGAAGAAACCTACGCTGGAAGTCAAGCACTTAATAGAG 3639
QY 1438 GluIleGluValLeuLysAlaGlnLeuLysAlaAlaGlnGluArgLeuGluIleLysAsp 1457
DB 3640 AAAAATCTGCTCTGCAAGAGTCTGATGATATTAAAGACAAAAGAAACAGTGAAT 3699
QY 1458 ArgAspTyrPheGluLeuValGlnThrAlaAsn----- 1468

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QY 371 AlaGlnAlaMetAlaLysGluGluIleHisThrGlnLeuLeuAlaGluIleLysGlnLeuHis 390
 Db 1144 -----CAAGCTCTGTG----- 1155
 QY 391 LysGluArgGluAspArgIleThrPheLeuThrAsnIleValValAlaSerSerGlnGlu 410
 Db 1155 ----- 1155
 QY 411 SerGlnGlnAspGlnArgValLysArgLysArgValThrTrpAlaProGlyLysIle 430
 Db 1155 ----- 1155
 QY 431 GlnAsnSerLeuHisAlaSerGlyValSerAspPheAspMetLeuSerArgLeuProGly 450
 Db 1156 -----CTACAGGCCCATGGA-----GTAACCTGCTCTGGA 1185
 QY 451 AsnPheSerLysLysAlaLysPheSerAspMetProSerPheProGluIleAspAspSer 470
 Db 1186 TCTATTAAGCTGTGGA-----CCATCA----- 1206
 QY 471 ValCysThrGluPheSerAspPheAspAlaLeuSerMetAspSerAsnGlyIle 490
 Db 1207 -----GAGATCTACATCTCCGTATGAGAAAGAT----- 1236
 QY 491 AspAlaGluTrpAsnLeuAlaSerLysValThrHisArgGluLysThrSer-----Leu 508
 Db 1237 -----CAGTCCCTGCTAGAGAAATGAAATAAATTAAGTCGTGTCTG 1278
 QY 509 HisGlnSerMetLeuAspPheGluGlnIleSerAspSerValGlnMetHisAspSerSer 528
 Db 1279 ACCGAGGCGAGCTGTGACAGACCCAGATGTTGGAAGAGATCTTTGGACAGAGCAAGG 1338
 QY 529 LysGluAsnGlnLeuGlnIleuPheProLysAspSerGlyAspMetAlaGluCysArgLys 548
 Db 1339 AATGAA-----AAATGAACGCCAAGCTAAGAAAGCTCAGCGAG 1377
 QY 549 ---AlaSerPheGluLysGluIleThrSerLeuGlnGlnLeuGlnSerLysGlu--- 566
 Db 1378 CATGCGCCTGCMAACTGCATCTTCAAAAGCTAGTGAGACTTTGGAAAGCAAGCATG 1437
 QY 567 GlnGluLysLysGluLeuValGlnSerPheGluLeuLysIleAlaGluLeuGluGln 586
 Db 1438 AAAGAAATGTAGAGATTAATTGTTACTGTCAGCAATTAATTAATCCAGTTATCGAGTGA 1497
 QY 587 LeuSerValLysAlaLysAsnLeuGluMetValThrAsnSerArgLysIleSerIleAsn 606
 Db 1498 -----ACTGTGCTGTGCATGCGTCGACGCATTAATCTGCGTGGAG 1539
 QY 607 AlaGluValGlnThrAspValGluLysGluValValArgLysGluMetSerValLeuGly 626
 Db 1540 CAAGAAAGCCCAAGTAAAGCCAGTCCAGAG----- 1569
 QY 627 AspSerGlyTyrAsnAlaSerAsnSerAspLeuGlnAspSerSerValAspGlyLysArg 646
 Db 1570 -----ACGACAGAGTCTTCTGACGCTTTTACCACTGAGATCTCTCCGT 1614
 QY 647 LeuSerSerSerHisAspLysCysIleGlnHisArgLysMetLeuGlnLysIleVal 666
 Db 1615 CAAGGCGAGATGTCTAAGAGAGCGGTGAGTTGAATTAAGCGCTTGCACTGAAA----- 1668
 QY 667 AspLeuGluGluPheIleGluAsnLeuAsnLysLys---SerGluAsnAspLysGln--- 684
 Db 1669 -----GAGGCCCTGCTAGAGATGATCAGATGACGCAACTG 1710
 QY 685 LysSerSerGluGlnAspPheMetGluSerIleGlnLeuCysGluAlaIleMetLeuGlu 704
 Db 1711 CAGCCTATTCTACCTACCATCAAGATACATA----- 1743
 QY 705 LysAlaAsnAlaLeuGluLeuAlaLeuMetArgAspAsnPheAspAsnIleIleLeu 724
 Db 1744 AAAGAGCCAGATTTGAAGTATCAATCTGCAAAAGGAAAG---GAAAGATTGGTCTT 1800

QY 725 GluAsnGluThrLeuLysArgGluIleAlaAspLeuGluArgSerLeuLysGluAsnGln 744
 Db 1801 GAACCTTCAGACAGCAAGAGAGATGCCAAACCAAGCCAAAGTTGATGAGCGCGCCGCAAA 1860
 QY 745 GluThrAsnGluPheGluIleLeuGluLysGluThrGlnLysGlnHisGluAlaGlnLeu 764
 Db 1861 CGCTTCACAGAGCTGAGAGGCTCAAAATGCTGATCTGAAAGAGAA----- 1905
 QY 765 IleHisGluIleGlySerLeuLysLeuValGluAsnAlaGluMetTyrAsnGlnAsn 784
 Db 1906 CTGAATGAGCAAGTCCAAACTTGAAGTAAAGAAATCCACAGACCGTAATCTCTCCAAA 1965
 QY 785 LeuGluGluAspLeuGluThrLysThrLysLeuLeuLysGluGlnGluIleGlnLeuAla 804
 Db 1966 CTGAACCCAGAGATA-----CGATGATGAAAAAACACAGCGGTACAGTTA--- 2010
 QY 805 GluLeuArgLysArgAlaAspAsnLeuGlnLysLysValArgAsnPheAspLeuSerVal 824
 Db 2011 ---ATGCGTCAATGAAGAAAGATGCTGAG---AAGTTTACACAGTGG----- 2052
 QY 825 SerMetGlyAspSerGluLysLeuCysGluGluIlePheGlnLeuLysGlnSerLeuSer 844
 Db 2053 -----AAGCAGAAAAGAGACAAAGAGATTAATACAGTTAAAGAA----- 2091
 QY 845 AspAlaGluAlaValThrArgAspAlaGlnLysGluCysSerPheLeuArgSerGluAsn 864
 Db 2092 -----CGAGACCGTAAAGAGCA-----TATGAGCTG 2118
 QY 865 LeuGluLeuLysGluLysMetGluAspThrSerAsnTrpTyrAsnGlnLysLysAla 884
 Db 2119 CTGAATCTGAAAGAACTTCCAGAAACAATCCAAATGCTTCAGACGTAACGAGAGAG 2178
 QY 885 AlaSerLeuPheGluLysGlnLeuGluThrGluLysSerAsnTyrLysLysMetGluAla 904
 Db 2179 GCAGCAGCTGCCAACAAGACGTCCTCAAGATGCTCCAGAAACAACGAGAGGTT---GCA 2235
 QY 905 AspLeuGlnLysGluLeuGlnSerAlaPheAsnGluIleAsnTyrLeuAsnGlyLeu--- 923
 Db 2236 GATTAAGCCGAAAGAGACTCCAGAGC-----CGTGCATGAGAA 2271
 QY 924 ---LeuAlaGlyLysValProArgAspLeuSerAsnArgValGluLeuGluLysLysVal 942
 Db 2272 GGCACGTGACGCTCCAGTAAGAATGCTTGAAACCAAAATTAAGCTTAATGCTCAATCT 2331
 QY 943 SerGluPheSerLysGlnLeuGluLysAlaLeuGluGluLysLysAsnAlaLeuGluAsnGlu 962
 Db 2332 GAGGAAGCCAAACGCACTGATGAATGACCTCTTGAAGTAAAGAAAGATCTGCTCAAGAT 2391
 QY 963 ValThrCysLeuSerGluTyrLysPheLeuProAsnGluValGluCysLeuLysAsnGln 982
 Db 2392 GTGGCTCAACTCAAGAA----- 2409
 QY 983 IleSerLysAlaSerGluGluIleMetLeuLysGlnGluGlnLysSerAlaSer 1002
 Db 2410 -----AAAAAGAACTGGGAGAAATCCACTCTCT 2439
 QY 1003 IleIleSerLysGlnGluIleIleMetGlnGlnGlnSerGluGlnIleLeuGlnLeuThr 1022
 Db 2440 AAATCCCGAGCGGATCAATCTCCCTTACTGAGAGCGGTGCTCAAGTT----- 2487
 QY 1023 AspGluValThrHisThrGlnSerLysValGlnGlnThrGluGluGlnTyrLeuGluMet 1042
 Db 2487 ----- 2487
 QY 1043 LysLysMetHisAspAspLeuPheGluLysTyrIleArgAsnLysSerGluAlaGluAsp 1062
 Db 2488 -----TCGAGTCAAGAT 2502
 QY 1063 ---LeuLeuArgGluMetGluAsnLeuLysGlyThrMetGluSerValGluValLysIle 1081
 Db 2503 TCTATTCAAGACAGATTGAAGCTTGAAGCTGAATGCAATTCAGAGAGTCCAGATT 2562
 QY 1082 AlaAspThrLysHisGluLeu-----GluGluThrIleArgAspLysGluGln--- 1097


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QY 153 ArgGluAspPheAsnArgValTyrValAlaAspLeuThrGluGluLeuValMetVal 172
   |||
Db 592 CGGGGAGATCTTAAGAGACATTAAGATGTGGGACTCACTGAGAGACGTTTACTT 651
QY 173 ProGluHisValIleGlnTrpIleValLeuValGluValAsnValGluValGluVal 192
   |||
Db 652 GCCTTGATCTACTGTTCTGTTTGGAGCAGGCAACACTCTAGACTGTGGCTCCACA 711
QY 193 LysMetAsnAspHisSerSerArgSerHisThrIlePheArgMetIleValGluSerArg 212
   |||
Db 712 GCTATGAACCTCCAGCTGCTCCGATCTCATCTTACATCTCTTACATCTCTTACAGCAAGA 771
QY 213 AspArgAsnAspProThrAsnSerGluAsnGluAsnGluValMetValSerHisLeu 232
   |||
Db 772 AAGAAAGGTGACAAAGATAGCAGC-----TTTCCTCCAGCTG 810
QY 233 AsnLeuValAspLeuValGluSerGluArgAlaSerGluThrGluValGluValArg 252
   |||
Db 811 CATCTGTAGACCTCGCTGATCAGAAAGACAGAGAAACCAAGCTGAGAGGAGATCGT 870
QY 253 LeuValGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 272
   |||
Db 871 CTAAAGAGGGGTATTAATTAATTAACCGAGGCTCTATGCTGGGAATGTAATCAGTCT 930
QY 273 LeuSerAspGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 292
   |||
Db 931 CTGGAGATGACAAAGAGGTAGCTTGTGCTCCCTACAGAGATTCAGATTACTCCAGCTG 990
QY 293 LeuGluAsnSerLeuGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 312
   |||
Db 991 CTGCAAGATCTCTAGAGAGTAAACAGCCACACTTATGATGACCTGTGAGATCTGCT 1050
QY 313 SerPheAspGluThrLeuSerThrLeuGluPheAlaSerThrAlaValHisVal 330
   |||
Db 1051 GACTCCATCTTAAGCAAGAACTTAAGTACCTTCGATGCTGACAGCAAGAAATATC 1110
QY 331 ArgAsnThrProHisValAsnGluValLeuAspAspGluAlaLeuLeuValArgTyr 350
   |||
Db 1111 AAGAACAAACCTTATGTTTAAAT-----ATTATCTCCACACA 1146
QY 351 LysGluIleLeuAspLeuValGluGluGluGluGluGluGluGluGluGluGluGlu 370
   |||
Db 1147 GCTGAAGTAACTTAAAGCAAGCAAGTAAACAGCTA----- 1185
QY 371 AlaGluAlaMetAlaLysGluGluGluGluGluGluGluGluGluGluGluGluGlu 390
   |||
Db 1186 -----CAAGCTTGTG----- 1197
QY 391 LysGluArgGluAspArgIleTrpHisLeuThrAsnIleValAlaSerSerGlnGlu 410
   |||
Db 1197 ----- 1197
QY 411 SerGlnGluAspGlnArgValValArgLysArgValThrTrpAlaProGluLysIle 430
   |||
Db 1197 ----- 1197
QY 431 GlnAsnSerLeuHisAlaSerGluValSerAspPheAspMetLeuSerArgLeuProGlu 450
   |||
Db 1198 -----CTACAGCCCATGGA-----GGTACCCTGCTGGA 1227
QY 451 AsnPheSerLysLysAlaLysPheSerAspMetProSerPheProGluIleAspAspSer 470
   |||
Db 1228 TCTATAAATGCAGAA-----CCATCA----- 1248
QY 471 ValCysThrGluPheSerAspPheAspAlaLeuSerMetMetAspSerAsnGluIle 490
   |||
Db 1249 -----GAGATCTACATCCCTGATGAGAGAAAT----- 1278
QY 491 AspAlaGluTrpAsnLeuAlaSerLysValThrHisArgGluLysThrSerLeuHisGln 510
   |||
Db 1279 -----CAG 1281

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QY 511 SerMetIleAspPheGluGlnIleSerAspSerValGlnPheHisAspSerSerGlu 530
   |||
Db 1282 TCCCTGTGAG-----GAGAAATGAA 1302
QY 531 AsnGlnLeuGlnTrpLeuProLysAspSerGluAspMetAlaGluCysArgLysAlaSer 550
   |||
Db 1303 AAATTAAGCTGTTGTCGAAAGCAGCTGTGTCAGACGCCCAATGTTGGAGAGATC 1362
QY 551 PheGluLysGluIleThrSerLeuGlnGlnLeuGlnSerLysGluGluGluLysVal 570
   |||
Db 1363 ATTTGACAG-----CAAGTGAATGAAATGAAACCGCCAGCTGAGAGCTCAGG 1416
QY 571 Glu-----LeuValGlnSerPheGluLeuLysIle 580
   |||
Db 1417 CAGCATGGGCGCTGACAGCTGATCTTCAAAAGCTAGTGGAGACTTGGAGACCAG-- 1473
QY 581 AlaGluLeuGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 600
   |||
Db 1474 ---GAATTGAAAGAAATGATGAGATATTGTAACCTGCAGCAACTGATTACCACTTA 1530
QY 601 ArgGluHisSerIle-----AspAlaGluValGlnThrAspValGluLysGluVal 617
   |||
Db 1531 TCAGATGAACCTGTTGCTTGCACGCGCTGCACCACTGATGCTGCGTGAAGAGAA-- 1587
QY 618 ValArgLysGluMetSerValLeuGluLysPheSerGluTyrAsnAlaSerAsnSerAsp 637
   |||
Db 1588 -----GCTCAAGTGAACCACT 1605
QY 638 GlnAspSerSerValAspGluLysArgLeuSerSerHisAspGluCysIleGluHis 657
   |||
Db 1606 CCAGAGACAAACAGCTCTTGCAGCCTTTTACCACTGAGCT-----GCTCTCCAT 1656
QY 658 ArgLysMetLeuGluGlnLysIleValAspLeuGluGluPheIle-----Glu 673
   |||
Db 1657 CAAGCTCAGAGCTTAAGAGCTGTTGATGAATTAACCCCTTGCACTGAAGAGGCC 1716
QY 674 AsnLeuAsnLysLysSerGluAsnAspLysGlnLysSerSerGluGlnAspPheMetGlu 693
   |||
Db 1717 CTAGTTGGAAGAGTCACTGACAGACCAACCA-----CTACAG 1755
QY 694 SerIleGlnLeuGluGluAlaIleMetAlaGluLysAlaAsnAlaLeuGluGluLeuAla 713
   |||
Db 1756 CCCATTAGTT----- 1767
QY 714 LeuMetArgAspAsnPheAspAsnIleIleLeuGluAsnGluThrLysValArgLysIle 733
   |||
Db 1768 CAATACAGAGATTAATTAATAATCTGAATTAAGATCAATCTGCAAAAGAGAAAG 1827
QY 734 AlaAspLeuGluArgSerLeu-----LysGluAsnGlnGluThrAsnGluPheGlu 750
   |||
Db 1828 GAGAAATTTGTTGTTGAACCTTCAAGACAGCAAAAGAAAGTCCAAACCAAGCAAGCTGAGT 1887
QY 751 IleLeuGluLysGluThrGlnLysGluHisGluAlaGlnLeu----- 764
   |||
Db 1888 GAGCAGCGTCGCAAACTTCCAGAGGCTGAGAGCTGAATATCTGATCTGAAGAGAA 1947
QY 765 IleHisGluIleGluSerLeuLysLysLeuValGluAsnAlaGluMetLysThrAsnGln 784
   |||
Db 1948 CTGAATGAGCAGTCCAAACTTCTGAATACTTAAGGAATCCACAGAGGCTACTGTCCAAA 2007
QY 785 LeuGluGluAspLeuGluThrLysThrLysLeuLeuLysGluGlnIleGlnLeuAla 804
   |||
Db 2008 CTGACACGAGATTA-----CGATGATGAAAAACAGCGGCTACAGTTA--- 2052
QY 805 GluLeuArgLysArgAlaAspAsnLeuGlnLysValArgAsnAspPheLeuSerVal 824
   |||
Db 2053 ---ATCGTCAATTAAGAGAGATGCTGAG---AAGTTAGACAGTGC----- 2094
QY 825 SerMetGluAspSerGluLysLeuGluGluIlePheGlnLeuLysGlnSerLeuSer 844
   |||
Db 2095 -----AAGCAAGAAAGAGACAAAGAGTAATTAAGTTAAAGAA--- 2133
QY 845 AspAlaGluAlaValThrArgAspAlaGlnLysGluCysSerPheLeuArgSerGluAsn 864

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Db- 2134 -----CGAGCCCTAGAGGCA-----TATAGCTG 2160
QY LeuGluLeuLeuGluLeuMetGluLeuSerAspThrTrpAsnGluLeuVala 884
Db 2161 CTGAAGACCTGAAAGAACTTCAGAAACAATGCTCAGAGCTGAAACGAGGAG 2220
QY AlaserLeuPheGluLeuGluLeuGluLeuThrGluLeuSerAspThrTrpAsnGluVala 904
Db 2221 GAGAGAGCTGCCAAGCGCTCAAGATGCTCTCCAGAAACAGGAGGTT--GCA 2277
QY AspleuGluLeuGluLeuGluLeuSerAlaPheAsnGluLeuAsnTrpLeuAsnGluLeu 923
Db 2278 GATAGCGGAAAGAGACTAGAC-----CGTGAATGGA 2313
QY 924 ---LeuAlaGlyLeuValProArgPheLeuLeuSerArgValGluLeuGluLeuVal 942
Db 2314 GGCACCTGCGAGCTCGAGTGAAGATTGCGCTTGGAATGAAATTGAGGTTATGCTCAGTACT 2373
QY SerGluPheSerLeuGluLeuGluLeuValaLeuGluLeuLeuValaAsnAlaLeuGluLeu 962
Db 2374 GAGAGAGCCAAAGCGCATGTGAATGACCTCTTGAAAGACAGAAAGATCTGCTCAGGAT 2433
QY ValThrCysLeuSerGluTrpTrpPheLeuProAsnGluValGluCysLeuValaAsnGlu 982
Db 2434 GTGCTCAACTCAAGAA----- 2451
QY 983 IleSerValaSerGluGluLeuMetLeuLeuGluGluGluGluHisSerAlaSer 1002
Db 2452 -----AAAAAGAAATCTCGGAGAAATCCACTCTCT 2481
QY 1003 IleIleSerLeuGluGluLeuIleLeuMetGluGluGluGluGluGluLeuLeuThr 1022
Db 2482 AAATCTCGGAATGTAACATTCTCCCTTCTGAGGTGCATGTCAGATTGTGAGTCAGA 2541
QY 1023 AspGluValaThrHisThrGluLeuSerValaGluGluGluGluGluGluLeuGluMet 1042
Db 2542 GATTGTATTACA-----AAACGATTGAAAGCTTGAGACATAAGTAAGAAC 2589
QY 1043 LysValaMetHis--AspAspLeuPheGluLeuValaArgAsnLysSerGluValaGlu 1061
Db 2590 AGGAGTGTCAAGATTGCTGCTACAGCAAGCTGCTGATGCAAGAAAGTGAAGATAGG 2649
QY 1062 AspleuLeuValaGluMetGluLeuAsnLeuLysGlyThrMetGluSerValaGluVala 1081
Db 2650 CG-BCAAAACAATGCTGGAGAAATATTCGCCACATTCTGGAAGCC-----AAGTGT 2699
QY 1082 AlaAspThrLysHisGluLeuGluGluLeuThrIleArgAspLysGluLeuLeuHisGlu 1101
Db 2700 GCC---CTGAATATTGATTGGAAGCTGCTCTCTCCAA-----ATACAT--- 2744
QY 1102 LysValaTrpPhePheGluAlaMetGluThrIlePheProIleThrProLeuSerAspSer 1121
Db 2745 -----GTCACCAAACTGAAAAACAGC 2765
QY 1122 LeuProProSerLeuLeuValaGluGluLeuSerGluAspProIleGluLeuAsnAspTrp 1141
Db 2766 CTGACAGACAGACAGCCAGCTGCTGCTGATGCAAGAACATGCTA---TTTGAGAGAACAA 2822
QY 1142 HisAsnLeuIleAlaLeuAlaThrGluArgAsnAsnIleMetValCysLeuGluThrGlu 1161
Db 2823 AATCTTTTCTGAGATAGACAGACAGATTCAAGCTGAGCTGCTGATGAGTGAACAGCAG 2882
QY 1162 ArgAsnSerLeuLysGluGluValaIleAspLeuAsnThrGluLeuGluSerLeuGlu 1180
Db 2883 CAC-----CAGAGAGAGGTGCTATCTTGCAGCCAGCTCAGAGAAAGCCAAATG 2933
QY 1181 ---AlaGluSerIleGluLysSer----- 1187
Db 2934 GCAGAGAGCAAGTGAAGAAATCACCAGTGAAGAAAGCAACAGTGTGTCAGCACACTG 2993
QY 1188 -----AspleuGluLysProLysGluAspLeuGluGluGluValaValaLys 1202

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Db 2994 CAGTGTCAAGATGAAGAACTTGAGAGATGCGAGAGTGTGTGACAAAATCAG---CAG 3050
QY 1203 LeuLeuLeuGluMetGluLeuLeuLysGlyHisIleThrAspSerGluLeuSerIleGlu 1222
Db 3051 CTTCTTCAAGAGAAATGAATATCATCAAGCAAGAACTGATCTCTCCAGGTACCGACAGA 3110
QY 1223 LysLeuGluLeuGluAsn-----LeuGluValaThrGluLysLeuGluThrLeuGlu 1239
Db 3111 CAGAAACATCTTCCATATGATACCTTCTATCTCCAGACTCTTCTTTGAAATATATCCCA 3170
QY 1240 GluGluMetLysAsnIleThrIleGluArgAsn-----GluLeuGluThrAsnPheGlu 1257
Db 3171 CTAAGCCAAAACCTTCTCGGTGTTAAAGAAAGTTTCTGAGCAAAAGATGACATCGAG 3230
QY 1258 AspleuLys-----AlaGluHisAspSerLeuLysGluAspLeuSerGluLeuIleGlu 1275
Db 3231 GATCTTAAATATATTGTCAGAGCATTTCTGTGAATGACATGAGATGCTGATGATGCG 3290
QY 1276 GluSerIleGluThrGluAspGlu-----LeuArgAlaAlaGlu 1288
Db 3291 CACAGTATGAGGGGAGATGATGAGAAATGGAAGCCCAAAATTGTCAGGTCTCCAG 3350
QY 1289 GluGluLeuArg-----GluGluLysGluLeuValaAspSer 1300
Db 3351 AAGAACATCCAAAGGCTGCTTCTGCAAGGCTGTGTGGAAACACAGACTGT-----GCG 3404
QY 1301 PheArgGluGluLeuLeuAspCysSerValaGlyIleSer---SerProAsnHisAspAla 1319
Db 3405 TGCAGAGAGCAAAAGTCAGACTGTGTGTGACTGTGACTGTGACCCCAAAAGTGTGCG 3464
QY 1320 ValAlaAsnGluGluLeuValSerLeuGluGlyValaAsnSerLeuGlu 1335
Db 3465 AACCCCGACAGAGCAAGATAGCTTGGGCACTGTGTAACAGACCCAG 3512

RESULT 11
US-09-722-139-1
; Sequence 1, Application us/09722139
; Patient No. 6355471
; GENERAL INFORMATION:
; APPLICANT: Berand, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6355471el motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1055
; CURRENT APPLICATION NUMBER: US/09/722,139
; CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4176
; TYPE: DNA
; ORGANISM: Human
US-09-722-139-1

Alignment Scores:
Pred. No.: 2,676-64 Length: 4176
Score: 915.50 Matches: 416
Percent Similarity: 40.59% Conservative: 246
Best Local Similarity: 25.51% Mismatches: 536
Query Match: 6,204 Indels: 433
DB: 4 Gaps: 71

US-09-724-584-1 (1-2954) x US-09-722-139-1 (1-4176)
QY 6 AlaValLysValaCysValaArgValaArgProLeuIleGluArgGluGluGluValaAspGluAla 25
Db 7 TCGGTCAAGGTGCGCGGTGAGGTCGCCCATGATGCCAGGAAAGAGACTGTGAGGCC 66
QY 26 Asn-----LeuGluTrpLysAlaGlyAsnAsnThrIleSerGluVala----- 39
Db 67 AAGTTCATTATTCAAGATGAGAAAGCAAAAGCAACAACTTAAGATACAGAA 126
QY 40 -----AspGlyThrLysSerPheAsnPheAspArgValaPhe 51

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Db      127 GAGGACATGGGACTCAGAGAGAGACGACCAAGACCTTACCTTGTCTTT 186
Qy      52 AenserHisGluSerThrSer-----GlnIleTyrGlnGlnIle 64
Db      187 TATTCGTGTATACAAAAGCCAGATTACGTTTCAACAAGAAATGGTTTCAAAACCTC 246
Qy      65 AlaValProIleIleArgSerAlaLeuGlnIleTyrAsnGlyThrIlePheAlaTyrGly 84
Db      247 GGCACAGATGTCGAACTCTGCACTTGAAGGTATATATGCTTGCTTGCTTGAATGG 306
Qy      85 GlnThrSerSerGlyLysThrTyr-ThrMetMetGlyThrProAsnSerLeuGlyIle 104
Db      307 CAACATGATCTGAAAGTCAATACATATGATGAGAAATTCGTGAGATTCGTGTTATA 366
Qy      105 ProGlnAlaIleGlnIleValPheLysIleIleGlnIle-----ProAsnArg 121
Db      367 CCTCGCATCTGTGAAGACTCTTCACTCGGATTAATGAACCCACAGATGGATGAAGCT 426
Qy      122 GluPheLeuLeuArgValSerTyrMetGlnIleTyrAsnGlyThrValLysAspLeu 141
Db      427 TCTTTTGAACTGAAGTCACTACTTAGAAATTTATACGAACTGTGAGAGATCTACTT 486
Qy      142 CysAspAspArgArgLysLysPro-----LeuGlnIleArgGlyAspPheAsn 157
Db      487 -----CGGGGGAAGTCACTAAACCTTCAATTGAGAGCTCGTGAGCATCCCAAA 537
Qy      158 ArgAsnValTyrValAlaAspLeuThrGlnGlnLeuValMetValProGlnHisValIle 177
Db      538 GAAGGCCCTTATTTGAGATTATCCAAACATTGATGACAAATATGATGATGATGATGAA 597
Qy      178 GlnThrIleLysLysGlyGlnLysAsnArgHisTyrGlyGlnThrLysMetAsnArgHis 197
Db      598 GAATCTATGATGATCGGCAATATCAACCGAACCGACGCTGGATGAGAACGACGTC 657
Qy      198 SerSerArgSerHisThrIlePhe-----ArgMetIleValGlnSerArgAspArgAsn 215
Db      658 AGTAGAGAGTCTCATGCACTTCCACATCAAGTCACTACAGGCTAAATTTGATTTCTGAA 717
Qy      216 AspProThrAsnSerGluAsnGlyAspGlyAlaValMetValSerHisLeuAsnLeuVal 235
Db      718 ATGCCA-----TGTGAA-----ACCGTCAAGTAAAGTCCACTTGTT 753
Qy      236 AspLeuAlaGlySerGlnArgAlaSerGlnThrGlyAlaGlnGlyValArgLeuLysGln 255
Db      754 GATCTTGGCGGAAGTGAAGGTGAGATGCCACCGAGCCACCGGGTTTACGTTTAAAGGA 813
Qy      256 GlyCysAsnIleAsnArgSerLeuPheIleLeuGlyGlnValIleLysLysLeuSerAsp 275
Db      814 GGGGGAATATTAAACAAAGTCCCTTGACTCTGGGAAAGCTCATTTCTGCTTACTGAT 873
Qy      276 GlnGlnAlaGlyGly-----PheIleAsnTyrArg 285
Db      874 TTATCTCAGGATCGCGAAATACTCTTGAAGAAAGAAAGCAAGTTTGTGCTTAAACGG 933
Qy      286 AspSerLysLeuThrArgIleLeuGlnAsnSerLeuGlyGlyAsnAlaLysThrValIle 305
Db      934 GATTCGTGCTTACTGCTGTTTAAAGTAGCTTGGAGAACTCTTAAACATATCATCG 993
Qy      306 IleCysThrIleThrPro-----ValSerPheAspGlyThrLeuSerThrLeuGlnPhe 323
Db      994 ATTGCCACCATTTTCACTGCTGATGTCAATTAAGAGAAACCTTAAAGTACTTCCGCTAT 1053
Qy      324 AlaSerThrAlaLysHisValArgAsnThrProHisValAsnGlnValLeuAspAspGln 343
Db      1054 GCAATATAGAGCAAAACATCATCAACAAGCTTACATTAATGAGATGCCAACGCTCAAA 1113
Qy      344 AlaLeuLeuLysArgTyrArgLysGlnIleLeuAspLeuLys----- 357
Db      1114 ---CTTATCCGTGAGCTCGAGCTGAATATAGCCAGACTGAAGAAAGCTGCTTCAAGGG 1170
Qy      358 LysGlnLeuGlnAsnLeuGlnSerSerSerGlnThrLysAlaGlnAlaMetAlaLysGln 377

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Db      1171 AATCAGATTGCCCTCTTAGACTCCCCACA-----GCTTAAAGTATGAG 1215
Qy      378 GluHisThrGlnLeu---LeuAlaGlnIleLysGlnLeuHisLysGlnArgGlnAspArg 396
Db      1216 GAAAAATTACAGAGATGAAGTAAAGCAAGAGTTCAAGATTTGACCAAGAAATGCAAAATAG 1275
Qy      397 IlePheIleLeuThrAsnIleValAlaAspSerGlnGlnSerGlnGlnAspGlnArg 416
Db      1276 ---TGAATGAAGAAC-----CAAAAT 1293
Qy      417 ValLysArgLysArgArgValThrTrpAlaProGlyLysIleGlnAsnSerLeuHisAla 436
Db      1294 ATTTTGAAAGAACAAACTCTA-----GCCCTCAGGAAA 1326
Qy      437 SerGlyValSerAspPheAspMetLeuSerArgLeuProGlyAsnPheSerLysAla 456
Db      1327 GAAGGATTTGCA-----GTTGTT 1344
Qy      457 LysPheSerAspMetProSerPheProGlyIleAspAspSerValCysThr----- 473
Db      1345 TTGATTTGAAAGTGGCTCATTTGATTTGGCATGATGATGACCTTTGAGTACTGCAATC 1404
Qy      474 -----GluPheSerAspPheAspAspAlaLeuSerMet 484
Db      1405 ATCTTATATCATTTAAAGAAAGTCAACATACCTGTGTAGAGACGATGCTTCCACGGAG 1464
Qy      485 MetAsp-----SerAsnGlyIleAspAlaGln-----TrpAsnLeu 496
Db      1465 CAAGATATGTTCTTTCATGAGCTGCTTGAATGAGAGTGAAGTCACTTGTGAAATATC 1524
Qy      497 AlaSerLysValThrHisArgGlnLysThrSerLeuHisGlnSerMetIleAspPheGly 516
Db      1525 GGGGGACAGTGACT---CTGATACCCCTGAGTGGTCCAGTGCCTGTGGAATGGTGT 1581
Qy      517 GlnIleSerAspSerValGlnPheHisAspSer-----LysGlnAsn 531
Db      1582 CAGATTCGTGGAGGCCACATCTTAATCAAGTGTGCTGTGATTTCTTGGGAAAGAACCAAT 1641
Qy      532 GlnLeuGlnTyr---LeuProLysAspSerGlyAspMetAlaGlyCysArgLys----- 548
Db      1642 ATGTTGCGCTTAAACATCCAAAGAAAGCCGCAAGCTCAGGAGAAAGAAAGATGGC 1701
Qy      549 -----AlaSerPheGlnLysGlnIleThrSerLeuGlnGlnIleGlnSerLysGln 566
Db      1702 CTCTGTGCTCTTCACTTGCATGATGACCCACCTC-----TGAAGTCC 1746
Qy      567 GlnGlnLysLysGlnLeuValGln-----SerPheGlnLeuLysIle 580
Db      1747 CGTGAAGAACTGTCTGAGTCACTGTGTATTAACCCGAGCTGAATTTGAGGCAACAG 1806
Qy      581 AlaGlnLeuGlnGlnLeuSerValLysAlaLysAsnLeuGlnMetValThrAsnSer 600
Db      1807 CGTGAAGAACTTGAATAATTAAGAAAGTAAAGAACTCATGAGAAATG---GAGGAA 1863
Qy      601 ArgGlnHisSerIleAsnIleGlnValGln---ThrAspValGlnLysGlnValValArg 619
Db      1864 AACGAGAAATCAGACAAGGCTGAATCGAGCGGATGCAACAGAGAGGTGAGACCCAGCC 1923
Qy      620 LysGlnMetSerValLeuGlnLysAspSerGlyTyrAsnAlaSerAsnSerAspLeuGlnAsp 639
Db      1924 AAGGAGACAGAAATCGTG-----CAGCTCCAG--- 1950
Qy      640 SerSerValAspGlyLysArgLeuSerSerHisAspGlnCysIleGlnHisArgLys 659
Db      1951 -----ATTCCAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1986
Qy      660 Met---LeuGlnGlnLysIleValAspLeuGlnGlnIleGlnLysLeuAsnLysLys 678
Db      1987 TTCACATGAGAGAACAGTAAAGATTTA-----CTTGGGAGAGAG 2028
Qy      679 SerGlnAsnAspLysGlnLysSerSerGlnGlnAspPheMetGlnSerIleGlnLeuLys 698
Db      2029 GAAAAATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2061

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QY 699 GluAlaIleMetAlaGluLysAlaAsnAlaLeuGluGluLeuAlaLeuMetArgAsp 718
 Db 2062 -----CAGGAATGCACTGCAGAAAGAGA 2088
 QY 719 PheAspAsnIleIleLeuGluAsnGluThrLeuLysArgGluIleAlaAspLeuArg 738
 Db 2089 -----CAGGAAGAGAGACCTTCTCCGCTCCAGGAAGAACTCCAGGA 2133
 QY 739 -----SerLeuLysGluAsnGlnIleThrasnGluPheGluIleLeuGluLys----- 754
 Db 2134 CTCAAGAACTCAACACAGAGAGAGCTGAGAGATTTCAGATTTTCAGAGAACTGAGC 2193
 QY 755 GluThrGlnLysGluHisGluAlaGlnLeuIleHisGluIleGlySerLeuLysLeu 774
 Db 2194 CAGCTCCAAAGAAAAGAAATGAAACAGATGCC--AAGCTGAACTGAAAAGAGAA 2250
 QY 775 ValGluAsnAlaGlu-----MetTyrAsnGlnAsnLeuGluAspLeuGlu 790
 Db 2251 CTAGAGAGCAGAGAGAGAGAGAGCTCATGCTCGGCCCATCTGGAAGAGAGCTCCGA 2310
 QY 791 ThrLys-----ThrLysLeuLeuLysGluGlnGluIleGlnLeuAlaGluLeuArg 807
 Db 2311 GAGAAAGCAGAGATGATCCAGCTCCTGCGCGCTGGAGAGTACAGTGGGTGGAAGAGAG 2370
 QY 808 LysArgAlaAspAsnLeuGlnLysLysValArgAsnPheAspLeuSerValSerMetGly 827
 Db 2371 AAGAGG----- 2376
 QY 828 AspSerGluLysLeuCyGluGluIlePheGlnLeuLysGlnSerLeuSer----- 844
 Db 2377 GACCTGAGAGCATTCGGGAATCCTCTCGCGGAGGAAGAGCTCGGCCGAGAGGAT 2436
 QY 845 ---AspAlaGluAlaValThrArgAspAlaGlnLysGluCySerPheLeuArgSerGlu 863
 Db 2437 GAAAGTGGCAGAGAGATTGAAAAGGCTCACTGCTTCTTCGAATTCAGAGAAAGCAG 2496
 QY 864 AsnLeuGluLysValGluLysMetGluAspThrSerAsnTyrTyrAsnGlnLysGlu 883
 Db 2497 CTTGTCAAGCTAGTGAACTTGAGAAAGAGCCTGCTTCAAGAAAGAGCTCTGAAAAA 2556
 QY 884 AlaAlaSerLeuPheGluLysGlnLeuGlnThrGluLysSerAsnTyrLysMetGlu 903
 Db 2557 GAAGTCCAAAGAGAGAGAGATCTTAGAGTGTAAATGTGAACATGACAAAGATCT 2616
 QY 904 AlaAspLeuGlnLysGluLeuGlnSerAlaPheAsnGluIleAsnTyrLeuAsnGlu 923
 Db 2617 AGATTGTTGAAAACATGATGAGTGCACAGAT----- 2652
 QY 924 LeuAlaGlyLysValProArgAspLeuSerArgValGluLeuGlnLysValSer 943
 Db 2653 ---GTCAGGAAAGTCCCAAGATTTGAGAAAATTAAGCCAGTGTACAGCTGCA 2709
 QY 944 GluPheSerLysGlnLeuGluLysAlaLeuGluGluLysAsnAlaLeuGluAsnGluVal 963
 Db 2710 TATTAAGAACCCCAAGCTACAG-----TACCTCTTCAGAAATCTCTTG 2751
 QY 964 ThrCySerLeuSerGlu-----TyrLysPheLeuProAsnGluValGluCyS 978
 Db 2752 CCAACTGCTTGGAAGAAAGAGAGAGCATTTGAAATTTCTGACAGAGGCCCTCAGC 2811
 QY 979 LeuLysAsn-----GlnIleSerLysAlaSerGluGluIleMetLeuLeuLysGln 995
 Db 2812 TTAGACAAACACTTTTATCAAGTAGAAAAGAAATAGAGAA----- 2853
 QY 996 GluGluGluHisSerAlaSerIleLeuSerLysGlnGluIleIleMetGlnGluGlnSer 1015
 Db 2854 -----AAAGAAAGACAGCTTGACACAGTACAGGCC 2883
 QY 1016 Glu-----GlnIleLeuGlnLeuThrArgGluValThr-----His 1027
 Db 2884 AATGCAAAACAGAGCTCAAAAGCTCCAAACCACTTGAATTCACAGCAACATTGCAGCT 2943

QY 1028 ThrGlnSerLysValGlnGlnThrGluGluGlnIleThrLeuGluMetLysLysMetHisAsp 1047
 Db 2944 CAGAGGAAAAGTACAGAAAAGAAAGAGAGATTTGGAGTCC----- 2988
 QY 1048 AspLeuPheGluLysTyrIleArgAsnLysSerGluAlaGluAspLeuLeuArgGluMet 1067
 Db 2989 -----AGAGAAAGCAGACAGAGAGAGCGCTGACCGGCCCTG 3027
 QY 1068 GluAsnLeuLysGlyThrMetGluSerValGluValLysIleAlaAspThrLysIleGlu 1087
 Db 3028 GCCAGGCTGAGAGAGAGACATTCGCGCTGAG-----AGGACATCC 3069
 QY 1088 ---LeuGluGluThrIleArgAspLysGluIleLeuLeuHisGluLysLysTyrPhePhe 1106
 Db 3070 ACCCTGGCAGAGATTGAAGAGACAGAGCAG----- 3102
 QY 1107 GlnAlaMetGlnThrIlePheProIleThrProLeuSerAspSerLeuProSerLys 1126
 Db 3103 -----AAA 3105
 QY 1127 LeuValGluGlyAsnSerGlnAspProIleGluIleAsnAspTyrHisAsnLeuIleAla 1146
 Db 3106 CTTGCCAGCTGAAACAGTGC----- 3126
 QY 1147 LeuAlaThrGluArgAsnAsnIleMetValCySerLeuGluThrGluArgAsnSerLeuLys 1166
 Db 3127 ---AGCAGAGAGCTCAGGCTCAGGCTCAGCTGAGCTGAGCTGAGAGAAAGCCCTGAG 3183
 QY 1167 GluGlnValIleAspLeuAsnThrGlnLeuGlnSerLeuGlnAlaGlnSerIleGluLys 1186
 Db 3184 AAGAGCCAGAGAGAGATTGAAATGAAATCAACAGAGCTGAAACAGAGATTATGAGATC 3243
 QY 1187 SerAspLeuGlnLysProLysGlnAspLeuGluGluVal---LysLeuLeuLeu 1205
 Db 3244 GATGCTGTCAAAAAGATCATCATGAGACCTGGAAGGAAAGTGGCTTTCCAGCTTG 3303
 QY 1206 GluMetGluLeuLeuLysGlyHisLeuThr-----AspSerGlnLeuSer----- 1220
 Db 3304 CCAGTCACTGTGAAAATTCACACCTGTTCCCTCATGATGCGCAGGATCAATGCTTAC 3363
 QY 1221 IleGluLysLeuGlnLeuGluAsnLeuGluValThrGluLysLeuGlnThrLeu----- 1238
 Db 3364 ATTGAAGA-----GAGTCCAAAGAGCCCTTCAGGATTTGCATGCT 3405
 QY 1239 -----GlnGluGluMetLys 1243
 Db 3406 GTGATTAGTAAGGCTGACATGATCTGACAGACAGATGAAGATTAAGAAAATTTAC 3465
 QY 1244 AsnIleThrIleGluArgAsnGluLeuGlnThrAsnPheGluAspLeuLys----- 1260
 Db 3466 AATGCAACCATTCAAAGTAATACTAAATATGAGCTGTGTCTGACCTCTGTGTCTG 3525
 QY 1261 -----AlaGluHisAspSerLeuLysGlnAspLeuSer 1271
 Db 3526 ATGCCAGAGCTGATGCCGCTGCTGCGCTATATGATCATCTTCTCCAGAAAGTCTG--- 3582
 QY 1272 GluAsnIleGluGlnSerIleGluThrGlnAspGluLeu-----Arg 1285
 Db 3583 ---GTTCACTTCTCTGATTGAGAAAACAGAAAATCTCTGATTAGTTTCCAAAT 3636
 QY 1286 AlaAlaGlnGluGluLeuArgGluGlnLysGlnLeuValAspSerPheArgGlnGlnLeu 1305
 Db 3637 GGAAGTCAAGGTGATCCAAATTCACAGATCACTTGTGTGACATGATT-----TACTTT 3660
 QY 1306 LeuAspCySerValGlyIleSerSerProAsnHisAspAlaValAlaAsnGlnLys 1325
 Db 3691 CTTGATGGAATATAGAAATCAATGCTCT----- 3720
 QY 1326 ValSerLeuGluGluValAsnSerLeuGlnSerGluMetLeuArgGlyGluArgAspGlu 1345
 Db 3721 ---TCCCTGGAGAAATTCACTTACTCTCTACCAACAGTGAAGATGAGGTGAGCT 3777
 QY 1346 LeuGlnThrSerCyLysValAlaLeuValSerGluLeuGluLeuLeuArgAlaHisValLys 1365

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Db      3778 GGCATGACCAAGTCCAGTGTGCTATGTC-----CTTCTGAACACCCACATTGCA 3825
QY      1366 SerValGlu-----
Db      3826 CTGTGTAGAGGAGACAGTGTGTTTATTCACGCATTCGATTCGAAACATACCTCTCGC 3885
QY      1369 GtYGLuAsnLeuGluLeuThrLysLysLeuAsnGluLeuGluLys-----Glu 1384
Db      3886 GGTGCACAAATTGATGATGATC-----AAATGCATGCTTTAAGTGAATTCAGGTGTGTTGTT 3942
QY      1385 lIeLeuGtYLYSserGluGluSerGluValLeuLysSerMetLeuGluAsnLeuLysGlu 1404
Db      3943 GTTCCAGAAAAGAAAATGTGTCAACAGTACAGTACTCTTTACAGAAAACCTCAAACT 4002
QY      1405 AspAsnAsnLysLeuLysGluGluAlaGluGluLysSerLysGluAsn-----Gln 1422
Db      4003 TCAGTGGTTCAGAAAATAGTCCACCTGACACCTTCAGGAAGCCCAATGTCCAGTTG 4062
QY      1423 PheSerLeuGluGluValPheSerGtYSerGlnLysLeuValAspGluLeuGluValLeu 1442
Db      4063 TTCACCAACCCCATGTGATCTTTCAGAGGAGTCAAGATGTGCACCT-----GAGGTCTGG 4116
QY      1443 LysAlaGluLeuLysAlaAlaGluGluLysLeu 1453
Db      4117 AAATTACTTTCATTCTCAAGATGAGGCTCTT 4149

RESULT 12
US-09-721-832-1
/ Sequence 1, Application US/09721832
/ Patent No. 6399346
/ GENERAL INFORMATION:
/ APPLICANT: Beraud, Christophe
/ APPLICANT: Freedman, Richard
/ TITLE OF INVENTION: No. 6399346el motor proteins and methods for
/ FILE REFERENCE: 1055
/ CURRENT APPLICATION NUMBER: US/09721,832
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 4176
/ TYPE: DNA
/ ORGANISM: Human
US-09-721-832-1

Alignment Scores:
Pred. No.: 2.67e-64 Length: 4176
Score: 915.50 Matches: 416
Percent Similarity: 40.59% Conservative: 246
Best Local Similarity: 25.51% Mismatches: 536
Query Match: 6.20% Indels: 433
Gaps: 71

US-09-724-584-1 (1-2954) x US-09-721-832-1 (1-4176)
QY      6 AlaValIysValCysValArgValArgProLeuIleGlnArgGluGlnGlyAspGlnAla 25
Db      7 TCGGTAAAGTGGCCCTGAGGTTCGGCCCATGATCGCAGGAAAAGCACTTGGAGGCC 66
QY      26 Asn-----LeuGlnTrpLysAlaGlyAsnAsnThrLysSerGlnVal----- 39
Db      67 AAGTTCATTATTCAATGATGAGAAAAGCAAAACGCAATCACTTAAGATACACGAA 126
QY      40 -----AspGtYThrLysSerPheAsnPheAspArgValPhe 51
Db      127 GGAGCACTGGGAGTCAAGAAAGCAAGCAAGCACTTCACTATAGACTTTCTTT 186
QY      52 AsnSerIleGluSerThrSer-----GlnIleYrGlnGluLeu 64
Db      187 TATTCGTGCTATCAAAAAGCCAGATTACGTTTCAAGAAATGGTTCAAAACCTC 246

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QY      65 AlaValProIleIleArgSerAlaLeuGlnGlyTyrAsnGlyThrIlePheAlaTyrGly 84
Db      247 GGCACAGATGTCGGAAGTCTGCATTGTAAGGTTATATGCTTGTCCTTGCATATGG 306
QY      85 GlnThrSerSerGtYLYSThrTrpMetMetGtYThrProAsnSerLeuGlyIle 104
Db      307 CAACCTGATCTGGAAGATCATACATATGATGAGGAAAATTCGAGATTCTGGCTTATA 366
QY      105 ProGlnAlaIleGlnGluValPheLysIleIleGlnGluLeu-----ProAsnArg 121
Db      367 CTTGGATGTGTGAAGAGCTTTCAGTCGGAATTAATGAACACCAAGATGGATGAAGCT 426
QY      122 GluPheLeuLeuArgValSerTyrMetGluLysIleTyrAsnGluThrValLysAspLeuLeu 141
Db      427 TCTTTTCGAACCGAAGTCACTACTATGAAATTTATACGAACGTCGAGAGATCTACTT 486
QY      142 CysAspAspArgValLysLysPro-----LeuGluIleArgGluAspPheAsn 157
Db      487 -----CGCGGAAGTCACTTAAACCTTCAATTGTGAGTCCGTGACATCCCAAA 537
QY      158 ArgAsnValTyrValAlaAspLeuThrGluGluLeuValMetValProGluHisValIle 177
Db      538 GAAGCCCTTATGTTGAGATTTATCCAAACATTTAGTACAGATTAATGATGACGTAAGA 597
QY      178 GlnTrpIleLysGtYLYSgltYLYSAsnArgHisTyrGtYLYSThrLysMetAsnAspHis 197
Db      598 GAACCTTATGATGCGGGCAATATCAACCGGACCGACGCGAGCTGGATGAAACGACGTC 657
QY      198 SerSerArgSerHisThrIlePhe-----ArgMetIleValGluSerArgAspArgAsn 215
Db      658 AGTGGACAGTCTCATGCAATCTTCAACATCAAGTCACTCAAGGCTAAATTGATTCGAA 717
QY      216 AspProThrAsnSerGluAsnCysAspGlyAlaValMetValSerHisLeuAsnLeuVal 235
Db      718 ATGCCA-----TGTGAA-----ACGTCAGATGATCACTTGAT 753
QY      236 AspLeuAlaGtYSerGluArgAlaSerGlnThrGlyAlaGluGlyValArgLeuLysGlu 255
Db      754 GATCTTCCGGAAGAGAGGTCATCAATGCCACCGAGGACCGGGGTTAGCTTAAAGGAA 813
QY      256 GlyCysAsnIleAsnArgSerLeuPheIleLeuGlnValIleLysLysLeuSerAsp 275
Db      814 GGGGAAATATTTAAAGATCCCTTGTGACTGTGGGAACGTCATTCTGCTTACGTAT 873
QY      276 GlyGlnAlaGlyGly-----PheIleAsnTyrArg 285
Db      874 TTATCTCAGATGTCGCAATACCTTGCAGAAAGACAGCAAGTTTTCGTGCTTACAG 933
QY      286 AspSerLysLeuThrPArgIleLeuGlnAsnSerLeuGtYLYSAsnAlaLysThrValIle 305
Db      934 GATTCGTGCTTGACTTGTGTTAAAGATGAGCTTGGAGGAAACTCTAAACTATCATG 993
QY      306 lIeCysThrIleThrPro-----ValSerPheAspGluThrLeuSerThrLeuGlnPhe 323
Db      994 ATTCCACCACTTTCACCTGCTGATGTCATATGAGAAAACCTTAAGTACTTTCGCTAT 1053
QY      324 AlaSerThrLysLysHisValArgAsnThrProHisValAsnGluValLeuAspAspGlu 343
Db      1054 GCAAAATGAGCCAAAACATCATCAACAGACCTTACATTAATGAGAGTCCAAAGCTCAA 1113
QY      344 AlaLeuLeuLysArgTyrArgLysGluIleLeuAspLeuLys----- 357
Db      1114 ---CTTATCCGTGAGCTGCGAGCTGAATATAGCCAGCTGAAAACGCTTCTCAAGGG 1170
QY      358 LysGlnLeuGluAsnLeuGluSerSerSerGluThrLysAlaGlnAlaMetAlaLysGlu 1170
Db      1171 AATCAGATTGCCCTTATGATCCGCCCA-----GCTTAAAGTATGAG 1215
QY      378 GluHisThrGlnLeu-----LeuAlaGluIleLysGlnLeuHisLysGluArgLysAspArg 1215
Db      1216 GAAAACCTTCAGCGAATGAGCAAGAGTTCAAGATTAACCAAGAAATGACAAATTAAG 1275
QY      397 lIeTrpHisLeuThrAsnIleValAlaSerSerGlnGluSerGlnGlnAspGlnArg 416

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Db	1276	---TGGAAATGAAACC-----	: :	-----CAAAT	1293
Qy	417	VallysArgLySArgArgValThrTrpAlaProGlybIleGlnAsnSerLeuHisla	417	VallysArgLySArgArgValThrTrpAlaProGlybIleGlnAsnSerLeuHisla	436
Db	1294	ATTTTGAAAGAAACAACCTCTA-----	: :	-----GCCCTCAGGAAA	1326
Qy	437	SerGlyValSerAspPheAspMetLeuSerArgLeuProGlyAsnPheSerLeuVala	437	SerGlyValSerAspPheAspMetLeuSerArgLeuProGlyAsnPheSerLeuVala	456
Db	1337	GAAGGGATTTGA-----	: :	-----GTTGTT	1344
Qy	457	LysPheSerAspMetProSerPheProGlyIleAspAspSerValCysThr-----	: :	-----	473
Db	1345	TTGGATTCTGAACCTGCCTCATTTGATTGGCATCGATGATGACCTTTTGAGTCTGGAATC	: :	-----	1404
Qy	474	-----	: :	-----GluPheSerAspPheAspAlaLeuSerMet	484
Db	1405	ATCTTATATCATTTTAAAGAAAGCTCAGACATACCTGGTATAGAGCAAGTCTTCCACGGAG	: :	-----	1464
Qy	485	MetAsp-----SerAsnGlyIleAspAlaGlu-----	: :	-----TrpAsnLeu	496
Db	1465	CAAGATATTGTTCTTTCATGAGCCCTTGACTGAGTGGAGTGCAGCTTCATCTTTGAAAAATATC	: :	-----	1524
Qy	497	AlaSerLyValThrHisArgGlybThrSerLeuHisGlnSerMetIleAspPheGly	497	AlaSerLyValThrHisArgGlybThrSerLeuHisGlnSerMetIleAspPheGly	516
Db	1525	GGGGGGACAGTACT--CTGATACCCCTGAGTGGGTCCACGTGCTGTGAAATGGTGT	: :	-----	1581
Qy	517	GlnIleSerAspSerValGlnPheHisAspSerSer-----	: :	-----LysGluAsn	531
Db	1582	CAGATCGTGGAGGCCACACATCTTAATTAAGTGTCTGTGATTCCTTGGAGAAACCAAT	: :	-----	1641
Qy	532	GlnLeuGlnTyr--LeuProLysAspSerGlyAspMetAlaGlyCysArgLyS-----	: :	-----	548
Db	1642	ATGTTTGCCTTTAACCATCCAAAGAGAACCCGCAAGCTCAGGAGAAAGAAAGATGGC	: :	-----	1701
Qy	549	-----AlaSerPheGlnLybGluIleThrSerLeuGlnGlnGlnLeuGlnSerLybGlu	549	-----AlaSerPheGlnLybGluIleThrSerLeuGlnGlnGlnLeuGlnSerLybGlu	566
Db	1702	CTTGTGCTCTCTTTCAGCTTGCTTCATGACCACTC-----	: :	-----TCGAATGCC	1746
Qy	567	GluGlnLybLybGluLeuValGln-----	: :	-----SerPheGluLeuLybIle	580
Db	1747	CGTGGAAACCTGTCTGCAGTATGTTGATTAACCCCGGACTTGAAATTTGAGAGCAACAG	: :	-----	1806
Qy	581	AlaGluLeuGlnGlnGlnLeuSerValLysAlaLysAsnLeuGlnMetValThrAsnSer	581	AlaGluLeuGlnGlnGlnLeuSerValLysAlaLysAsnLeuGlnMetValThrAsnSer	600
Db	1807	CGTGAAGAACTTGAAAAATTGAAAGTAAAGAAACTCATAGAAGAAATG--GAGGAA	: :	-----GAGGAA	1863
Qy	601	ArgGluHisSerIleAsnAlaGluValGln--ThrSerValGlybGluValValArg	601	ArgGluHisSerIleAsnAlaGluValGln--ThrSerValGlybGluValValArg	619
Db	1864	AAGCAGAAATCAGCAAGCTGAACTGGAGGGATGCAGCAGGAGGTGGAGAACCCACAGCC	: :	-----	1923
Qy	620	LybGlnMetSerValLeuGlybAspSerGlyTyrrAsnAlaSerAsnSerAspLeuGlnAsp	620	LybGlnMetSerValLeuGlybAspSerGlyTyrrAsnAlaSerAsnSerAspLeuGlnAsp	639
Db	1924	AAGAGACACAAATCTGT-----	: :	-----CAGCTCAC--	1950
Qy	640	SerSerValAspGlybLybArgLeuSerSerSerHisAspGlyCysIleGluHisArgLyS	640	SerSerValAspGlybLybArgLeuSerSerSerHisAspGlyCysIleGluHisArgLyS	659
Db	1951	-----ATTGCGAAGCAGAGGAGACCTTCAAAACGCCGCGACG	: :	-----	1986
Qy	660	Met---LeuGlnGlnLybIleValAspLeuGlnGluPheIleGluAsnLeuAsnLybLyS	660	Met---LeuGlnGlnLybIleValAspLeuGlnGluPheIleGluAsnLeuAsnLybLyS	678
Db	1987	TTCCACACATCGGAACAAGCTTAAGGATTTA-----	: :	-----CTTGGCGAGAAAG	2028
Qy	679	SerGluAsnAspLybGlnLybSerSerSerGlnGlnAspPheMetGluSerIleGlnLeuCys	679	SerGluAsnAspLybGlnLybSerSerSerGlnGlnAspPheMetGluSerIleGlnLeuCys	698
Db	2029	GAATAATTGGAAGAGAGGCTGAGGAAAG--	: :	-----	2061
Qy	699	GluAlaIleMetAlaGluTybAlaAsnAlaLeuGlnGluLeuAlaLeuMetArgAspAsn	699	GluAlaIleMetAlaGluTybAlaAsnAlaLeuGlnGluLeuAlaLeuMetArgAspAsn	718
Db	2062	-----CAGGAAATCGAGCTGCGAAGAAAGAGA	: :	-----	2088
Qy	719	PheAspAsnIleIleLeuGluAsnGluThrLeuLybArgGlybIleAlaAspLeuGlnArg	719	PheAspAsnIleIleLeuGluAsnGluThrLeuLybArgGlybIleAlaAspLeuGlnArg	738

Db	2089	-----CAAGAAAGAGACCTTTCTCCCGGCTCAAGAAAGAACTCCAAACA	2133
Qy	739	-----SerLeuYsGluApsngIngluThraBngluPhegluIleLeuGluYs	754
Db	2134	CTCAAGAAACTTCACACAAACGAGAGCTGAGAACTTCAGATATTTCAGAACTGGAC	2192
Qy	755	GIuThrGlnYsGluIhISgluAlaGlnleuIleHISgluIleGlySerLeuYsYsleu	774
Db	2194	CAGCTCCAAAAGGAAAAAGATGAACAGATATGCC--AAGCTTGAACCTGAAAAAAGAGA	2256
Qy	775	ValgluApsnAlaGlu-----MetTryApsnIleApsnleGluIhApsnleuGlu	790
Db	2251	CTAGAGGAGCAGAGAGAGAGACAGCTACTGCTCGGGGCCATCTGGAAGAGCAGCTCCGA	2310
Qy	791	ThlYs-----ThlYsleuLeuYsGluGlnGluIleGlnleuAlaGluLeuArg	807
Db	2311	GAGAAAGCAGAGATGATCAGCTCCTCGCGCGGTGGAGGATGACAGTGGGTGGAAAGAGAG	2370
Qy	808	LYsAlaGAlaApsnleuGlnIhYsValArgApsnleuApsnleuSerValSerMetGly	827
Db	2371	AAGAGG-----	2378
Qy	828	ApsnserGluYsleuCyGluGluIhPheGlnleuYsGlnSerLeuSer-----	844
Db	2377	GACTCGAAGGCGATTCCGGAAATCCCTCTCGGGGTGAAGAGGCTCGTCCGGAGGGAT	2433
Qy	845	--ApsnAlaGluAlaValThraArgApsnAlaGlnYsGluCySerPheLeuArgSerGlu	863
Db	2437	GAAAGTGGCGAGAGACTTGAAGAAAGGCTCACTGGCTTCTTGAAATTCAGAGAAAGCGAG	2496
Qy	864	ApsnleuGluLeuYsGluYsMetGluApsnThraSerApsnTryApsnGlnYsGluYs	883
Db	2497	CTTGCAAGCTAGTGAACACTTGAGAGAGAGCTGGTTCAGCAGAAAGACATCTCGTAAAAA	2556
Qy	884	AlaAlaSerleuApsnleuGlnYsGlnleuGlnIhArgYsSerApsnTryYsleuYsMetGlu	903
Db	2557	GAACTCCAGAGAGACAGAGATCTCTAGAGTGTAAATGATGAACATGACAAAGAACTT	2616
Qy	904	AlaApsnleuGlnYsGluLeuGlnSerAlaPheApsnGluIleApsnTryLeuApsnGluYs	923
Db	2617	AGATTGTTGAAAAAATCATGATGAGATGCTACAGAT-----	2652
Qy	924	LeuAlaGluYsValProArgApsnleuSerArgValGluLeuGluYsYsValSer	943
Db	2653	--GTCACGAGAAAGTCCCTCAAGATTTCCAGAAAAATAAAGCCAGTGGAGTACAGCGTCCAA	2709
Qy	944	GluPheSerYsGlnleuGlnYsAlaApsnleuGluYsApsnAlaApsnleuGlnYsVal	963
Db	2710	TATAAAGAACCCACGACTACAG-----TACTCTCTGCAAAATCACTTGG	2751
Qy	964	ThraYsleuSerGlu-----TyrIhPheleuProApsnGluValGluCyS	978
Db	2752	CCAACCTCTGTTGGAAGAAAGAACAGAGCATTGAAATCTTGACAGAGGCCCTCTCAGC	2811
Qy	979	LeuYsApsn-----GlnIleSerYsAlaSerGluGluIleMetLeuLeuYsGln	995
Db	2812	TTAGACAAACACTTTTATCAAGTGAAGAAAGAAATGCAAGAA-----	2853
Qy	996	GluGluGluIhApsnSerAlaSerIleIleSerYsGlnGluIleIleMetGlnGlnSer	1015
Db	2854	-----AAAAGAAACAGCTTTGCACTACATCCAGGCC	2883
Qy	1016	Glu-----GlnIleLeuGlnleuThraApsnGluValThr-----His	1027
Db	2884	AATGCAAAACAGCTGCAAAAGCTCCAAAGCCCTTTGAAATTCACCTGCCAATTCAGACT	2943
Qy	1028	ThraGlnSerYsValGlnGlnThraGluGlnGlnIhYsleuGlnMetYsYsMetHisAps	1047
Db	2944	CAGAGGAAAAAGTGAAGAAAAAGAAAGAGATTTTGAGCTCC-----	2988
Qy	1048	ApsnleuPheGluYsTryIleArgApsnYsSerGluAlaGluApsnleuApsnArgGlnMet	1067
Db	2989	-----AGAGAGAAAGCAGAGAGAGAGAGCGCTGAGACGGGCGCTTG	3027

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QY 1068 GUAAsnLeuIleGlyThrMetGluSerValGluValIleAlaAspThrIleHisGlu 1087
DB 3028 GCCAGGCTGGAGAGAGACATTCTGGCTGCAG-----AGGCACATCC 3069
QY 1088 ---LeuGluGluThrIleArgAspIleGluIleLeuHisGluIleGlyTyrPhe 1106
DB 3070 ACCCTGGGACGAGATTGAAAGACAGAGCAG----- 3102
QY 1107 GlnAlaMetGlnThrIlePheProIleThrProLeuSerAspSerLeuProSerIle 1126
DB 3103 -----AAA 3105
QY 1127 LeuValGluGlyAsnSerGlnAspProIleGluIleAsnAspTyrHisAsnLeuIleAla 1146
DB 3106 CTTGCCAGCTGCAACAGTGC----- 3126
QY 1147 LeuAlaThrGluArgAsnAsnIleMetValCysLeuGluIleThrGluArgAsnSerLeuIle 1166
DB 3127 ---AGCAGAGAGACATCGGGCTCCAGGCTAGCCTGAGGCTGAGGAGGAGGAGCCTTGAG 3183
QY 1167 GlnGluValIleAspLeuAsnThrGlnLeuGlnSerLeuGlnAlaGlnSerIleGluIle 1186
DB 3184 AAGGACGAGAGAGGTTAGTAATGAAATCCAGACGCTGAAACGAAATTTAGAGTC 3243
QY 1187 SerAspLeuGlnIleProIleGluAspLeuGluGluGluVal---LysLeuLeuLeu 1205
DB 3244 GATGCTGTTCAAAAGATCATCATGAGACCCCTGAGGAGGAGGAGGCTTCTTCAGCTTG 3303
QY 1206 GlnMetGluLeuLeuIleGlyIleLeuThr-----AspSerGlnLeuSer 1220
DB 3304 CCAGCTAGGCTGAAAATACACCTGTTCCCTCATGATGCCAGGATCAATGCTTAC 3363
QY 1221 IleGluIleLeuGlnLeuGluAsnLeuGluValThrGluIleGlnIleThrLeu 1238
DB 3364 ATTTAAGAA-----GAAGTCAAGAGGCTTCAGATTGATCTGT 3405
QY 1239 -----GlnGluGluMetIle 1243
DB 3406 GTGATTAGTAGAGGCTGCATACATCTGCAGACACATGAAAGATATATGAAACTTCAC 3465
QY 1244 AsnIleThrIleGluArgAsnGluLeuGlnIleThrAsnPheGluAspLeuIle 1260
DB 3466 AATGGACCCATTCAAGCTAACTAAATATGAGCTGTGTGAGCTCTGTGTCTGTG 3525
QY 1261 -----AlaGlnHisAspSerLeuIleGluAspLeuSer 1271
DB 3526 ATGCCAGAGCCTATGCCCTGCTGCTTAATCATCTCTCCAGCAAGATCTG--- 3582
QY 1272 GlnAsnIleGluGlnSerIleGlnThrGlnAspGluLeu-----Arg 1285
DB 3583 ---GTTCAAGCTTCTCTGTATGGAACAGAAATCCGATTAGTTTGGCAAT 3636
QY 1286 AlaAlaGlnGluGluLeuArgGlnIleGlnIleValAspSerPheArgGlnIle 1305
DB 3637 GGAAGTTCAGGTGATCCAAATTCAGACTCTGTGTTGACATGAT---TACTTT 3690
QY 1306 LeuAspCysSerValGlyIleSerSerProAsnHisAspAlaValAlaAsnGlnIle 1325
DB 3691 CTTTCATGGAATATGGAATGATGCTCT----- 3720
QY 1326 ValSerLeuGlyGluValAsnSerIleGlnMetLeuArgGlyGluArgAspGlu 1345
DB 3721 ---TCCCTGGCAGAAATTCACTTACTGTCTACACACAGGAAAGATGAGGAGCTCT 3777
QY 1346 LeuGlnThrSerCysIleAlaLeuValSerGluLeuGluLeuAlaGlnHisValIle 1365
DB 3778 GGCATGACGACGAGTCACTGCTGCTTCAACACAGGAAAGATGAGGAGCTCT 3825
QY 1366 SerValGlu-----CTTTCGAACACCCACATTCGA 3885
DB 3826 CTGGAGAGGAAAGACTGTGTTTTTATTCACGACATTCGATTCGAACATACCTCCTCG 3885

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QY 1369 GlyGluAsnLeuGluIleThrIleIleIleIleIleIleIleIleIleIleIleIle 1384
DB 3886 GGTGACCAATTTGATGTATC---AATGCCATGCTTTAAGTAATTCAGGTGTGTGT 3942
QY 1385 IleLeuGlyIleSerGluGluSerGluValIleIleIleIleIleIleIleIleIle 1404
DB 3943 GTTCCAGAAAGAAATAATGTGTCAACAGTACGATCTTCTTACAAACTCAAACT 4002
QY 1405 AspAsnAsnIleLeuIleGluGlnIleGluIleIleIleIleIleIleIleIle 1422
DB 4003 TCAGTGGCTTCCAGAAATATGTCACCTTACAGACCTTCAGAAAGCCCAATGTCAGTTG 4062
QY 1423 PheSerLeuGluGluValPheSerGlySerGlnIleLeuValAspGluIleGluValIle 1442
DB 4063 TTCACACCCCATTTGATCTTCAAGGACGTCAGATGCGACCT---GAGGTCTGG 4116
QY 1443 LysAlaGlnLeuIleValAlaGlnGluValArgLeu 1453
DB 4117 AAATCTTCTCAATTCATTCAGATGAGGCTCTT 4149

RESULT 13
US-09-721-689-1
/ Sequence 1, Application US/09721689
/ Patent No. 6440685
/ GENERAL INFORMATION:
/ APPLICANT: Beraud, Christophe
/ APPLICANT: Freedman, Richard
/ TITLE OF INVENTION: No. 6440685: motor proteins and methods for
/ TITLE OF INVENTION: their use
/ FILE REFERENCE: 1055
/ CURRENT APPLICATION NUMBER: US/09/721,689
/ CURRENT FILING DATE: 2000-11-24
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 4176
/ TYPE: DNA
/ ORGANISM: Human
US-09-721-689-1

Alignment Scores:
Pred. No.: 2,67e-64 Length: 4176
Score: 915.50 Matches: 416
Percent Similarity: 40.59% Conservative: 246
Best Local Similarity: 25.51% Mismatches: 536
Query Match: 6.20% Indels: 433
DB: 4 Gaps: 71

US-09-724-584-1 (1-2954) x US-09-721-689-1 (1-4176)
QY 6 AlaValIleValCysValArgValArgProLeuIleGlnArgGluGlnIleAspGlnAla 25
DB 7 TCGGTCAAGGTGCGGTGAGGCTCGGCCATGATCCAGGAAAGAGACTTGAGGCGC 66
QY 26 Asn-----LeuGlnIleIleValIleValAsnThrIleSerGlnVal----- 39
DB 67 AAGTTTATTATTCAGATGAGGAAAGCAAAACGCAATACCAAACTTAAGATACAGAA 126
QY 40 -----AspGlyThrIleSerPheAsnPheAspArgValPhe 51
DB 127 GGAGGACACTGGGAGCTCAGAAAGAGAGACGACCAAGACTTTCACCTTTCTTTT 186
QY 52 AsnSerIleGluSerThrSer-----GlnIleIleGlnIle 64
DB 187 TATTTGCTGTATACAAAAGCCAGATTACGTTTACAGAAATGTTTCAAAACCTC 246
QY 65 AlaValProIleIleArgSerAlaLeuGlnIleIleIleIleIleIleIleIleIleIle 84
DB 247 GGCACAGATGTCGGAAGTCTGCATTGGAAGTTATATGCTGTGTGTTGATATGAGG 306
QY 85 GlnThrSerSerGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIle 104
DB 307 CAATCTGATCTGGAAGATCATACATATGATGAGAAATTCGAGATTCGTGCTTAATA 366

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105 ProGlnAlaIleGlnIleValAlaPheLysIleIleGlnIle-----ProAsnArg 121
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 367 CTTGGATGTGTGAAGACTCTTCACTGGATTAATGAACCAACGATGGATGAAGCT 426
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 122 GluPheLeuLeuArgValSerTyrMetGluIleTyrAsnGluThrValLysAspLeu 141
 |||||
 427 TCTTTTGAAGTGAAGTCACTAGTAATTTATTAACGAACGTGTGAAGATCTACTT 486
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 142 CysAspAspArgArgLysPro-----LeuGluIleArgGluAspPheAsn 157
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 487 -----CGCGGAAGTCATCTAAACCTTCAATTGAGAGTCGTGAGATCCCAAA 537
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 158 ArgAsnValTyrValAlaAspLeuThrGluGluLeuValMetValProGluHisValIle 177
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 538 GAAGCCCTTATGTAGGATTTATCTCAACATTATTAACAAGATTATGACATGAGA 597
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 178 GlnTrpIleLysLysGluLysAsnArgHisTyrGluGluThrLysMetAspHis 197
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 198 SerSerArgSerHisThrIlePhe-----ArgMetIleValGluSerArgAspArgAsn 215
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 658 AGTACGAGGTCTCATGCGCATCTTCAACCATCAAGTTCACAGGCTAAATTGATCTGAA 717
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 718 ATGCA-----TGAGAA-----ACCGTCAGTAAAGTCACTTGCTGTT 753
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 754 GATCTTCCCGGAAGTGAAGCTGCAATGCGCACCGGACCAACCGGGTTAGGCTTAAAGAA 813
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 256 GlyCysAsnIleAsnArgSerLeuPheIleLeuGluValIleLysLysLeuSerAsp 275
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 814 GGGGAATATTAACAAGTCCCTTGATGCTGGGGAAGCTCATTTCTGCTTACGTGAT 873
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 276 GlyGlnAlaGlyGly-----PheIleAsnTyrArg 285
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 874 TTATCTCAGATGTCGCAAACTCTTGCMAAGAAAGAACGATTCTCGCTTACAG 933
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 286 AspSerLysLeuThrArgIleLeuGluAsnSerLeuGluValAsnAlaLysThrValIle 305
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 934 GATTCGTGCTTACTGTTGTTAAAGTACCTTGGAGAACTCTTAAACTATCAAG 993
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 306 IleCysThrIleThrPro-----ValSerPheAspGluThrLeuSerThrLeuGlnPhe 323
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 994 ATTGCACCATTTCACTGATGTCATTAATGAGAAACCTTAAGTACTCTTGCTAT 1053
 |||||
 324 AlaSerThrAlaLysHisValArgAsnThrProHisValAsnGluValLeuAspArgGlu 343
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 1054 GCAAAATAGAGCCAAACATCATCAACCAAGCTTACCATTATGAGATGCCAACGTCAAA 1113
 |||||
 344 AlaLeuLeuLysArgTyrArgLysGluIleLeuAspLeuLys----- 357
 |||||
 1114 ---CTTATCTCGAGCTGCGACTGAATAAGCCAAAGTGAACCGCTGCTCTCAAGG 1170
 |||||
 358 LysGlnLeuGluAsnLeuGluSerSerGluThrLysValAlaIleAsnAlaLysGlu 377
 |||||
 1171 AATCAGATTGCCCTCTAGACTCCCAACA-----GCTTAAAGTATGAG 1215
 |||||
 378 GluHisThrGlnLeu-----LeuAlaGluIleLysGlnLeuHisLysGluArgGluAspArg 396
 |||||
 1216 GAAAAAATTCAAGCAATGAAAGCAAGAGTTCAAGAAATTGACCAAGAAATGCAAAATAG 1275
 |||||
 397 IleTrpHisLeuThrAsnIleValAlaAlaSerSerGlnGluSerGlnAspArgGlu 416
 |||||
 1276 ---TGAATGAAC-----CAAAAT 1293
 |||||
 417 ValLysArgLysArgArgValThrTrpAlaProGluLysIleGlnAsnSerLeuHisAla 436
 |||||
 1294 ATTTGAAAGAAACAAGTCTA-----GCCCTCAAGAA 1326
 |||||

437 SerGluValSerAspPheAspMetLeuSerArgLeuProGluValAsnPheSerLysValAla 456
 |||||
 1327 GAAGGATTTGGA-----GTTGTT 1344
 |||||
 457 LysPheSerAspMetProSerPheProGluIleAspAspSerValCysThr----- 473
 |||||
 1345 TTGATTTGAACTGCTCATTTGATTTGATGTCATGATGATGACCTTTTGAGTACTGGAATC 1404
 |||||
 474 -----GluPheSerAspPheAspAspAlaLeuSerMet 484
 |||||
 1405 ATCTTATATCATTTAAAGAAAGTCAGACATACGTTGTAGAGACATGCTTCCACGAG 1464
 |||||
 485 MetAsp-----SerAsnGlyIleAspAlaGlu-----TrpAsnLeu 496
 |||||
 1465 CAAGATATTTGTTCTTCATGAGCTTCACTTGGAGAAGTGAACATTCATTTTAAATATTC 1524
 |||||
 497 AlaSerLysValThrHisArgGluLysThrSerLeuHisGlnSerMetIleAspPheGly 516
 |||||
 1525 GGGGGACAGTACT---CTGATACCCCTGAGTGGTCCAGTGTCTGTGAATGTGTT 1581
 |||||
 517 GlnIleSerAspSerValGlnPheHisAspSerSer-----LysGluAsn 531
 |||||
 1582 CAGATCGTGAAGGCCACACATCTAAATCAAGGTCTGTGATTCCTTGGAAAGAACAT 1641
 |||||
 532 GlnLeuGlnTyr---LeuProLysAspSerGluAspMetAlaGluCysArgLys----- 548
 |||||
 1642 ATGTTTCCGTTTAACCATCAAGAGACCGCCAAAGCTCAGGAGAAAGGAAAGTGGC 1701
 |||||
 549 -----AlaSerPheGluLysGluIleThrSerLeuGlnGlnLeuGlnSerLysGlu 566
 |||||
 1702 CTTCGTCTCTCTTCAAGTTCATGACCAACGCTC-----TCGAAGTCC 1746
 |||||
 567 GluGluLysLysGluLeuValGln-----SerPheGluLeuLysIle 580
 |||||
 1747 CGTGAGAACCTGTCTGCAGCTCATGTTGTATTAACCCCGACCTTGAATTGAGAGCAACAG 1806
 |||||
 581 AlaGluLeuGluGluLeuSerValLysValLysAsnLeuGluMetValThrAsnSer 600
 |||||
 1807 CGTGAAGAACTTGAAGAAATTGAAGAACTGAAGAACTCATTAAGAAATG---GAGAA 1863
 |||||
 601 ArgGluHisSerIleAsnAlaGluValGln---ThrAspValGluLysGluValAlaValArg 619
 |||||
 1864 AAGCAAGAAATCAGCAAGAGCTGAACTGAGAGCGAGATGACAGAGAGTGAGACCCAGCGC 1923
 |||||
 620 LysGluMetSerValLeuGluLysAspSerGluTyrAsnAlaSerAsnSerAspLeuGlnAsp 639
 |||||
 1924 AAGCAGACAGAAATGCTG-----CAGCTCCAG--- 1950
 |||||
 640 SerSerValAspGluLysArgLeuSerSerHisAspGluCysIleGlnHisArgLys 659
 |||||
 1951 -----ATTGCAAGCAGAGAGAGAGCTTAAACGCCGCAAGC 1986
 |||||
 660 Met---LeuGluGlnLysIleValAspLeuGluGluPheIleGluAsnLeuAsnLysLys 678
 |||||
 1987 TTCCATCTGAGACAACTAAAGATTTA-----CTTCCGAGAGAG 2028
 |||||
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 |||||
 2029 GAAAAATTGTAAGAGAGAGCTGAGGAGACG----- 2061
 |||||
 699 GluAlaIleMetAlaGluLysAlaAsnAlaLeuGluGluLeuAlaLeuMetArgAspArg 718
 |||||
 2062 -----CAGAAATCTGAGCTCAGAAAGAGAG 2088
 |||||
 719 PheAspAsnIleIleLeuGluAsnGluThrLysLysArgGluIleAlaAspLeuGluArg 738
 |||||
 2089 -----CAAGAAAGAAAGACTTCTCCGCGTCCAAAGAAACTCAAGCA 2133
 |||||
 739 -----SerLeuLysGluAsnGlnGluThrAsnGluPheGluIleLeuGluLys----- 754
 |||||
 2134 CTCAAAGAACTCAACAAACAGAGAGAGTGTGAGATTTTCAGATTTTCAAGAACTGAGAC 2193
 |||||
 755 GluThrGlnLysGluHisGluAlaGlnLeuIleHisGluIleGlySerLeuLysLysLeu 774
 |||||

Db 2194 CAGCTCCAAAAGGAAAAAGATGAACAGTATGCC---AAGCTGAAGTCACTGAAAAAAGAGA 2250
Qy ValGluAsnIagi-----MetTyrAsnGlnAsnLeuGluIuAspLeuGlu 790
Db 2251 CTAGAGAGACAGAGAAAGACAGCTATGCTCTGCGCCATCTGGAAAGGACGCTCCGA 2310
Qy ThrLys-----ThrLysLeuLeuGluGlnGluIleGlnLeuIagiLeuArg 807
Db 2311 GAGAAAGCAGAGATGATCAGCTCTCGCGCGTGGGAGGTACAGTGGTGAAGAGAGAG 2370
Qy LysAlaArgAlaAspAsnLeuGlnLysValArgAsnPheAspLeuSerValSerMetGly 827
Db 2371 AAGAGG----- 2376
Qy AspSerGluLysLeuGluGlnGluIlePheGlnLeuGlnSerLeuSer 844
Db 2377 GACCTGGAAAGGCACTTGGGAAATCCCTCTCGGGGTGAAGAGGCTGCTGCGGAGGGGAT 2436
Qy 845 ---AspAlaGluAlaValThrArgAspAlaGlnLysGluCysSerPheLeuArgSerGlu 863
Db 2437 GAAGATGCGCAGAGAGATTAGAAAGGCTCAACTGCTTTTCGAATTCAAGAGAGAGCAG 2496
Qy 864 AsnLeuGlnLeuLysGluLysMetGluAspThrSerAsnTrpTyrAsnGlnLysGluLys 883
Db 2497 CTGTCAAGCTACTGAACCTTGAGAAAGACCTGGTTCCAGACGAAGACATCTCGAAAAA 2556
Qy 884 AlaAlaSerLeuPheGluLysGlnLeuGlnThrGluLysSerAsnTyrLysMetGlu 903
Db 2557 GAAGTCCAGAAAGAACAGAGATCCTAGAGCTTTAAATGTGAACATGACAAAGATAT 2616
Qy 904 AlaAspLeuGlnLysGlnLeuGlnSerAlaPheAsnGluIleAsnTyrLeuAsnGluLeu 923
Db 2617 AGATTGTTGAAAAACATGATGAGAGTGCACAGAT----- 2652
Qy 924 LeuAlaGlyLysValProArgAspLeuLeuSerArgValGluLeuGluLysValSer 943
Db 2653 ---GTCACGGAAGTGCCTCAAGATTTCGAGAAAATTAAGCCAGGTGAGTACAGGCTGCA 2709
Qy 944 GluPheSerLysGlnLeuGlnLysAlaLeuGlnLysAsnAlaLeuGlnLysAsnGluVal 963
Db 2710 TATTAAGAACGCCAGCTACAG-----TACCTCTGAGATCACTTG 2751
Qy 964 ThrCysLeuSerGlu-----TyrLysPheLeuProAsnGluValGluCys 978
Db 2752 CCAACTCTGTGAAAGAAAAGACAGAGCATTGAAATCTTGACAGAGGCCCTCTCAGC 2811
Qy 979 LeuLysAsn-----GlnIleSerLysAlaSerGluGluIleMetLeuLeuLysGln 995
Db 2812 TTAGACAAACACTCTTTATCAAGTAAAGAAAAGAAATGGAAGAA----- 2853
Qy 996 GluGlyGlnHisSerAlaSerIleIleSerLysGlnGluIleIleMetGlnGlnSer 1015
Db 2854 -----AAAAGAAACAGCTTGACACAGATCCAGGCC 2883
Qy 1016 Glu-----GlnIleLeuGlnLeuThrAspGluValThr-----His 1027
Db 2884 AATGCAAAACAGCTGCAAAAGCTCCAGGACCTTTGAATTCACGCGCAACATTGACAGT 2943
Qy 1028 ThrGlnSerLysValGlnGlnThrGluGlnGlnTyrLeuGlnMetLysLysMetHisAsp 1047
Db 2944 CAGAGGAAAAAGTAGGAAAAAGAAAGAGATTTTGAGTCC----- 2988
Qy 1048 AsnLeuPheGluLysTyrIleArgAsnLysSerGluAlaGluAspLeuLeuArgGluMet 1067
Db 2989 -----AGAGAGAAAGCAGACAGAGAGCGCTGAGGCGGCGCTG 3027
Qy 1068 GluAsnLeuLysGlyThrMetGluSerValGluValLysIleAlaAspThrLysHisGlu 1087
Db 3028 GCCAGGCTGGAGAGAGACATTCTGCGCTGCGAG-----AGGACATCC 3069
Qy 1088 ---LeuGlnGluThrIleArgAspLysGlnLeuLeuHisGluLysLysTyrPhePhe 1106

Db 3070 ACCCTGGCAGCGAGATTGAAGAGAGAGCGAG----- 3102
Qy 1107 GlnAlaMetGlnThrIlePheProIleThrProLeuSerAspSerLeuProProSerLys 1126
Db 3103 -----AAA 3105
Qy 1127 LeuValGluGlyAsnSerGlnAspProIleGluIleAsnAspTyrHisAsnLeuIleAla 1146
Db 3106 CTGGCAGCTGCAACAGTGC----- 3126
Qy 1147 LeuAlaThrGluArgAsnAsnIleMetValCysLeuGlnIuThrGluArgAsnSerLys 1166
Db 3127 ---ACGACAGAGCAGTCCAGGCTCCAGGCTAGGCTGAGGCTGAGCAGAGAGCCCTGAG 3183
Qy 1167 GluGlnValIleAspLeuAsnThrGlnLeuGlnSerLeuGlnAlaGlnSerIleGluLys 1186
Db 3184 AAGGACAGAGAGAGTGAATGAAATGCAAGCAGCTGAAACAGAAATTTATGAGGTC 3243
Qy 1187 SerAspLeuGlnLysProLysGlnAspLeuGlnGluGlyGluVal---LysLeuLeuLeu 1205
Db 3244 GATGGTGTCAAAAAGATCATGAGGACCCCTGGAAGGAGGTGGCTTCCAGCTTG 3303
Qy 1206 GluMetGluLeuLeuLysGlyHisLeuThr-----AspSerGlnLeuSer----- 1220
Db 3304 CCAGTCAAGTGTGAAAAATCACACCTGGTCCCTCATGATGATGACAGGATCAATGCTTAC 3363
Qy 1221 IleGluLysLeuGlnLeuGlnAsnLeuGlnValThrGluLysLeuGlnThrLeu----- 1238
Db 3364 ATTGAAGAA-----GAAGTCCAAAGACGCTTCAGAGATTGCAATGCT 3405
Qy 1239 -----GlnGluGluMetCys 1243
Db 3406 GTGATTAGTGAAGGCTGAGTACATCTGCAGACACGATGAAGCATATAGAAATTCAC 3465
Qy 1244 AsnIleThrIleGluArgAsnGlnLeuGlnThrAsnPheGluAspLeuLys----- 1260
Db 3466 AATGCAACATTAACGTAACGTAATAATATGAGCTGTGTGTCACCTCTGTGTCTG 3525
Qy 1261 -----AlaGlnHisAspSerLeuLysGlnAspLeuSer 1271
Db 3526 ATGCCAGAGCCTGATGCCGCTGCTGAGCTATATCATCTTGTCTCCAGCAAGATCTG--- 3582
Qy 1272 GluAsnIleGlnGlnSerIleGluThrGlnAspGluLeu-----Arg 1285
Db 3583 ---GTTCAAGCTTCTCTTGAATTGGAAAAACGAATCCGATTAAGTTTGGCAAT 3636
Qy 1286 AlaAlaGlnGluLysLeuArgGlnGlnLysGlnLeuValAspSerPheArgGlnGlnLeu 1305
Db 3637 GGAAGTCAAGGTGATCCAAATTCAGACTTACCTTGGTGAATGAT-----TACTTT 3690
Qy 1306 LeuAspCysSerValGlyIleSerSerProAsnHisAspAlaValAlaAsnGlnLys 1325
Db 3691 CTTGATGAATAATGAAAGTCAATGTCCCT----- 3720
Qy 1326 ValSerLeuGlnGluValAsnSerLeuGlnSerGluMetLeuArgGlyGluArgAspGlu 1345
Db 3721 ---TCCCTGGCAGAAAGTTCACTTACTGCTTACACAACAGTGAAGATCAGGTGACTCT 3777
Qy 1346 LeuGlnThrSerCysLysAlaLeuValSerGluLeuGlnLeuLeuArgAlaHisValLys 1365
Db 3778 GGCATACCAAGTGCAGTGCCTAGTC-----CTTGTGAACACCCACATTTGCA 3825
Qy 1366 SerValGlu----- 1368
Db 3826 CTGGTGAAGAGAGACTGTGTTTTTATCCAGCATTCGATCTGAAACATACCTCTCCG 3885
Qy 1369 GlyGluAsnLeuGlnIleThrLysLysLeuAsnGlyLeuGlnLys-----Glu 1384
Db 3886 GGTGCACAAATTTATGATGATC---AAATGCCAGCTTTAAGTAATCAGGTGTGTTGT 3942
Qy 1385 IleLeuGlyLysSerGlnGlnSerGluValLeuLysSerMetLeuGlnAsnLeuLysGlu 1404
Db 3943 GTTCCAGAAAAAGAAATGTGTCAACAGTGAAGTACTGTTCTTACAGAAATCCAAACCT 4002


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Db      1237 -----CAGTCCCTGCTAGAGAGAAATGAAATAATTAAGTCGTCTG 1278
QY      509 HtsgInserMetIleAspPheGluIleSerAspSerValGlnPheHisAspSer 528
Db      1279 AGCGAGGACGCTGTCAGACACCAGATGTTGGAGAGATCATTTGGACAGACGACG 1338
QY      529 LysGluAsnGlnLeuGlnTyrLeuProLysAspSerGlyAspMetAlaGlyCysArgLys 548
Db      1339 AATGAA-----AAATGAACGCCAGCTAGAGAAAGACTCAGGCAG 1377
QY      549 ---AlaSerPheGluLysGluIleThrSerLeuGlnGlnGlnLeuGlnSerLysGlu 566
Db      1378 CATGGCGCTGCAAACTGATCTTAAAGCTAGAGACTTTGGAAAGCCAGAAATTG 1437
QY      567 GlnGluLysLysGluLeuValGlnSerPheGluLeuLysIleAlaGluLeuGluGln 586
Db      1438 AAAGAAATGTAGAGATTAATTTGTAACTCGACGCAATTGATTACCCAGTTATGGATGAA 1497
QY      587 LeuSerValLysAlaLysAsnLeuGluMetValThrAsnSerArgLysIleSerIleAsn 606
Db      1498 -----ACTGTTGCTTGATGCTGCGCTGACGCAATTGATCTGCGGTGAG 1539
QY      607 AlaGluValGlnThrAspValAlaGluLysGluValAlaArgLysGluMetSerValLeuGly 626
Db      1540 CAAGAGCCCAAGTAAAGAAACCAATCCAG----- 1569
QY      627 AspSerGlyTyrAsnAlaSerAsnSerAspLeuGlnAspSerValAspGlyLysArg 646
Db      1570 -----ACAGCAGGCTCTTCTGACCGCTTTTACCACTGACCTGATGCTCTCCCT 1614
QY      647 LeuSerSerSerHisAspGluCysIleGluHisArgLysMetLeuGlnLysIleVal 666
Db      1615 CAAGCGAGATGCTTAAGAGAGCTGTTGAGTTGAAATTAAGCTTGCACCTGAAA----- 1668
QY      667 AspLeuGluGluPheIleGluAsnLeuAsnLysLys---SerGluAsnLysGln 684
Db      1669 -----GAGGCCCTGCTAGAGAGATGATGATCAGATGACAGCCCAACG 1710
QY      685 LysSerSerGluGlnAspPheMetGluSerIleGlnLeuGluAlaIleMetAlaGlu 704
Db      1711 CACCTATTTCAGTACCAATTCAGATTAACATA----- 1743
QY      705 LysAlaAsnAlaLeuGluGluLeuAlaLeuMetArgAspAsnPheAspAsnIleLeu 724
Db      1744 AAAGAGCCAGAAATTAGATCATCATCTGCAAAAGAAAG---CAAGAAATGGTCTT 1800
QY      725 GluAsnGluThrLeuLysArgGluIleAlaAspLeuGluArgSerLeuLysGluAsnGln 744
Db      1801 GAACTTCAGACGCAAGAGAGATGCCAACCAAGCCAAAGTGAAGACGCGCGCCGCAAA 1860
QY      745 GlnThrAsnGluPheGluIleLeuGluLysGluThrGlnLysGluHisGluAlaGlnLeu 764
Db      1861 CCTCTCCAGAGCTGAGGCTCAAAATGCTGATCTGAAGAGAAA----- 1905
QY      765 IleHisGluIleGlySerLeuLysLeuValGluAsnAlaGluMetTyrAsnGlnAsn 784
Db      1906 CTGAATGACAGCTCAAACTTCTGAACCTAAAGGAATCCACAGACCTGATGCTCCAAA 1965
QY      785 LeuGluGluAspLeuGluThrLysThrLysLeuLysGluGlnGlnIleGlnLeuAla 804
Db      1966 CTGAACCAAGAGATTA-----CGGATGATGAAAAACAGCGGATCACTTA--- 2010
QY      805 GluLeuAlaGlyLysArgAlaAspAsnLeuGlnLysLysValArgAsnPheAspLeuSerVal 824
Db      2011 ---ATGCGCTCAAAATGAAGAGATGCTGAG---AAGTTTACACAGTGG----- 2052
QY      825 SerMetGlyAspSerGluLysLeuGluGlnLysIlePheGlnLysGlnSerLeuSer 844
Db      2053 -----AAGCGAAAAAGACACAAAGAGTAAATACAGTTTAAAAAGAA----- 2091
QY      845 AspAlaGluAlaValThrArgAspAlaGlnLysGluCysSerPheLeuArgSerGluAsn 864

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Db      2092 -----CGAAGCCGTAAAGAGCAAA-----TATGAGCTG 2118
QY      865 LeuGluLeuLysGluLysMetGluAspThrSerAsnTyrTyrAsnGlnLysGluLysAla 884
Db      2119 CTGAACCTTGAAAGAAACTTCAGAAACAATCAATGCTCTCAGACGTTAAACGAGAG 2178
QY      885 AlaSerLeuPheGluLysGlnLeuGluThrGluLysSerAsnTyrLysLysMetGluAla 904
Db      2179 GCAGCAGCTGCCAACAGAGGCTCTCAAGATGCTCTCCAGAAACAAACGAGAGTT---GCA 2235
QY      905 AspLeuGlnLysGluLeuGlnInserAlaPheAsnGluIleAsnTyrLeuAsnGlyLeu 923
Db      2236 GATTAAGCGGAAAGAACTCAAGAC-----CGTGAATGAA 2271
QY      924 ---LeuAlaGlyLysValProArgAspLeuSerArgValGluLeuGluLysVal 942
Db      2272 GGCAGCTGACGCTCGAGTAAAGAAATTGGCTTGAAACGAAATTGAGTTATGCTCAGTACT 2331
QY      943 SerGluPheSerLysGlnLeuGluLysAlaLeuGluGluLysAsnAlaLeuGluAsnGlu 962
Db      2332 GAGGAAGCCAAACGCATCTGAATGACCTCTTGAAGATGAAAGATCTTGGCTCAAGAT 2391
QY      963 ValThrCysLeuSerGluTyrLysPheLeuProAsnGluValGluCysLeuLysAsnGln 982
Db      2392 GTGGCTCAACTCAAAAGAA----- 2409
QY      983 IleSerLysAlaSerGluGluIleMetLeuLeuLysGlnGluGlnLysIleSerAlaSer 1002
Db      2410 -----AAAAAGAACTGGGGGAGATCCACCTCT 2439
QY      1003 IleIleSerLysGlnGluIleIleMetGlnGlnInserGluGlnIleLeuGlnLeuThr 1022
Db      2440 AAATCCCGAGCGGTATATTCCTCCCTACTGAAGTGCCTGAGTAACTTGGAGTCAAGAA 2499
QY      1023 AspGluValThrHisThrGlnSerLysValGlnGlnThrGluGlnGlnLysGluMet 1042
Db      2500 GATTCTTATTCACA---AAGCAGATTGAAGCCTGAGACATGAATGAATGACAGGAGTCT 2556
QY      1043 LysLysMetHisAspAspLeuPheGluLysTyrIleArgAsnLysSerGluAlaGluAsp 1062
Db      2557 CAGATTGCT-----GACCTACAGCAGAGCTGCTG---GATCCAGAAATGTAAGAC 2604
QY      1063 LeuLeuArgGlu-----MetGlu 1068
Db      2605 AGACAAACAAACAGCTGGAGAAATATTCACCACTTCTGAAAGCCAAAGTGCCTCCGAAA 2664
QY      1069 AsnLeuLysGlyThrMetGluSerValGluValLysIleAlaAspThrLysHisGluLeu 1088
Db      2665 TATTTGATTTGAGAGCTGCTCTCTCCAAATATCAGGTACGAACTTGAAAGCAGCTG 2724
QY      1089 GluGlu-----ThrIleArgAspLysGlnGlnLeuLeuHisGluLysLysTyrPhe 1105
Db      2725 AAACAGAGCAAGACAGCTGCTGCTGATGACAGAAAGTCTGTTGAGAAAGCAAAATCAT 2784
QY      1106 PheGluAlaMetGlnThrIlePheProIleThrProLeuSerAspSerLeuProSer 1125
Db      2785 TTTCGCGAGATGAGCAGAGTTA-----CAAGCT 2814
QY      1126 LysLeuValGluGlyAsnSerGlnAspProIleGluIleAsnAspTyrHisAsnLeuIle 1145
Db      2815 GAGCTGTGCAAGATGAGACACAGACACCCAGAGAAAGTG---CTGTAC 2859
QY      1146 AlaLeuAlaThrGluArgAsnAsnIleMetValCysLeuGluThrGluArgAsnSerLeu 1165
Db      2860 CTTCCTCAGCAGCTGCAACAAAGCCAAATGCA-----GAGAACAGATT 2904
QY      1166 LysGluGlnValIleAspLeuAsnThrGlnLeuGlnInser---LeuGlnAlaGlnSerIle 1184
Db      2905 GAGGAAATCAGTACAGTAAAGAAAGAAACAGACCTGCAAGACACATGATGCTCAGAT--- 2961
QY      1185 GluLysSerAspLeuGlnLysProLysGlnAspLeuGlnGluGlnValLysLeuLeu 1204
Db      2962 -----GAAGAACTTGAGAAATATCGAAGATGCTGAGCAAAATCAG---CAGCTTCTC 3012

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OY	198	SeSerAAspSerHISThrILePheArgMetILEValGluSerArgAspArgAsnAspPro	217
Db	942	TCCTTCGCATCCCACTCACTGATATCTCTTAATCAATGTAG-----	980
OY	218	ThraAsnSerGluAsnCyAspGlyAlaValMetValSer---HisLeuAsnLeuValAsp	236
Db	981	-----CAGCGAATCTGGAGAACCCAGAAACTATCTCGGCMAACTTACTCTGGTGGAT	103
OY	237	LeuAlaGlySerGluArgAlaSerGlnThrGlyAlaIleGluValArgLeuIysGluGly	256
Db	1035	TTGGCCCGGTTCCGAAAGAGTTTCCAAAGACTGGAGCGGAGGAAACCGTTCTTGAATGAAGCC	109
OY	257	CysAsnILEAsnArgSerLeuPheILELeuGlyGlnValILEIlysLysLeuSerAspGly	276
Db	1095	AAGAAACATCAACAAGTGTGCTGGCTGGCCCTTGGGCACATATTTCTGCGCTGGCGACGGA	115
OY	277	GlnAlaGlyGlyPheILEAsnITyArgAspSerILEuThrArgILEuGlnAsnSer	296
Db	1155	AACAAA---ACGCACATCCCTTACCGGATTCCAACTAACCGGCATCTCTGACAGAGTGC	121
OY	297	LeuGlyGlyAsnAlaLysThrValILEILECysThrILEThrProValSerPheAsp---	315
Db	1212	CTGGAGAGGCACACGACCAACCATCGTCATGCTGCTCTCCAGCCATTTCACAGAA	1271
OY	316	---GlnThrLeuSerThrLeuGlnPheAlaSerThrAlaLysHisValArgAsnThrPro	334
Db	1272	TCGAAACGAACTCAACGCTGCATCTCGGTCTGTAGCCCAACAGTGAAGAACCTGGTCT	1331
OY	335	HisValAsnGluValLeuAspArgGluAlaLeuLeuLYArgITyArgGlyGluILEu	354
Db	1332	TGCGTTAAAGAGAGCTTACTGCCAGAGAAATGAAGACGCTTAAGAAAGAG---	1385
OY	355	AspLeuLYLysGlnLeuGlnLeuAsnLeuGluSerSerGlnThrLysAlaGlnAlaMet	374
Db	1385	-----	1385
OY	375	AlaLYsGlnGlnHisThrGlnLeuLeuAlaGluILELysGlnLeuHisLYsGlu---	392
Db	1386	---AAGAAAGAAGACCGCCGATTAAGGTTAAGCGTGAAGACTGGAATCGAATCGCTTCCG	1442
OY	393	-----ArgGluAspArgILEThrPHisLeuThrAsnILE	403
Db	1443	CGCTGACAGCGGGTGAACTGTTAAGCGGAGGAGCAAACTC---AACTATGAGAGATCTC	1499
OY	404	ValValAlaSerSerGlnGluSerGlnAsp---GlnArgValLysArgLysArgVala	423
Db	1500	ATGAGGCGAAGACCGCCCACTGGAAATGAGAGCGACAGACGGCGCGCGAAGGCC	1559
OY	423	IThrThrAlaProGlyLYsILEglnAsnSerLeuHisAlaSerGlyValSerAspPheAs	443
Db	1560	GCTTTGGCGCCCGACGAA-----	1578
OY	443	PMetLeuSerArgLeuProGluAsnPheSerLYsLeuAlaLysPheSerAspMetProse	463
Db	1579	-----CGGCTCTC-GCCCAATATGTCCTCGCATCGGTGCTCCGTGAACGACGCCGAG	1627
OY	463	rPheProGluILEAspAspSerValCysThrGlnPheSerAspPheAspAlaLeuSe	483
Db	1628	GCTGAGCTACAGAGTCGACGCTCTCTCAACAGACCTGACAGACAAAGATGAG-----	1679
OY	483	rMetMetAspSerAsnGlyILEAspAlaGluITyPAsnLeuAlaSerLYsValThrHisAsr	503
Db	1679	-----	1679
OY	503	gGluLYsThrSerLeuHisglnSerMetILEAspPheGlyGlnILEAspAspValGln	523
Db	1680	-----GAGATCAATACAGACAGCA	1699
OY	523	pPheHisAspSerSerLYsGluAsnGlnLeuGlnITyLeuProLYsAspSerGlyAspMe	543
Db	1700	GTACGCGGAGAGCTCAAGACGACGGATGAG-----CAGAGGAAGTAATCAT	1747

QY	543	ctaaagtcuayarglys-----alaserpnehluysgluilethserleuenglncgl	561
Db	1748	CGCTAACGCTCGCGCTGACGTATGAGACTTTGGACGTGGAGATGGCCGGAATCAACAGCA	1807
QY	561	nleuGlSerLysgluGlunluyLysgluLeuValGlnserPnehluleuilei	581
Db	1808	GAACCAATCCCGCAAGAGAGAGGTTAAGAGGGTCTCCAAAGCTCTCGAA	1855
QY	581	agluLeuGlunluyLysSerValLysAlaLysAsnLeuGlumetValThAsnSerAr	601
Db	1857	-GAGCTGACTGTAACCTACGACCAGAAATCCACAGAGATCGAT-----	1895
QY	601	ggluHisSerIleasnAlaGluValGlnThrAspValGluLysGluValValArgLysGl	621
Db	1899	-----AACAGAACAGAGATTCGATCCCTCCACAGACAGACCTCCAGCAGAA	1945
QY	621	umetSerValLeuGluyAspSerGlyTyTrAsnAlaserAsnSerAspLeuGlnAsp	639
Db	1946	GCACTCTGTG-----TTCAACCCCCCTCCACAGAGCTTACAGAGCTCAAC	1990
QY	640	-----SerSerValAspGlyLysArgLeuSerSerHisAspGluCysIleGlnHi	657
Db	1991	TCGATCATCTCTCCACACCAAGAAACCGCATACG-----	2024
QY	657	sargLysMetLeuGlunluyLysIleValAspLeuGlunluehileGluAsnLeuAsnLys	677
Db	2025	---GAAAGCTAACCAACTACTCGCGACCTCGCGAATGGGCGCAGCCATTGGCCC	2080
QY	677	slYsSerGluAsnAspLysGlnLysSerSerGluAsnAspMetGluSerIleGlnLe	697
Db	2081	CGCGCAGTCGACATCGACTTAAAGATAG-----	2111
QY	697	uCySgluAlaIleMetAlaGluLysAlaAsnAlaLeuGlunluy-----	711
Db	2112	---GCTCTGCGTGGCACGAGATCGCACAGAGTGAGAGAAATTTCACCAATGGCGC	2164
QY	712	-----LeuAlaLeuMetArgAspAsnIleIleLeuGlunluyLysLe	729
Db	2165	TTTGTGTTTTCAGCAAGTGAAGACGAGGCCAAGAACATTGCCAGGATGCTTCAACAT	2224
QY	729	uLysArgLysIleAlaAspLeuGluArgSerLeuLysGlu---AsnGlnLysThrAsnG	748
Db	2225	GGAAACACAGCAGGCTGATCCCAACAGAAAGATCTCCGATTGAGAAATCTGGCGCA	2284
QY	748	uPheGluLeuGlunluySgluThrGlnLysGluHisGluAlaGlnLeuIleHisgluI	768
Db	2285	GTACCGGTACTCT-----ATTTCGACGACGAGAGCAGCATG-----	2321
QY	768	egLysLeuLysLysLeuValGluAsnAlaGluMetTyAsnGluAsnLeuGlunluyAs	788
Db	2322	-AAGTCGCTGACAGAGTCGATCGCGGAGCAGAGAACAGACGCGACGCTTCAGGAAACA	2380
QY	788	pleuGlunluyr-----LysThrLysLeuLeuLysgluGlnluyIleGl	802
Db	2381	AATGATTCGCTGCGCAGAGAAATGCGCAAGCTCAAGCGCGCGAGACGATTCCGCGGT	2440
QY	802	nLeuAlaGluLeuArgLysArgAlaAspAsnLeuGlnLysLysValArgAsnPheaspLe	822
Db	2441	TAAAGCCGAGAGAAACAGCGGCTGAGGAGCTGGCC-----	2477
QY	822	uSerValSerMetGlyAspSerGluLysLeuCysGluGlnIlePheGlnLeuLysGlnSe	842
Db	2478	-----TTCATGTTGATTCCTCAG-----ATGACAGAGCTA-----	2507
QY	842	rLeuSerAspAlaGluAlaValThrArgAspAlaGlnLysGluCysSerPheLeuArgSe	862
Db	2508	-----CGGAAAGCCACACCCCG-----CAGGTGTCGAGCTCCGGGA	2545
QY	862	rGluAsnLeuGluLeuLysGluLysMetGluAspThrSerAsnTrpTyAsnGlnLysGl	882
Db	2546	CGAAATTGGCCGCCAACAGACAGAAATGACGATGAAAGAT---GTCCATCAAAAG-2600	
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Db 2654 GGATGCCGAGAAAGTCCAGGAGCTTCAG-----AACAT 2686
QY 922 yLeuLeuAlaGlyValProArgAspleuLeuSerArgValGluLeuGluYsLYsVa 942
Db 2687 CATCCTCACC----- 2696
QY 942 lSerGluPheSerLYsGlnLeuGluYsAlaLeuGluGluYsAsnAlaLeuGluAsnG1 962
Db 2697 -----AACGAGCCTCGGAGACCAAGCGCCAAAGACTCAAGCGCCTGGAGAC-- 2744
QY 962 uValThrCYsLeuSerGluTYrLYsPheLeuProAsnGluValGluCYsLeuLYsAsnG1 982
Db 2745 -----ACGCTGGCCAAAGAGTTCACAGACGCTACACAACCTGCGAAAACTTTTCCTTCAGGA 2800
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QY 1002 rIleIleSerLYsGlnGluIleIleMetGlnGluGlnSerGluGluIleLeuGlnLeuTh 1022
Db 2861 ACTGCGCGAAGAAACGAAGATTCTCTTGGAGAACAC-----CT 2902
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QY 1062 pLeuLeuArgGluMetGlu---AsnLeuLYsGLYThrMetGluSerValGluValLYsI1 1081
Db 2960 CGAGCTGCCCAAGCTGGAGAAAGCTGTACGCTGTACCATGGAGCGGATGAAGCTCTGGA 3019
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QY 1101 u 1101
Db 3080 G 3080
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Search completed: October 22, 2003, 21:22:47
Job time : 930 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 22, 2003, 21:01:12 ; Search time 1494 Seconds
(without alignments)
5302.570 Million cell updates/sec

Title: US-09-724-584-1

Perfect score: 14769
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Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1792395 seqs, 134090451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100
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-MAXLEN=200000000 -USER=US09724584.@CGN_1.1.1053@runat_22102003_161414_1215
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	3615.5	24.5	7992	11	US-09-893-519A-140 Sequence 140, App

2	3613.5	24.5	8493	13	US-10-071-766-51	Sequence 51, App1
3	3613.5	24.5	8503	14	US-10-037-270-130	Sequence 130, App
4	3611.5	24.5	8491	12	US-10-133-013-260	Sequence 260, App
5	1153	7.8	10300	10	US-09-960-253-145	Sequence 145, App
6	1152	7.8	10096	10	US-09-960-253-163	Sequence 163, App
7	1149	7.8	10281	14	US-10-084-817-361	Sequence 361, App
8	1147	7.8	10281	12	US-10-240-965-201	Sequence 201, App
9	1139	7.7	10190	10	US-09-864-864-292	Sequence 292, App
10	1139	7.7	10211	10	US-09-954-456-1153	Sequence 1153, App
11	1139	7.7	10211	10	US-09-967-768A-186	Sequence 186, App
12	1139	7.7	10211	11	US-09-918-624B-2	Sequence 2, App1
13	1050	7.1	4775	14	US-10-146-473-81	Sequence 81, App1
14	1032.5	7.0	7694	12	US-10-096-534-14	Sequence 34, App1
15	1032.5	7.0	8063	12	US-09-814-353-21776	Sequence 7, App1
16	1024.5	6.9	12313	14	US-10-171-311-7	Sequence 3, App1
17	1024.5	6.9	12438	14	US-10-171-311-3	Sequence 5, App1
18	1022.5	6.9	12337	14	US-10-171-311-5	Sequence 1, App1
19	1022.5	6.9	12462	14	US-10-171-311-1	Sequence 134, App
20	998	6.8	11677	14	US-10-082-830-134	Sequence 668, App
21	946	6.4	3753	12	US-10-116-712-668	Sequence 661, App
22	941.5	6.4	4348	12	US-10-116-712-661	Sequence 667, App
23	941.5	6.4	4348	12	US-10-116-712-667	Sequence 40, App1
24	900.5	6.1	6386	13	US-10-098-841-40	Sequence 175, App
25	891.5	6.0	7497	10	US-09-960-253-175	Sequence 359, App
26	891.5	6.0	7792	13	US-10-044-090-359	Sequence 2651, App
27	888.5	6.0	3366	14	US-10-205-823-418	Sequence 418, App
28	872	5.9	6452	14	US-10-205-823-418	Sequence 336, App
29	848	5.7	6773	10	US-09-864-864-336	Sequence 1601, App1
30	836	5.7	14800	10	US-09-954-456-1601	Sequence 61, App1
31	836	5.7	14800	12	US-10-269-909-61	Sequence 115, App
32	829	5.6	7065	9	US-09-874-923-115	Sequence 115, App
33	829	5.6	7065	9	US-09-991-496-115	Sequence 115, App
34	828	5.6	580073	12	US-10-205-220-1	Sequence 1, App1
35	814	5.5	14833	12	US-10-240-965-113	Sequence 113, App
36	797	5.4	15231	10	US-09-917-800A-1505	Sequence 1505, App
37	795.5	5.4	5641	12	US-10-032-585-6646	Sequence 6646, App
38	795	5.4	10625	9	US-09-727-384-5	Sequence 5, App1
39	795	5.4	10625	14	US-10-023-219-3	Sequence 3, App1
40	786.5	5.3	6586	10	US-09-954-456-1115	Sequence 1115, App
41	786.5	5.3	6586	10	US-09-954-456-1190	Sequence 1750, App
42	786.5	5.3	6586	14	US-10-157-031-17	Sequence 37, App1
43	776	5.3	8948	9	US-09-735-705-119	Sequence 119, App
44	776	5.3	8948	10	US-09-850-716A-119	Sequence 119, App
45	776	5.3	8948	10	US-09-897-778-119	Sequence 119, App

ALIGNMENTS

RESULT 1
US-09-893-519A-140
Sequence 140, Application US/09893519A
Publication No. US20030027243A1
GENERAL INFORMATION:
APPLICANT: ANADYS PHARMACEUTICALS, INC.
APPLICANT: THOMPSON, Craig
APPLICANT: MOORE, Jeffrey
APPLICANT: BURMAN, Ed T.
APPLICANT: BRADLEY, John
APPLICANT: DESILVA, Thamara
APPLICANT: HARRIS, Sandra
APPLICANT: KOMARNITSKY, Svetlana
APPLICANT: MENDILLO, Marc
APPLICANT: MOORE, Daniel
APPLICANT: MCCOY, Melissa
APPLICANT: SANDERSON, Karen
APPLICANT: HAO, Tariq
APPLICANT: ZHU, Shuhao
APPLICANT: LONG, Fan
APPLICANT: DAVIDOV, Eugene
TITLE OF INVENTION: ANTI-FUNGAL COMPOUNDS AND METHODS OF USE
FILE REFERENCE: 0342/IG548-US2
CURRENT APPLICATION NUMBER: US/09/893, 519A
CURRENT FILING DATE: 2001-06-28

QY 598 ThrAsnSerArgGluHisSerIleAsnAlaGluValGlnThrAspValGluIleArgGluVal 617
 DB 1498 TTGAACCTCA----- 1506
 QY 618 ValArgLySGluMetSerValIleuGlyAspSerGlyTyrAsnAlaSerAsnSerAspIleu 637
 DB 1506 ----- 1506
 QY 638 GlnAspSerSerValAspGlyLyAsrGluSerSerSerHisAspGluCysIleGluHis 657
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 DB 1507 -----CTGCTGCT 1515
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 QY 858 SerPheLeuArgSerGluAsnIleuGluIleuLySGlnIlyMetGluAspThrSerAsnTrp 877
 DB 1924 GCCTTTCTTAAGATGAAATATCTGAGTTTGAAAGGAAATGAAAGAACTTCAACTACA 1983
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 DB 1984 TACAAGCAAAATGAAATATGATTCAGTTATATCAAGCAATTTGAGGCAAAA----- 2037
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 DB 2038 -----AAGAAATGCAAGTTGATCTGAGAAAGAAATTAACATCTGCTTTTATAGATA 2091
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 QY 1488 -----SerIleAspArgSerGluIlyMet-----GluIleIlyValLeu 1501
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 QY 1502 GlyIlyIly-----LeuGluArgAsnGlnIlyLeuLeuGluArgLeuGlnIlyIlySer 1520
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 QY 1521 GluLeuSerAsnIlyLeuGluIleLeuGlnIlySerGluMetGluThrSerValLeuLeuIly 1540
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 QY 1601 GluIlySerGlu-----ThrSerAlaAspCysValHisProLeuGluGluIlyLeu 1617
 Db 4213 GAGATGAGCAATTAACAAACCAAGATTCAGACACTTAAGAGATGAATGAATGAATGCTC 4272
 QY 1618 LeuLeuThrGluGluLeuHisGlnIlyThrAsnGluGlnIlyIlyLeuHisIlyGluIly 1637
 Db 4273 GGATTTGTCAAAGAAAGCTTCAAGAAAGTCAATGATGAAATGAATCTGTAGTCAAGAGAA 4332

QY 1638 AsnGluLeuGluGlnAlaGlnIlyValGluLeuIlyCysGluValGluHisIleuMetIlySer 1657
 Db 4333 GATGACCTTACAGAGGCTGCAGAAAGTTCTTCAATCTGAAAGTACACAGCTC----- 4383
 QY 1658 MetIleGluSerIlySerSerLeuGlnSerLeuGlnHisGluIlyHisAspThrGluGln 1677
 Db 4384 -----AAAGAAACATTAAGAAATTTAGCTTAACACCTGGAAACTGAAG 4431
 QY 1678 GlnLeu-----LeuAlaLeuIlySerGlnIlyMetGlnIlyValIleGlnIlyIly 1693
 Db 4432 GAACCTTAAAGTCTCATATTGTTGCTGAAGAAAGAGAGAACTTAAATGATGAAGAA 4491
 QY 1694 IlyGluLeuGlnIlyThrHisGluHisIleuThrAlaGluValAspHisIleuSerGluAsn 1713
 Db 4492 GTGAATCTTTCAGAAAGAAAG-----ACTGAATATATCAACCATTCMAAGCAG 4539
 QY 1714 IleGlu-----LeuGlyLeuAsnPheIlyAsnGluAlaGlnIlyIlyThrIlySerGluGln 1732
 Db 4540 TTAGAAAGCAATCAATGATTAATTAACAGAAAGAGATCCAAAGAGATTTATGAGAAAGAGAA 4599
 QY 1733 CysLeuLeuAsnGluAsnIlySerGluLeuGlnIlySerGlnHisIlyArgLeuIlyCysGluIle 1752
 Db 4600 CAACTT-----ATATTAACCAATTAATGATGAGTTCAAGAAACGTGAAT--GAAGT 4650
 QY 1753 GluGluLeuMetIlySerSerLeuIlyAspIlySerGluSerAlaLeuGluThrLeuIlySer 1772
 Db 4651 AAACATATTCAGAGAGATCGCAAGAGCCAGAGATTCAGACCTTAACAAGATAT----- 4701
 QY 1773 GluGlnIlyValIleAsnLeu-----AsnGlnIlyMetGluMet 1785
 Db 4702 GAAAGTAAAGATGCTCGAGTTACCAACAGACTTCAAGAAAGTCAAGAAATCAAAAT 4761
 QY 1786 ValMetLeuGluMetGluGluLeuIlyAsnSerGlnArgThrValIleAlaGluArgAsp 1805
 Db 4762 ATGATTTAAGAAAAAGAGAAATGAATAAGAACTACAGAGCCCTTCAGATGAAGAGAGAC 4821
 QY 1806 GlnLeuGlnAspAspLeuArgGluSerValGluMetSerIleGluThrGlnAspAspLeu 1825
 Db 4822 CAACGAAAGAAACACTTAAAGAAATTTAGCTTAAATTAAGAAAGATCTCAAGAA----- 4875
 QY 1826 ArgIlyAlaGlnGluAlaLeuGlnGlnIlyAspIlyValGlnIlyLeuThrSerGln 1845
 Db 4876 AAAGAAATATCACTTTTAAGATGACAGCTGTCAATGAGACTCGAGAAATATGTGAA 4935
 QY 1846 IleSerValLeuGlnIlyIlySerLeu-----LeuGluAsn----- 1858
 Db 4936 ATTAAGACATTTGAAGAGCAATTTGAGAACCCAGAAAGTTAAACCTGGAAGAACTGAAGAC 4995
 QY 1859 -----GlnMetLeuTyr--AsnValAlaThrValIlySerGluThrLeu 1871
 Db 4996 GAGAAATTAAGTTGACTCAGATCTACTACATAAAACCTTGAAGAAATGAGATCTGAACA 5055
 QY 1872 SerGluArgAspAspLeuAsnGlnSerIlySerGlnHisIleuPheSerGluIleGluThrLeu 1891
 Db 5056 AAAGAAAGAGATGACTTGAAGAGTGTGAGAGAACTCTCAAGATGAGAGAGACCAAGCTC 5115
 QY 1892 SerLeuSerLeuIlySerGluIly-----GluPheAlaLeuGluGlnAlaGluIlyAspIly 1909
 Db 5116 AAGGAAAGAACTTTAGAGAACTATTAATCAAGAGCTTAAGAAAGAAAGAGAGCTTAAGAAAT 5175
 QY 1910 -----AlaAspAlaIleArgIlyThrIleAspIleThrGluIlyIleSerAsn 1925
 Db 5176 GTTCACATGATCTGAAGAGACACCAAGAAATCTATTCAT-----AAACTTAAGAGAG 5226
 QY 1926 IleGluGluGlnLeuLeuGlnIlyAlaIleThrAsnIlySerGluThrLeu--TyrGluArg 1944
 Db 5227 ATTGTTTCAAGAAAAACAATGAATTAATCAATTAAGAAAGAGACTTAAGAACTGAAT 5286
 QY 1945 GluSerLeu-----IleGlnCysIlyGluGlnIleuAlaLeuAsnThrGluHis 1960
 Db 5287 GATGCTTAAAGACACAGATCTGAAGAAATTAACAGAGAACTTAAGAAATGCTCAATGAT 5346

QY 1961 LeuArgGluThrLeuLeuSerLeuSerLeuAlaLeuGluLeuMetGluGlnGluArgAsp 1980
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 QY 1991 GUAUAAlaAsnLysValIleAlaLeuThrGluLysMetSerSerLeuGluGlnIle 2000
 DB 5407 AAACATCATCAATATCAAAAAAGATTAGAAAATTCAAAATGCTAAATTACAGAAAAGATT 5466
 QY 2001 AsnGluAsnValThrThrLeuLysGluGluGluGluGluGluGluThrPheThrLeuGln 2020
 DB 5467 CAAAGAA-----CTTAAGCCAAATGAACATCACTATTATACGTTAAAAAAGAT 5514
 QY 2021 ArgProSerLysGlnLysSerSerGlnMetGluGluLeuArgGluSerLeuLysThr 2040
 DB 5515 GTCATATGACACACAAAAAAGTGTGAAATGAGCAACTAAAGAAAATAAATGAAGC 5574
 QY 2041 LysAspLeuGlnLeuGluGluAlaGluLysGluLysSerGluAlaThrAsnGluLys 2060
 DB 5575 CAAACCTTAACCTCTAGTAATTA-----GAAATAGAG 5607
 QY 2061 AsnLeuThrAlaLysIleSerSerLeuGluGluGluIleLeuGlnAsnAlaSerIleLeu 2080
 DB 5608 AATTTA-----AATTGGCTCAAGAACTTCATGAAAACCTTGAGAAAATG 5652
 QY 2081 AsnGluAlaValSerGluArgGluAsnLeuArgHisSerLysGlnLeuValSerGlu 2100
 DB 5653 AAATGTGTAATGAAAGAAAGATATCTTAAGAAAGTAGAGAGACACTCAAACTGAG 5712
 QY 2101 LeuGlnLeuSerLeuThrLeu-----LysSerArgAspHisAlaPheAlaGln 2117
 DB 5713 AGAGACCAACTCAAGAAAGCTGCAGAAACCAAAAGCTAGAGATGTGAAATACACAG 5772
 QY 2118 -----SerLysArgGluLys-----AspGluAlaVal 2126
 DB 5773 GAACAAAAAAGTCTCGATGCTATCAAAAGAAACAAAGAACTGTGATTAAGT 5832
 QY 2127 AsnLysIleAlaSerLeuAlaGluGluIleLysIleLeuThrLysGluMetAspGluPhe 2146
 DB 5833 GAAAAATTTTCGAAAAGACAACTCAAAATTTCAAGACATTCAAAAGGATTTAATTA 5889
 QY 2147 ArgAspSerLysGluSerLeuGlnGlnLysSerHisLysSerGluGluLeuCysThr 2166
 DB 5890 -----TCAAAAGATGAATTAAGAAAAGATCCAAAGAACTTCAG----- 5928
 QY 2167 TyrLysThrGluLeuGlnMetLeuLysGlnIleLysGluAspIleAsnAsnLysLeuAla 2186
 DB 5929 ---AAAAAGAACTTCAACTGCTTAGA---GTGAAAGAAAGATGTCAATATGAGT---CAT 5979
 QY 2187 GluLysValLysGluValAspGluLeu----- 2195
 DB 5980 AAAAAAATTAAATGAATGAAATGAAAGATTAAGAAAGCAATTTGAGCCAAACTATATGCAAG 6039
 QY 2196 -----LeuGlnHisLeuSerSerLeuLysGluGlnLeuAspGlnIleGln 2210
 DB 6040 TGTGATGATGATTAACCTTCAGTTGACTTAAGAAACTTCATGAAGAGCTTGAAGAAATTAAGA 6099
 QY 2211 MetGluLeuArg--AsnGluLysLeuArgAsnTyrGluLysCysGluLysMetAspIle 2229
 DB 6100 ATTGATGCTAAAGAAAGAGATGAGCTTAAGAGAGATTAAGAAAGATCTCTCAAAATGGA 6156
 QY 2230 MetGluLysGluLysSerValLeuArgLeuMet-----Gln 2241
 DB 6157 AGGACCAATTCATGCAACTTAAGGAAATGATAGTAGAGACCGACAGAACCAACCA 6216
 QY 2242 AsnGluProGlnGlnGlu-----GluAspAspValAlaGluArgMetAspIleLeuGlu 2259
 DB 6217 GTAAGAACTGAAAAAGCTTAAGTAGATGATGACAAAGCACCCTTAATGAAAGCCTTGAGA 6276
 QY 2260 SerArgAsnGlnGluIleGlnIleLysMetGluLysIleSerAlaValTyrSerGluGln 2279
 DB 6277 GAAAGATGCTAGATAAAGAGCTTTTGAAGAGATACTCAGAGATG---GATGATCAT 6333
 QY 2280 HisThrLeuLeuSerSerLeuSerGluLeuGlnLysGluThrGluAlaHisLysHis 2299

DB 6334 TATGAGTGTGTAATGATGATTTGCTCTGTGACTTGGAGAAAGAAATTAATTCACAGAA--- 6390
 QY 2300 CysMetLeuAsnIleLysGluSerLeuSerSerThrLeuSerArgSerPheGlySerLeu 2319
 DB 6390 ----- 6390
 QY 2320 GlnThrGlnIleValLysLeuAsnThrGlnLeuGlnThrLeuLeuAsnLysPheLysVal 2339
 DB 6391 -----ATCATAGAAAGTCAAGTAT 6411
 QY 2340 Val-----TyrArgThrAlaAlaValLysGluAsnHisSerLeuIleLysAspTyrGlu 2357
 DB 6412 GTGTTAAAGCTATGTTACAAAAATAAAGAAAGAAACATGATGATCATTAATTTGAA 6471
 QY 2358 LysAspLeuAlaAlaGluGlnLysArgHisAspGluLeuAspGluGlnLeuGlnCysLeu 2377
 DB 6472 ATGGAATTTTATGATGAAGTGGAAAAGCAAGAAATGCTTAATTAATAATACAGCACTT 6531
 QY 2378 GlnGlnHisGluArgLysTyrSerAspSerAlaSerGluGluLysPheCysGluIle 2397
 DB 6532 CAACAAAGAT-----TGTGATGTACCATCCACAGAAATTAAGGATTTCAAAATTG 6579
 QY 2398 GluPheLeuAsnGluLeuLeuPheLysValAsnIleIleGlnSerValGlnAspAsp 2417
 DB 6580 AACCAAGATATGATGATTA-----CATATTGACAGAAATTTCAAAAGAT 6621
 QY 2418 PheSerGluValGlnValPheLeuAsnGlnValGlySerThrLeuGlnGluGluGlu 2437
 DB 6622 TTCTCGAAGAAAGTGAAG-----TTCCCTAGCATTAAGAACTGAATTTCAACAACTAATGAT 6675
 QY 2438 HisLysLysGluLysPheMetGlnThrLeuGlnIlePheGluAspLeuHisValAspAlaLys 2457
 DB 6676 AATAGAAAAGAAATGACACAGTTTGTGAAGAGTGTGAATTAAGTCTGTTTGAATTAAGA 6735
 QY 2458 LysLeuSerGluGluMetGlnGlnGlnLysAsnArgAspGluAlaSerThrIleGlnLeuLeu 2477
 DB 6736 AAGCTTAATAATGCGATCCAGAAAGAAATATGATAGATTTTGCMAAGTAATTAATCTTT 6795
 QY 2478 ThrLysArgLeuLysValValGlnSerLysIle-----GlnArgGluIleThr 2494
 DB 6796 AATAACAGAAATATGTCATATGATGAATCAATCAACAGAGTTTGAAGAAAGAGTCTAC 6855
 QY 2495 ValTyrLeuAsnGlnPheGluAlaLysLeuGlnGlnLysLysGluGlnAsnLysValLysAsp 2514
 DB 6856 ATA---TCAAGAGATGGAAACAGGACCTGAATCTAGAAAGAAAAATGAAGAACTA 6912
 QY 2515 MetArgAspMetGlnHisHisGlyProSerAlaSerValMetGluGluGlnLysAsnLysArg 2534
 DB 6913 TTTAAAACTACCAAACTTGAAGACTTCTTGCGATCTGCGCCAGCTTAAT----- 6966
 QY 2535 LeuLeuGluIleLeuLysThrValGlnAspGlu-----SerLysLys 2548
 DB 6967 -----CTTACACACACACACATAGATATCCATGTTATCAATCAAGAGCT 7011
 QY 2549 LeuGln-----SerArgIleLysMetLeuGlnGlnGlnLysLeuAsnLysValLysAsp 2565
 DB 7012 ACACAGTTAACACACAGAAATTTGAGAGCTGGAAATTTCACTGCAAGAACTTAAGAA 7071
 QY 2566 AspAlaMetHisLysGluGluLysValAlaIleLeuGlnAspLysLeu--LeuSerArg 2584
 DB 7072 AGTGTATGCTTAAGAAAGCAAGATTTAAAGATGCGAAAGAACTTGAGCTGACTAAT 7131
 QY 2585 AsnAlaGluAlaGluLeuAsnAlaMetGlnValLysLeuThrLysLysGlnAspAsnLeu 2604
 DB 7132 GACATTAATAGCAAACTT-----CAAGCAAAAGTTCAATGAATTAATAGCTT 7182
 QY 2605 GlnAlaAlaMetLysGluIleGluAsnLeuGlnLysMetValAlaLysGluValAlaPro 2624
 DB 7183 GAAAAACAAAGAGACAAATTCAGTACTTCAGACAAAGTTGCTTTAGAGACTTAAGCA 7242
 QY 2625 TyrLysGluGluIleAspAsnLeuLysThrLysValValLysIleGlnMetGluLysIle 2644

Db 7243 TATAAGAGAAATTTGAAGTCTCAAAATGAGCTGTGAAATAGCCTTAGAGAAAATG 7302
 Oy 2645 LysTyrSerLysAlaThrAspGlnGluLeuAlaTyrLeuLysSerCysLeuGluAspLys 2664
 Db 7303 AAAAATGCCAAAGAAATTTGAAAAGAAATCAGTCTCAAAAACCACTGTAGAAATTCAA 7362
 Oy 2665 GlnGluGluLeuArgArgLeuLysGlnGluLeuArgArgAlaGlnAlaAspAsnAspThr 2684
 Db 7363 AAGGAAGTTTAAAGCTATTGAGAGAAAATCTCAGAGAAATGACAGGCCCAAGATACC 7422
 Oy 2685 ThrValCysValProLysAspTyrGlnLysAlaSerThrPheProValThrCysGlyGly 2704
 Db 7423 TCAGTGTATACAGAACTACTGATCTCTCAGCTTCAATTAACCTTAACCTTACTGTGGAGGT 7482
 Oy 2705 GlySerGlyIleValGlnSerThrAlaMetLeuValLeuGlnSerGluLysAlaAlaLeu 2724
 Db 7483 GGCAGCGCGCATGTGTACAAAACAAAGCTTATTATTGAAAAGTACACTATTAAGGCTTA 7542
 Oy 2725 GluArgGluLeuSerIleTyrLysLysTyrHisIleLeuSerArgThrMetSerSer 2744
 Db 7543 GAAAAAGAAATTTCTAAGTTAAAGCAGCAAAATGAAACAGCTA----- 7584
 Oy 2745 SerGluAspArgLysThrLysAlaLysSerAspAlaHisSerSerHisThrGlySer 2764
 Db 7585 -----ATAAAACAAAGAAATGAAATTTGTAAGCAATTAATCAGCATCTT 7626
 Oy 2765 SerHisArgGlySerProHisLysThrGluThrTyrArg-----HisGlyProVal 2781
 Db 7627 TCCAAATGAGGTCAAAACCTTGAAAGAAAGAACCCCTTAAAGAGAGGCTCACAAACAGTA 7686
 Oy 2782 ThrProGluArgSerGluMetProSerLeuHisLeuGlySerProLysLysSerGluSer 2801
 Db 7687 ACTGTGAG-----AATTCCTCAAG----- 7707
 Oy 2802 SerThrLysArgValValSerProAsnArgSerGluIleTyrSerGlnLeuValMetSer 2821
 Db 7708 -----TCT 7710
 Oy 2822 ProGlyLysThrGlyMetHisLysHisIleLeuSerProSerLysValGlyLeuHisLys 2841
 Db 7711 CCTAAAGTACTGGAAACA-----GCTTCTAA 7737
 Oy 2842 LysArgAlaLeuSerProAsnArgSerGluMetProThrGlnHisValIleSerProGly 2861
 Db 7738 AAGAAACAAATTACACC----- 7755
 Oy 2862 LysThrGlyLeuHisLysAsnLeuThrGluSerThrLysPheAsnLeuSerSerPro 2881
 Db 7756 -----TCTCA 7761
 Oy 2882 CysLysGlnGlnLysValGlnGlnLeuLeu-----AsnSerProLysGlyLysLeuPhe 2899
 Db 7762 TGCAGAGAAACGGAATTTACAGATCTGTGCCAAAGAAATCACCAAAATCTGTTTTTTT 7821
 Oy 2900 AspValLysSerLysSerMetProTyr---CysProSerGlnPhePheAsnSerLys 2918
 Db 7822 GATACCCATCAAGTCTTTTACCATCACTCATCTCAAGTTCCGCTATTGATTAACCTCAAGT 7881
 Oy 2919 LeuGlyAspPheSerGluLeuAsnThrAlaGluSerAsnAspLysSerGlnAlaGluAsn 2938
 Db 7882 TTAGGCTTTTTCAGAGAGGTGCAAAATGACAGAGACAGAGAGTGTGATTTCTCAGCAGAGT 7941
 Oy 2939 TrpTyrTyrGluAlaLysLysGluThrAlaProGlyCysLysThr 2953
 Db 7942 CTTGGCAGCGCTCTCAGGCAAGATGTGCTGAGTGCAAAACCT 7986

FILE REFERENCE: PA-0043 US
 ; CURRENT APPLICATION NUMBER: US/10/071,766
 ; CURRENT FILING DATE: 2002-02-07
 ; NUMBER OF SEQ ID NOS: 144
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 51
 ; LENGTH: 8493
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20020192678A1 441283.3
 US-10-071-766-51
 Alignment Scores:
 Pred. No.: 4,456-220 Length: 8493
 Score: 3613.50 Matches: 995
 Percent Similarity: 50.34% Conservative: 573
 Best Local Similarity: 31.94% Mismatches: 932
 Query Match: 24.47% Indels: 615
 DB: 13 Gaps: 86
 US-09-724-584-1 (1-2954) x US-10-071-766-51 (1-8493)
 Oy 1 MetSerGluGlyAspAlaValLysValCysValArgValArgProLeuIleGlnArgGlu 20
 Db 91 ATGGCGGAGAAAGAGCGCGTGTGCGTGTGCGAGTGGCGGCGCTGACAGCAGAGAA 150
 Oy 21 Gln-----GlyAspGlnAlaAsnLeuGlnThrProLysAlaGlyAsnAsnThrIleSerGln 38
 Db 151 GAATACCTTGAGAAAGAACTGCCCAAGTTTACTGAAAACCTGACAAATTAATGATTCATTATCA 210
 Oy 39 ValAspGlyThrLysSerPheAsnPheAspArgValPheAsnSerHisGlySerThrSer 58
 Db 211 GTTGATGGAAGTAATATCTTCAATTTGATGCTGTCTTCTGATGTAATGAACCTACCAA 270
 Oy 59 GlnIleTyrGlnGlnIleAlaValProIleIleArgSerAlaLeuGlnGlyTyrAsnGly 78
 Db 271 AATGTATGTAAGAAATATGACGACCAATCATCTTCATCTGCAATACAGCTTACAAATGCT 330
 Oy 79 ThrIlePheAlaTyrGlyGlnThrSerSerGlyLysThrTyrThrMetMetGlyThrPro 98
 Db 331 ACTATATTGCTGCTATGACAGACTGCTTCAGAAAACATATATACATGATGGTTCAGAA 390
 Oy 99 AsnSerLeuGlyIleIleProGlnAlaIleGlnGluValPheLysIleIleGlnGluIle 118
 Db 391 GATCATTTGGAGATTAATACCGAGGCAATTCATGACATTTTCCAAAATTAAGAGATT 450
 Oy 119 ProAsnArgGluPheLeuLeuArgValSerTyrMetGluIleTyrAsnGluThrValLys 138
 Db 451 CCTATAGGGAATTTCTTTACGTTATCTTAACATGAGAAATATACAAATGAAGCAATTAACA 510
 Oy 139 AspLeuLeuCysAspAspArgLysLysProLeuGluIleArgGluAspPheAsnArg 158
 Db 511 GATTACTCTGTGCACTCAAAAAATGAACCTTTAATTATTCAGAGATGTAATGAAGG 570
 Oy 159 AsnValTyrValAlaAspLeuThrGlnGluLeuValMetValProGlnHisValIleGln 178
 Db 571 AATGTATATGTTGCTGATCTCACAGAGAAAGTTGTATATGATCATCAGAAATGGCTTGAAA 630
 Oy 179 TrpIleLysLysGlyGlyLysAsnArgHisTyrGlyGluThrLysMetLeuAspHisSer 198
 Db 631 TGGATTACAAAGGAGAAAAGAGAGGCAATTAAGAAAACAAAAGAAATCAAGAAAGAC 690
 Oy 199 SerArgSerHisThrIlePheArgMetIleValGluSerArgAspArgAsnAspProThr 218
 Db 691 AGTGTCTCATACCACTTTAGATGATCTTTGGAAAAGCAGAGAAAGGAGTCAACTCTTCT 750
 Oy 219 AsnSerGluAsnCysAspGlyAlaValMetValSerHisLeuAsnLeuValAspLeuAla 238
 Db 751 -----AATGTGAAGATCTGTTAAGTATCCATTTGAATTTGGTTGATCTTGCA 801
 Oy 239 GlySerGluArgLysSerGlnThrGlyAlaGluGlyValArgLeuLysGlnGlyCysAsn 258

RESULT 2

; Sequence 51, Application US/10071766
 ; Publication No. US20020192678A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Huel-Mei Chen
 ; TITLE OF INVENTION: GENES EXPRESSED IN SENESENCE

Db	802	GGCAGTGAAGAGCTGCTCAAAAGCGCTGCAGGTGTGGCTCAAGGAAGCTTAAT	861
Qy	259	IIeAsnAArgSerLeuPheIleLeuGIgInValIleLeuLeuSerAspGIgInAla	278
Db	862	ATTAATCGAAGCTTATTTATTTGGGACAAGTATCAAGAACTTGATGACAAAGTT	921
Qy	279	GIgLYPheIleAsnTYrArgAspSerLYLeuThrArgIleLeuGlnAsnSerLeuGIY	298
Db	922	GGTGGTTTCATTAATTTATGAGATACCAATTAAACCAATTTCTTGAAATTTCTTGGGA	981
Qy	299	GIYAsnAlaLYleThrValIleIleCYthrIleThrProValSerPheAspGIuThrLeu	318
Db	982	GGAAATCCAAACACAGTATTATCTGCACAATTAATCCAGTACTTTTGAATGAACCTTT	104
Qy	319	SeTrnLeuGlnPheAlaSerThrAlaLYSHIleValArgAsnThrProHIleValenGlu	338
Db	1042	ACTGCTCTCCAGTTTGGCCAGTACTGCTTAATATATATAAGAAATCTCTTATGTATGAG	110
Qy	339	ValLeuAspAspGIuAlaLeuLeuLYsArgTYrArgLYsGIuIleLeuAspLeuLYs	358
Db	1102	GTAACAACGATGAAGAGCTCTCTCGAAAGATAGAAAGAAATATGATCTTAAAAA	116
Qy	359	GIuLeuGIuAsnLeuGIuSerSerGIuTYrTrnLYsAlGIuAlaMetAlaLYsGIuGIu	378
Db	1162	CAATTAGAG-----GAGGTTCTTTAGAGACGCGGGCTCAGGCAATGGAAGAAAGCCAA	121
Qy	379	HIstrnGIuLeuLeuAlaGIuIleLYsGIuLeuHIleLYsGIuArgGIuAspArgIleTrp	398
Db	1216	TTGGCCCCAATTTTGGAGAAAAAGATTTGCTTCAGAAAGTACAGATAGAAAAATTGAA	127
Qy	399	HIleuTrnAsnIleValAlaIleSerSerGIuSer---GlnGlnAspGlnArgVal	417
Db	1276	AACTTAACACGAGATGCTGTGACCTCTTCTCCCTCAGCTTGCAACAGGAATTAAGGCT	133
Qy	418	LYsAlaGLYsArgArgValThrTrpAlaP-roGIuLYsIleGlnAsnSerLeuHIleAlaSer	437
Db	1336	AAAAAGAAAAAGAGATTACTTGCTGCTGCCTTGCCAAATTAACAAATGAAGAACTCAAC	139
Qy	438	GIYAlaSerAspPheAspMetLeuSerArgLeuProGIYAsnPheSerLYsLYsAlaLYs	457
Db	1396	TATGCAGATCAATTAAT-----ATACCAACAATTAACAACAATAACACT	144
Qy	458	PheSerAspMetProSerPheProGIuIleAspAspSerValCYstrnGIuPheSerAsp	477
Db	1444	AAGCTTTCATTAATTTATTAGAGAAATTTGATGATCTGTCTGTACAGTCTGATGT	150
Qy	478	PheAspAspAlaLeuSerMetMetAspSerAsnGIYIleAspAlaGIuTrpAsnLeuAla	497
Db	1504	TTCACTAACACTCTTGATCACTTAAGT-----GAGATGAAGATGAATCCAGCA	155
Qy	498	SerLYsValIleThrIleArgGIuLYstrnTrnSerLeuHIleGlnSerMetIleAspPheGIuGln	517
Db	1552	ACAAATGCTACTTAATACAGAG-----	157
Qy	518	IleSerAspSerValGlnPheHIleAspSerSerLYsGIuAsnGlnLeuGlnTYrLeuPro	537
Db	1572	-----	157
Qy	538	LYsAspSerGIYAspMetAlaGLUCYsArgLYsAlaSerPheGIuLYsGIuIleThrSer	557
Db	1572	-----	157
Qy	558	LeuGlnGlnGlnLeuGlnSerLYsGIuGIuGIuLYsLYsGIuLeuValGlnSerPheGIu	577
Db	1572	-----	157
Qy	578	LeuLYsIleAlaGIuLeuGIuGlnGlnLeuSerValLYsAlaLYsAsnLeuGlnMetVal	597
Db	1573	-----AATTATGAAGCTGAG	158
Qy	598	ThrAsnSerArgGIuHIleSerIleAsnAlaGIuValGlnThrAspValGIuLYsGIuVal	617

[illegible]


```

4423 GATGACCTACAGAGCTGCAAGAGTCTTCAATCTGAAAGTACACAGCTC----- 4473
QY 1658 MetIleuglyserlyserleuglyserleuglnhiieglulysihisapthrglugln 1677
Db 4474 -----AAAGAAAACATTAAGAAATGAGTCTTAACCTGGAACCTGAAGAG 4521
QY 1678 Glnleu-----LeuAlaleuylvglnlmetglnvalvalthrglnlulys 1693
Db 4522 GAACTTAAGAGTTGCTGATTTGCTGGAAGAGAACTATTAATGATTAAGAG 4581
QY 1694 lvsleuglnleuglnthrhieglulysleuthralagluvalasphihisleuylsgluen 1713
Db 4582 GTGAATCTTTCAGAGAGAGAA-----ACGAAATATCAACCTTCAAAAGCAG 4629
QY 1714 lileglu---leuglyleuhsnphelysengluvalaglnlulysrthrlrgslugln 1732
Db 4630 TTAGAAGCAATCAATGATTAATTACAGAAACAAGATCAAGATTTATGAGAAAGAGAA 4689
QY 1733 Cysleuleuasngluasnlysgluluglnleuglnserglnhiisargleuincysgluile 1752
Db 4690 CAATTT-----AATTAATAACAATTAAGTGTGAGCTTCAGAAAAGTGAAAT--GAACGTG 4740
QY 1753 GluGluLeuMetlyserleuylserylsygluyserylaleuglnluthrleuylsgluser 1772
Db 4741 AAACAATTCAGAGAGATCGCAAAAGCCAGATTCAGCACTACAAAGTATA----- 4791
QY 1773 GluGlnlysevalileasnleu-----Asnglnlunmetglumec 1785
Db 4792 GAAATTAAGATGCTCGAGTTGACCAACAGACTTCAAGAAAGTCAAGAAATACAAAT 4851
QY 1786 ValMetleuGluMetGluGlnleuylsasnserglnargthrvallleaglunargap 1805
Db 4852 AGGATTTAAGCAAAAAGAGAAATGAAAAGATACAGAGAGCCCTTCAGATAAGAGAGAC 4911
QY 1806 GlnleuGlnAspAspserleuylserValGluMetserileuglnthrhieaspserleu 1825
Db 4912 CAACCTGAAAAGAAAACCTAAAGAAATTTGCTAAATAAGAAAGAACTCAAGAA----- 4965
QY 1826 Arglysalaglnlualaleuglnleuglnlulysasphlysalaglnluleuthrsergln 1845
Db 4966 AAAGATATCACTTCTTAAGATGACAGCTGCAATGACACTCAGAGAAAATGTGTGAA 5025
QY 1846 lleservalileuglnlulyslileserleu-----Leuglnasn----- 1858
Db 5026 ATAGAACACTTGAAAGCAATTTGAGACCAGAACTTAACCTGAAAACCTAGAAAGC 5085
QY 1859 -----GlnMetleuTyr---AsnValAlathrvalllysgluthrleu 1871
Db 5086 GAGAAATTAAGCTGACTCAGATCTACTACTGAAAACCTTGAAGAAATGAGATCTGTAA 5145
QY 1872 SerGluArgAspAspserleuasnleuglnserlysglnhisleupheserGluilegluthrleu 1891
Db 5146 AAAAGAAAGATGACTTAGAGGTGTGAGAGACTCTCAAAAGTACAGAGAACCGCTC 5205
QY 1892 SerleuSerleuylsglulys---GluPheAlaleuglnlualaglnlulysasphly--- 1909
Db 5206 AAGAAAACCTTAGAGAACTTAACCTAGAGACTTAGAAAACAGAGAGAGCTTAATAAT 5265
QY 1910 -----AlaAspAlaAlarglysrthrlleasphilethrglnlulyslileserAsn 1925
Db 5266 GTTCATGATCATCTGAAGAGACCAAGAAACTATTTGAT-----AAACTTAAGAGGG 5316
QY 1926 lilegluglnleuGlnleuglnlualathrasnleuylsgluthrleu---TyrGluArg 1944
Db 5317 ATTGTTTCAGAAAAAACAATATCAATATGCAAAAGAGACTTGAACACCTCAAT 5376
QY 1945 Gluserleu-----lileglnCyslysgluginleuAlaleuhsnthrglulhis 1960
Db 5377 GATGCTTAAAGCAACAGATCTGAATAATACAAAGAGAACTAAGATGCTCACAATGAT 5436
QY 1961 LeuArgGluThrleuylserylsasphleuAlaleuGlylyMetGlnleuglnlunargap 1980

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Db 5437 CTGAAAAGACAGACAGAAACTATGACAAACTCAGAGAGATTTGTTCTGAGAAACAGAT 5496
QY 1981 GluAlaAlaAsnlysevalilealaleuthrglulysmeeserleuGlnleuglnle 2000
Db 5497 AAACATCAAAATATGCMAAAAGATTTAGAAAATTCAMATGCTAAATTTACMAAAGAAAT 5556
QY 2001 AsnglnAsnValThrThrleuylsglulysgluluglnlulysgluthrpheryleugln 2020
Db 5557 CAAGAA-----CTTAAGCCAAATGAACATCAACTTAATACGTTAAAAAAAGAT 5604
QY 2021 ArgProserlysglnlserserserglnmetglululeuargluserleuylsrth 2040
Db 5605 GTCAATGAGACACAGAAAAAGCTGTGAAATGAGCAACTAAGAAAACAATTAAGAAC 5664
QY 2041 lvsasphleuGlnleuglnlualagluylsglulileserglnlualathrasnluilelys 2060
Db 5665 CAACCTTAACCTGATTAATA-----GAAATAGAG 5697
QY 2061 AsnleuthralalylliserleuGlnlulileuglnlhasnlaserileu 2080
Db 5698 AATTTA-----AATTTGCTCAAGAACTTCATGAACCTTGACAGAAATG 5742
QY 2081 AsngluAlaValSerGluArglulasnleuarghiserylsglnleuvalserglu 2100
Db 5743 AAATCTGTAATGAAGAAAGAGATATCTAAGAGAGTGAAGAGACACTCAAACTGAG 5802
QY 2101 LeuGlnleuSerleuThrleu-----lyserArgAspHisAlaPheAlagln 2117
Db 5803 AGAGACCAACTCAAGAAAGCCCTGCAGAAACCAAGCTAGAGATCTGAAATACAAACAG 5862
QY 2118 -----SerlyAsnGluLys-----AspGlnAlaVal 2126
Db 5863 GAACATAAAACCTCGTCATGCTATCAAAAGAACCAAAAGAACTGTTGATTAATCTTGA 5922
QY 2127 AsnlysalaleaserleuAlaglnlulileylsileuthrlysglnmetasphluphe 2146
Db 5923 GAAAAAATTTTCAGAAAGCAATTCAAATTTGACACATCAAAAGAGATTTAATTAATAA--- 5979
QY 2147 ArgaspherylsgluserleuGlnleuglnlulysasphihisleuSerGlnleucythr 2166
Db 5980 -----TCMAAAGATGAATTCAGAAAAGATCAAGAACTTCAG----- 6018
QY 2167 TyrlysrthrglnleuGlnMetleuylsglnlulysglunarglileasnAsnlyseuAla 2186
Db 6019 ---AAAAAGAACTTCAACTGCTTGA---GTAAAGAGATGCAATTAATGACT---CAT 6069
QY 2187 GlulysVallysgluvalasphluleu----- 2195
Db 6070 AAAAAAATTAATGAATGGAACAGTTGAAGAAAGCAATTTGAGCCAAACTATCTATGCAAG 6129
QY 2196 -----LeuglnhisleuSerleuylsgluginleuAspGlnleugln 2210
Db 6130 TGTGAGATGATTAACCTTCACTGACTTAAGAAACCTTCAAGAAAGCTTGAAGAAATTAAGA 6189
QY 2211 MetGluLeuArg---Asnglnlulysleuargasnryrgluleucyglulysmetasphile 2229
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QY 2230 MetGluylsglulileservalileuylrgleuMet 2241
Db 6247 AGGCAACATTCATATGCAACTTAAGGGAATGATAGCTAGAGACCGACAGAACCAACCA 6306
QY 2242 AsnglnlulysleuValleuylrgleuMet 2259
Db 6307 GTAAACCTGAAAAAGGTTACTTAAGTATGACAAACCACTTATGAAAGCTTGAGA 6366
QY 2260 SerArgAsnglnlulileglnluleuMetGluylsileservalvaltyrserglugln 2279
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QY 2280 HisThrleuLeuSerleuSerleuSerleuGlnleuglnlulysgluthrgluAlahiselyshis 2299
Db 6424 TATGAGTCTTGAATGAATGTGCTTGAATCTTGAAGAGAAAGAAATTTGAATTCACAGAA--- 6480

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QY 2300 CysMetLeuAsnIleLysGluSerLeuSerThrLeuSerArgSerPheGlySerLeu 2319
 Db 6480 ----- 6480
 QY 2320 GluThrGluHisValLysLeuAsnThrGlnLeuGlnThrLeuLeuAsnLysPheLysVal 2339
 Db 6481 -----ATCATGAGAAATCGAAGTAT 6501
 QY 2340 Val-----TyrArgThrAlaAlaValLysGluAspHisSerLeuIleLysAspTyrGlu 2357
 Db 6502 GTGCTAAGCATGTTACAAAATAAAGAGAACACATGATGATCATATAATTGAA 6561
 QY 2358 LysAspLeuAlaIleGluGlnLysArgHisAspGluLeuArgLeuGlnLeuGlnCysLeu 2377
 Db 6562 ATGGATTTTATTTGATGAAAGTGAAAGCAAAAGCAATTCCTAATTAATAACAGCACCTT 6621
 QY 2378 GluGlnHisGlyArgLysTrpSerAspSerAlaSerGluGluLeuLysPheCysGluIle 2397
 Db 6622 CAACCAAGAT-----TGTGATGTAACCATCCAGAGAAATTGAAGGATCTCAAAATTG 6669
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 Db 6670 AACCAAGATATGATGATCTA-----CATATTGAGGAATTCCTCAAGAT 6711
 QY 2418 PheSerGluValGlnValPheLeuAsnGlnValGlySerThrLeuGlnGluLeuGlu 2437
 Db 6712 TTCTCGAAGAGTCAG-----TTCCCTAGCATTAAGCATGAATTCACAAAGTCACTAAGT 6765
 QY 2438 HisLysLysGlyPheMetGlnTrpLeuGlnGluPheGlyAspLeuHisValAspAlaLys 2457
 Db 6766 AATGAGAAAGAAATGACACAGTTTGGAAAGTGGTTAAATCTGTTTGTATAGAA 6825
 QY 2458 LysLeuSerGluGlyMetGlnGlnGlnLeuAsnArgArgIleAlaSerThrIleGlnLeuLeu 2477
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 QY 2478 ThrLysArgLeuLysAlaValAlaGlnSerLysIle-----GlnArgGluIleThr 2494
 Db 6886 AATTAACAGATATATTTGCCATTAATGAATCAACAGACTTTGAGAAAGAAAGTGTCTAC 6945
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 Db 6946 ATA-----TCCAAAGAGTGGGAAACAGGACCTGAATATCTGAAAGAGAAATAAATACTA 7002
 QY 2515 MetArgArgMetGluHisIleGlyProSerAlaSerValMetGluGlnLysAlaArg 2534
 Db 7003 TTTAAATACTAACCAACATTGAAGACTTCTGTGGCATCTGTGCCAGGTTAAT----- 7056
 QY 2535 LeuLeuGlyIleLeuLysThrValGlnAspGlu-----SerLysLys 2548
 Db 7057 -----CTTACCAACAAGCAATTAAGATCTCTCATGTTACCAAGAGCT 7101
 QY 2549 LeuGln-----SerArgIleLysMetLeuGlnAsnGluLeuAsnLeuValLysAsp 2565
 Db 7102 ACACAGTTAAACACAGAGAAATTCGAGAGCTGGAAATTCCTCATGATCAACTAAAGAA 7161
 QY 2566 AspAlaMetHisLysGlyGlyLysValAlaIleLeuGlnAspLeu-----LeuSerArg 2584
 Db 7162 AGTGTATGTCATTAAGAAAGCAAGATTTAAAGATGACAGAAAGAACTTGAGGTGACTAAT 7221
 QY 2585 AsnAlaGluAlaGluLeuAsnAlaMetGlnValLysLeuThrLysLysGlnAspAsnLeu 2604
 Db 7222 GACATTAATAGCAAACTT-----CAAGCCAAAGTTCATGAATTCAAATTAATGCTT 7272
 QY 2605 GlnAlaAlaMetLysGluIleGluAsnLeuGlnLysMetValAlaLysGlyAlaValPro 2624
 Db 7273 GAAAAACAAAAAGACACATTCAAGTACTGAGCAAAAGTTCCTTGGAGCTAAGCA 7332
 QY 2625 TyrLysGluGlnLysAspAsnLeuLysThrLysValValLysIleGluMetGluLysIle 2644
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QY 2645 LysTyrSerLysAlaThrAspGlnGluIleAlaTyrLeuLysSerCysLeuGluAspLys 2664
 Db 7393 AAAAAATGCCAAAGAAATTTGAAAAGAAATCACTGCTACAAAAGCCACTGATGATATCA 7452
 QY 2665 GluGluGlyLeuArgArgLeuLysGluGluLeuAlaGlnAlaGlnAlaAspAsnAspThr 2684
 Db 7453 AAGGAAGTTATAGGCTATTGAGAGAAAATCTCAAGAGAGTCAACAGCCCAATATCC 7512
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 Db 7513 TCAGTGAATATCGAACATATGATCTGATCTCAAGCTTCAAAATTAACCTTAACTTGTGAGCT 7572
 QY 2705 GlySerGlyIleValGlnSerThrAlaMetLeuValLeuGlnSerGluLysAlaIleLeu 2724
 Db 7573 GGCACGGCATTTGTCAAAACACAAAGCTTATTTGAAAAGTGAACATATAAGGCTA 7632
 QY 2725 GluArgGluLeuSerHisTyrLysLysLysTyrHisIleLeuSerArgThrMetSerSer 2744
 Db 7633 GAAAAAGAAATTTCTAAGTTAAAGCAAAATGAAGACAGCTA----- 7674
 QY 2745 SerGluAspArgLysLysThrLysAlaLysSerAspAlaHisSerSerHisThrGlySer 2764
 Db 7675 -----ATAAAACAAAGAAATGATTTGTAAGCAATATCAGATCTT 7716
 QY 2765 SerHisArgGlySerProHisLysThrGluThrTyrArg-----HisGlyProVal 2781
 Db 7717 TCCAAATGAGGTCAAAATCTTGAGAGAGAAAGAACCCCTTAAAGAGAGGCTCACAAACAAAGTA 7776
 QY 2782 ThrProGluArgSerGluMetProSerLeuHisIleGluLysSerProLysLysSerGluSer 2801
 Db 7777 ACTTGTGAG-----AATTCTCCAAAG----- 7797
 QY 2802 SerThrLysArgValLysSerProAsnArgSerGluIleTyrSerGlnLeuValMetSer 2821
 Db 7798 -----TCT 7800
 QY 2822 ProGlyLysThrGlyMetHisLysHisIleLeuSerProSerLysValGlyLeuHisLys 2841
 Db 7801 CCTAAAGTACTGGAACA-----GCTTCTTAAA 7827
 QY 2842 LysArgAlaLeuSerProAsnArgSerGluMetProThrGlnHisValIleSerProGly 2861
 Db 7828 AAGAAACAAATTAACACC----- 7845
 QY 2862 LysThrGlyLeuHisLysAsnLeuThrGluSerThrLeuPheAsnLeuSerSerPro 2881
 Db 7846 -----TCTCAA 7851
 QY 2882 CysLysGlnGlnLysValGlnGluAsnLeu-----AsnSerProLysGlyLysLeuPhe 2899
 Db 7852 TGCAAGGAAACGGAATTTACAAAGATCTGTGCAAAAGAAATCACCAAAATCTTGTTTT 7911
 QY 2900 AspValLysSerLysSerMetProTyr-----CysProSerGlnPhePheAspAsnSerLys 2918
 Db 7912 GATAGCCGATTAAGTCTTTACATCACCTCATCTCACTGCTATTTGATTAATCTCAAGT 7971
 QY 2919 LeuGlyAspPheSerGluLeuAsnThrAlaGluSerAsnAspLysSerGlnAlaGluAsn 2938
 Db 7972 TTAGGCTTTGTCCAGAGGTCGCAAAATGACAGAGCAAGAGTGTGATCTTCACCCAGT 8031
 QY 2939 TrpTrpTyrGluAlaLysLysGluThrAlaProGluLysLysThr 2953
 Db 8032 CTTTGGACCGCTCTCTCAGGCAAGAGATGTGCTGAGTGCAAAATCT 8076

RESULT 3

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US-09-724-584-1 (1-2954) X US-10-037-270-130 (1-8503)

Db	511	GATTTACTCTGTGGACACTCAAAAATGAACCTTAAATTATTCGAGAAAGATGCTCAATAGC	570
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Db	571	AATGTGTATGTGTGGATGATCTCACAAGAAAGAGTGTATATACATCGAAATAGGCTTTGA	630
Qy	179	TrpIleValblybGlyGluIleValAsnArgHisIstYrGlyGluThrIleValbMetAsnAspHisSer	198
Db	631	TGGATTACAAAGGGGAGAAAGAGCGCGCATTTATGAGAAACAAATAATAACTCAAGAACG	690
Qy	199	SerArgSerHisIstThrIlePheArgMetIleValGluSerArgAspArgAsnAspProThr	218
Db	631	AGTCGTTCTCATACCATCTTTAGATGATGATTTTGGAAAGCACAAGACAGAAAGGCGTAACCTTCT	750
Qy	219	AsnSerGluAsnCyAspGlyAlaValMetValSerHisIleuAsnLeuValAspLeuAla	238
Db	751	-----AATTGGAAGGATCTGTTAAAGTATCCCATTTGAAATTTGTTGATCTTGCA	801
Qy	239	GlySerGluArgAlaSerGlnThrGlyAlaIleGluGlyValAlaGlyLeuIleValGlyCysLeuAsn	258
Db	802	GGCGATGAAAGCGCTGCTCAAAACGGCCCTCAGATGTGCGCGCTCAAGAAAGCGCTGAAT	861
Qy	259	IleAsnArgSerLeuPheIleLeuGlyGlnValIleValblybLeuSerAspGlyGlnAla	278
Db	862	ATAAATCGACGCTTATTTATTTTGGACAAGATGATCAAGAAACTTAGTAGTGACAACTT	921
Qy	279	GlyGlyPheIleAsnYrArgAspSerIleValbThrArgIleLeuGluAsnSerLeuGly	298
Db	922	GGTGGTTTCATTAATATTATCGATGACAAAGTTATTCACAGAAATTCCTTCAGAAATTCCTTGGA	981
Qy	299	GlyAsnAlaValbThrValIleIleIleCysThrIleThrProValSerPheAspGluThrLeu	318
Db	982	GGAATATCCAAAGACACGATATTATGTGCAAAATTTCTCCAGATATCTTTTGAATGAACCTTT	1041
Qy	319	SerThrLeuGluHisPheAlaSerThrAlaHisHisValArgAsnThrProHisValAsnGlu	338
Db	1042	ACTGCTCTCCAGTTTGGCCAGTACTGCTAAATATATGAAGAAATACTCCTTATGTTAAATGAG	1101
Qy	339	ValLeuAspArgGluAlaLeuLeuIleValbIstYrArgIleValbGluIleLeuAspLeuIleValb	358
Db	1102	GTATCAACTGATGAAGCTCTCTGTAAGAAAGTATGAAGAAAGAAATATATATGATCTTAAAAA	1161
Qy	359	GlnLeuGluAsnLeuGluSerSerSerGluThrIleValbAlaGlnAlaMetAlaIleValbGluGlu	378
Db	1162	CAATTAGAG-----GAGGTTCTCTTTAGAGACGCGGCGCTCAGCAATGGAATAAGAACCCAA	1215
Qy	379	HisThrGlnLeuLeuAlaGluIleValbGluLeuHisIleValbGluAlaGluAlaAspArgIleThr	398
Db	1216	TTGGCCCAACTTTTGGAAAGAAAGATTTGCTTCAGAAAGTACAGAAATGCAAAATTTGAA	1275
Qy	399	HisLeuThrAsnIleValAlaIleSerSerGlnGluSer---GlnGluAspGluArgVal	417
Db	1276	AACTTACACGGAGATGCTGGTGAACCTTTCTTCCCTCACGTGGCAACAGAAATTTAAAGCT	1335
Qy	418	LysArgIleValbArgValbThrIleAlaArgProGlyIleValbIleGluAsnSerLeuHisIleSer	437
Db	1336	AAAAGAAAACGAAGAGTACTTGGTGCCTTGGCAAAATTTAAACAATATGAAGAACTCAAC	1395
Qy	438	GlyAlaIleSerArgPheAspMetLeuSerArgLeuProGluAsnProHisSerIleValbAlaValb	457
Db	1396	TATCGACATCAATTAAT-----ATACCAACAATATATACAAACAAACAT	1443
Qy	458	PheSerAspMetProSerPheProGluIleAspArgSerValCysThrGluPheSerArg	477
Db	1444	AAGCTTTCTAATAATTTATATCGAGAAATTTGATATCTGCTGTTCCAGAGTCTGATGTT	1503
Qy	478	PheAspArgAlaLeuSerMetMetAspSerAsnGlyIleAspAlaGluThrPheAsnLeuAla	497
Db	1504	TTTCAGTAAACACTTGTATACATTAAGT-----GAGATAGAAATGGAATCCAGCA	1551
Qy	498	SerIleValbThrHisArgGluIleValbThrSerLeuHisIleGlnSerMetIleAspPheGlyGln	517
Db	1552	ACAAAGCTACTAAATACGAGAG-----	1572

QY 518 ILeSerAspSerValGlnPheHIsAspSerSerIysGlnsGlnLeuGlnTyrLeuPro 537
 Db 1572 ----- 1572
 QY 538 LysAspSerGlyAspMetAlaGluCysArgLysAlaSerPheGlnIysGlnIleThrSer 557
 Db 1572 ----- 1572
 QY 558 LeuGlnGlnLeuGlnSerIysGlnGlnIulLysLysGlnLeuValGlnSerPheGln 577
 Db 1572 ----- 1572
 QY 578 LeuLysIleAlaGlnLeuGlnGlnLeuSerValLysAlaLysAsnLeuGlnMetVal 597
 Db 1573 -----AATATAGAAAGCTGAG 1587
 QY 598 ThrAsnSerArgGlnHisSerIleAsnAlaGlnValGlnThrAspValGlnIysGlnVal 617
 Db 1588 TTGAAGCTCA----- 1596
 QY 618 ValArgLysGlnMetSerValLeuGlnIysAspSerGlyTyrAsnAlaSerAsnSerAspLeu 637
 Db 1596 ----- 1596
 QY 638 GlnAspSerSerValAspGlyLysArgLeuSerSerSerHisAspGlnCysIleGlnHis 657
 Db 1596 ----- 1596
 QY 658 ArgLysMetLeuGlnGlnIysIleValAspLeuGlnGlnPheIleGlnAsnLeuAsnLys 677
 Db 1596 ----- 1596
 QY 678 LysSerGlnAsnAspLysGlnIysSerSerGlnAspPheMetGlnSerIleGlnLeu 697
 Db 1596 ----- 1596
 QY 698 CysGlnAlaIleMetAlaGlnIysAlaAsnAlaLeuGlnGlnLeuAlaLeuMetArgAsp 717
 Db 1597 -----CTTCGTGCT 1605
 QY 718 AsnPheAspAsnIleIleLeuGlnAsnGlnIulThrLeuLysArgGlnIleAlaAspLeuGln 737
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 Db 1726 AAAGATCAAGAGATGCACTAAATTCATGAATTTGCAACTTAAAGAAATTTAGTTAGCAT 1785
 QY 778 AlaGlnMetTyrAsnGlnAsnLeuGlnIulThrAspLeuGlnIulThrLysThrLysLeuLys 797
 Db 1786 CGAGAAGTATATATCAAGATCTTGAGATGAACTCAAGTCAAAAGTAGAGCTGCTTACA 1845
 QY 798 GlnGlnGlnIleGlnLeuAlaGlnLeuArgLysArgAlaAspAsnLeuGlnIysLysVal 817
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 QY 818 ArgAsnPheAspLeuSerValSerMetGlyAspSerGlnLysLeuGlnIulThrPhe 837
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 QY 838 GlnLeuLysGlnSerLeuSerAspAlaGlnAlaValIThrArgAspAlaGlnLysGlnCys 857
 Db 1954 CAATAGAGACAGACTCTGTTGATGCTGAACTGTAGCCCTTGATGAGCCCAAGAGAAATCA 2013
 QY 858 SerPheLeuArgSerGlnAsnLeuGlnIulThrLysGlnIulThrMetGlnAspThrSerAsnTyr 877
 Db 2014 GCCTTTCTTAGAAGTGAATCTGAGATTGAAAGAAATGAAGAACTTGCAACTACA 2073

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 Db 2074 TACAAGCAAAATGCAAAATGATATTCAGTTATATCAAGCAATTCGAGGCAAAA----- 2127
 QY 898 AsnTyrLysLysMetGlnAlaAspLeuGlnIulThrGlnLeuGlnSerAlaPheAsnGlnIle 917
 Db 2128 -----AAGAAAATGCAAGATGATCTGAGAAAGAAATTAACAATCTGCTTTTAATAGATA 2181
 QY 918 AsnTyrLeuAsnGlnLysLeuAlaGlnLysValProArgAspLeuLeuSerArgValGln 937
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 QY 938 LeuGlnLysLysValSerGlnPheSerIysGlnLeuGlnIulThrAlaLeuGlnIulLysAsn 957
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 QY 958 AlaLeuGlnAsnGlnValThrCysLeuSerGlnIulThrLysPheLeuProAsnGlnValGln 977
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 QY 978 CysLeuLysAsnGlnIleSerLysAlaSerGlnIulThrMetLeuLeuLysGlnGlnIul 997
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 QY 998 GlnHisSerAlaSerIleIleSerLysGlnIulThrIleMetGlnGlnSerGlnGln 1017
 Db 2422 GATTAATTTGTTCTGAGATGATCTCATAGAGAGTAGTAGTTCAAGGTTTACTTGAAAGAA 2481
 QY 1018 ILeuGlnLeuThrAspGlnValThrIleThrGlnSerLysValGlnGlnIulThrGlnGln 1037
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 QY 1038 GlnTyrLeuGlnMetLysLysMetHisAspAspLeuPheGlnIulThrTyr----- 1053
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 QY 1054 -----IleArgAsnLysSerGlnAlaGlnAspLeuLeuArgGlnMetGlnAsnLeu 1070
 Db 2602 GAGGAGAAATGAGAGAAATGAATCAGAAATAGTTATCTCTTAAAGAAAGCCCAAAATTT 2661
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 QY 1111 ThrIlePheProIleThrProLeuSerAspSerLeuProSerLysLeuValGlnGln 1130
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 QY 1131 AsnSerGlnAspProIleGlnIleAsnAspTyrHisAsnLeuIleAlaLeuAlaThrGln 1150
 Db 2836 AAATGCAAGCAAACTTTAGAA-----GAGCTAAAACTTTAACTCAAGAAAAAGATGAT 2889
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 Db 2890 CTTAAACAACTCCAAAGAAAGCTTGCAAAATTGACAGGAGCAACAACCAAAAGTATATCAC 2949
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 Db 2950 GATTCGTAAACATGATATATGATATCTCAAGAAACAAATTTAGAAAGCTCTTGAGTCTCG 3009
 QY 1183 SerIleGlnLysSerAspLeuGlnLysProLysGlnAspLeuGlnGlnGlnIulThrValLys 1202
 Db 3010 AAACAACATCAAGAAACAAATTAATATACCTAAATTCGAAATTTCTGAG--GAAAGTTCC 3066
 QY 1203 LeuLeuLeuGlnMetGlnLeuLeuLysGlyHisLeuThrAsp-----SerGln 1218
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 QY 1219 LeuSerIleGlnLysLeuGlnLeuGlnAsnLeuGlnValIThrGlnLysLeuGlnIulThrLeu 1238

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Db      3127 GTTGCATGATATAAAACAG-----GATTGGAA--GCTAAAAATACCAAAACACTA 3177
Qy      1239 GInGluGluMetLysAsn1LeThr1Le----- 1247
Db      3178 ACTGCAGATGTTAAGATATGAGATTAATTGACAAACAAGAGATATTTCTTTAATA 3237
Qy      1248 ---GUAAGAenGluLeuGlnThrAsnPhenGluAspLeuValAGluHnAspSerLeu 1266
Db      3238 CAGGAGAAATGAAATCCACAATAATGTTAGAGAGTGTATAGCAGAAAGAACAAATGG 3297
Qy      1267 LysGlnAspLeuSerGluAsn1LeGluGlnSer1LeGluThrGlnAspGluLeuValA 1286
Db      3298 AAGACTGACCTTAAGAGAAATATTTGAAATGACCATTTGAAACACAGAAATTAAGACT 3357
Qy      1287 AlAGInGluGluLeuArgGluGlnLysGlnLeuValAspSerPheArgGlnLeuLeu 1306
Db      3358 CTTGGGATGAACTTAATAAACACACAGAGATAGTTGCACAAGAAAGAACCATGCCATA 3417
Qy      1307 AspCysSerValGly1LeSerSerProAsnH1AspAlaValAlaAsnGlnLysVal 1326
Db      3418 AAG---AAAGAGAGAGCTTTCTAGAGACTGTGACAGACTGCAGAAAGTTAAGAAAA 3474
Qy      1337 SerLeuGluGluValAsnSerLeuGlnSerGluMet-----LeuArgGly 1341
Db      3475 CTAAAGGAAAGAGCCAGCACTCCAGAAAAACAGCAACAACCTTTAATATACAGAA 3534
Qy      1342 GluArgAspGluLeuGlnThrSerCysValAlaLeuValSerGluLeuGluLeuArg 1361
Db      3535 GAGATGAGTGAATCAGAAAAAG-----ATTAATGAATAGAGAAATTAAG 3582
Qy      1362 AlaHnValLysSer-----ValGluGlyGluAsnLeuGluLeu 1374
Db      3583 AATGAATTAAGAACAAAGAAATTGACATTGAAACATATGAAACAGAGGCTTAGTGG 3642
Qy      1375 ThrLysLysLeuAsnGlyLeuGluGluLeuGluLysSerGluGlnSerGluVal 1394
Db      3643 GCTCGAAATCTTAAGAAAAATTTATGAGAGAGTGAATCTATTAACCAAGAAAGAAAGTT 3702
Qy      1395 LeuLysSerMetLeuGluAsnLeuLysGluAspAsnLysLeuLysGluGlnAlaGlu 1414
Db      3703 CTAAAGGAATTAACAGAGCTATTGAAACAGAGAGACCTTAAGAGATAT----- 3756
Qy      1415 GluTyrSerSerLysGluAsnGlnPheSerLeuGluGluValPheSerGlySerGlnLys 1434
Db      3757 -----ATMAAGAAATTAAGAGCTTAACAGCCTTAACA 3786
Qy      1435 LeuValAspGluLeuGluValLeuLysAlaGlnLeuValAlaGluGluArgLeuGlu 1454
Db      3787 ACCAAAGAAAGACTAAATATTCCTCATATTCACTTAAGAAACACCAAGAAATTAATGAT 3846
Qy      1455 IleLysAspArgAspTyrPheGlu---LeuValGlnThrAlaAsnThrAsnLeuValGlu 1473
Db      3847 GAACTAAGAAGAGCGTATCTGAGAAAGACAGCTCAATTAATAATACAGACTTAAGA 3906
Qy      1474 GlyLysLeuGluThrProLeuGlnAlaAsp-----HisGluGluAsp----- 1487
Db      3907 ---AAATCCCATACCAATTAACMAAGAGATCCAGTGCCTTCATGAGAGAACAGAGTTA 3963
Qy      1488 -----Ser1LeAspArgArgSerGluGluMet---Glu1LeLysValLeu 1501
Db      3964 CTGCCTAATGTGAAAAAGTCTGAGACTCAGGAAACATGAATGAATGAGAGTTATTA 4023
Qy      1502 GlyLysLys---LeuGluArgAsnGlnTyrLeuLeuGluArgLeuGlnGluLysLeu 1520
Db      4024 ACAGAAAGAGTCCACAACAGAGCTCAACAACACTGGCAAGAAATGAATGAAGAGCTC 4083
Qy      1521 GluLeuSerAsnLysLeuGluLysGluGlnLysGluMetGluThrSerValLeuLysLys 1540
Db      4084 AGGTGTAATGAAAAATTTCAAGAAAGTCAAGAGAGATTAATAATCTCTTAACCAAGAAAGA 4143
Qy      1541 AspAspLeuGlnGlnLysLeuGlnSerLeuLeuSerGluAsn1Le1LeuLysGluAsn 1560

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Db      4144 GACAACCTTAAAAAGATAAAAAGAGCCCTTGAAGTTAAATACAGACCACTGAAAGACAT 4203
Qy      1561 IleAspThrThrLeuLysHn1HisSerAspThrGlnAlaGlnLeuGlnLysThrGlnGln 1580
Db      4204 ATTAGAGAAACTTGT-----GCTAAATATCAGAGACTCAAAAGC 4242
Qy      1581 GluLeuValAlaLysLeuValAlaLeuAlaLysAspAspValPro1LeThrGln 1600
Db      4243 AAACAAGAAACAGCTCTTAATATGAAAGAAAAAGCAATGAATACCAAAATCTCGACT 4302
Qy      1601 GlyLysGlu-----ThrSer1LeAspCysValHn1ProLeuGluGluLys1Leu 1617
Db      4303 GAGATGAGAGCAATTAACCAACCAAGATTCAGACATACTAAGATGAATGAATGAGCTC 4362
Qy      1618 LeuLeuThrGluGluLeuHn1GlnLysThrAsnGlnGlnGluGlnLysLeuLysVal 1637
Db      4363 GGATGTCCAAAGACTTCAAGAAAGTATGATGAATGAATCTGTAGTGAAGAGAA 4422
Qy      1638 AsnGluLeuGluGlnAlaGlnValGluLeuLysCysGluValGlnHn1LeuMetLysSer 1657
Db      4423 GATGACCTACAGAGCTCCAAAGAGCTTCAATCTGAAATGAGCACTC----- 4473
Qy      1658 Met1LeuSerLysSerSerLeuGluSerLeuGlnHn1GluLysValAspThrGluGln 1677
Db      4474 -----AAAGAAACATAAAGAAATTTAGCTTAACACCTGAAACCTGAAAGC 4521
Qy      1678 GlnLeu-----LeuAlaLeuLysGlnGlnMetGlnValAlaThrGlnLysLys 1693
Db      4522 GAACCTTAAGTGTCTCATTTGTGCTCGAAAGAAACAGAGAACTTAATGAGTTAAGA 4581
Qy      1694 LysGluLeuGlnGlnThrHn1GlnHn1LeuThrAlaGlnValAspHn1LeuLysGluAsn 1713
Db      4582 GTGAATCTTTCAAGAGAGAA-----ACTGAATATTAACCACTTAACAAAGCAG 4629
Qy      1714 IleGlu---LeuGlyLeuAsnPhenLysAsnGluAlaGlnGlnLysThrLysGluGln 1732
Db      4630 TTAGAGAGCAATCAATGATTAATTAACAGAAACAAGATCCAAAGATTTATGAGAAAGAGAA 4689
Qy      1733 CysLeuLeuAsnGluAsnLysGluLeuGlnGlnSerGlnHn1ValGluGlnCysGluLeu 1752
Db      4690 CAACCTT-----AATATTAACCAATTAAGTAGCGTTCCGAGAAAGTCAAT---GMACTG 4740
Qy      1753 GluGluLeuMetLysSerLeuLysAspLysArgGlnSerAlaLeuGlnThrLeuLysGluSer 1772
Db      4741 AAACATTTCAAGAGACATCGCAAGAGCCAAAGATTCAGACATTAACAAAGTATA----- 4791
Qy      1773 GluGlnLysVal1LeAsnLeu-----AsnGlnGluMetGluMet 1785
Db      4792 GAAAGTAAAGTCTCGAGCTTGAACCAAGACTTCAAGAAATCAAGAAATTAACAATT 4851
Qy      1786 ValMetLeuGluMetGluGluLysLeuLysAsnSerGlnArgThrVal1Le1LeGluArgAsp 1805
Db      4852 ATGATTAAAGAAAAAGAGAAATGAAAGATACAGAGGCCCTTCAGATGAGAGAGAC 4911
Qy      1806 GlnLeuGlnAspAspLeuArgGluSerValGluMetSer1LeGluThrGlnAspAspLeu 1825
Db      4912 CAACGAAAGAAACACTTAAGAAATTTAGCTTAATAATGAAGAAATTCGAAAGAA----- 4965
Qy      1826 ArgLysAlaGlnGlnAlaLeuGlnGlnGlnLysAspLysValGlnGluLeuThrSerGln 1845
Db      4966 AAAGAAATTCAGTTTCTTAATGATGACAGCTGCAATGAGACTCAGAGAAAAATGTGTAA 5025
Qy      1846 IleSerValLeuGlnGluLys1LeSerLeu-----LeuGluAsn----- 1858
Db      5026 ATAGAAACACTTGAAGAGCAATTTGAGACCCAGAAAGTTAAACCTGGAAGAAATAGAAAGC 5085
Qy      1859 -----GlnMetLeuTyr---AsnValAlaThrValLysGluThrLeu 1871
Db      5086 GAGAAATTAAGCTTGACTCAATATCTATATAAAACCTTGAAAGAAATGAGATCTGTAAACA 5145
Qy      1872 SerGluArgAspAspLeuAsnGlnSerLysGlnHn1LysLeuPheSerGlu1LeGluThrLeu 1891
Db      5146 AAAGAAAGATGACCTTAGAGAGTGTGAGAGAGACTCAAAAGTAAAGAGAGACAGCTC 5205

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QY	1892	SerLeuSerLeuLysGluLys---	GluPheAlaLeuGluGlnAlaGluLysAspLys---	19079
Db	5206	AAAGAAAACCTTAGAAACCTTA	CTAAGACACCTTAGAAAAACAAGAGAGCTTAAATAAT	52655
QY	1910	-----Ala	AspAlaAlaArgLysThrIleAspIleThrGluLysIleSerAsn	19255
Db	5266	GTTTCATCATCTGTGAAGAGAC	CAAGAACTATTGAT-----AAACTAAGAGCG	53166
QY	1926	IleGluGluGlnLeuLeuGlnAla	ThrAsnLeuLysGluThrLeu---TyrGluArg	19444
Db	5317	ATTGTTTCAGAGAAAA	CAAAATGAAATATCAAAATATGCAAAAGGACTTGAAACATCAAAAT	53767
QY	1945	GluSerLeu-----	IleGlnCysLysGluGlnLeuAlaLeuAsnThrGluHis	19606
Db	5377	GATGCCTTAAAGACACAGAT	GTGAAATACAGAGGAACTTAGAATTGCTCATCATGAT	54366
QY	1961	LeuArgGluThrLeuLysSerLys	AspLeuAlaLeuGlyLysMetGluGlnGluArgAsp	19808
Db	5437	CTGAAGAAGACACAGAAAC	TATTCACAAACTCAAGAGAAATGTTTTCAGAAAGACAGAT	54966
QY	1981	GluAlaAlaAsnLysValIle	AlaLeuThrGluLysMetSerSerLeuGluGlnIle	20000
Db	5497	AAACTATCAAAATATGCAAA	AGATTATAGAAAATTCAAAATGCTAAATTACAGAAAAAGTT	55566
QY	2001	AsnGluAsnValThrThrLeu	LysGluGlyGluGlyLysGluThrPheTyrLeuGln	20200
Db	5557	CAAGAA-----	CTTAGGCAAAATGAAACATCAACTATTATAGCTTAAAAAAGAT	56046
QY	2021	ArgProSerLysGlnGlnSer	SerSerGlnMetGluLeuArgGluSerLeuLysThr	20400
Db	5605	GTCAAATGAGACACAGAAAA	AGCTGCTGTAATGAGCAACTTAAGAAACAAATTAAGAC	56646
QY	2041	LysAspLeuGlnLeuGluAla	GluLysGluLysSerGluAlaThrAsnGluLys	20600
Db	5665	CAAACTTAACCTGAGTAA	ATT-----GAAATAGAG	56976
QY	2061	AsnLeuThrAlaLysLys	SerSerLeuGluGluGluLysLeuGlnAsnAlaSerLysLeu	20800
Db	5698	AAATTAA-----	AAATTGGCTCAAGAACTTCATGAAGAACTTGAAGAAATG	57426
QY	2081	AsnGluAlaValSerGlu	LysLysLeuArgHisSerLysGlnLeuValSerGlu	21000
Db	5743	AAATGCTAAATGAAGAA	AGAGATATATTAAAGAGAGTACAGACACTAACTGAAG	58026
QY	2101	LeuGluGlnLeuSerLeuThr	-----LysSerArgAspHisAlaPheAlaGln	21176
Db	5803	AGAGACCACTCAAGAAAG	CGCTGCAGAAACCAAAAGCTTAGAGATCTGAATATCAACAG	58626
QY	2118	-----	SerLysArgGluLys-----AspGluAlaVal	21266
Db	5863	GAACATAAACTGCTCGAT	CTCTCAAAACAAACAAAGAACTGTTGATAAACCTTAGA	59226
QY	2127	AsnLysIleAlaSerLeu	AlaGluLysLysIleLysIleLeuThrLysGluMetAspGluPhe	21466
Db	5923	CAAAAAATTTCAAGAAAG	ACAATTCAAATTTCAAGCAATTCAAAGATTTAGATAA--	59796
QY	2147	ArgAspSerLysGluSerLeu	GlnGluGlnSerSerHisLeuSerGluGluLeuCysThr	21666
Db	5980	-----TC	AAAGATGAATTACAAAAAGATCCAGAAACCTTCG-----	60186
QY	2167	TyrLysThrGluLeuGln	MetLeuLysGlnGlnLysGluAspIleAsnAsnLysLeuAla	21866
Db	6019	-----AAAAAGAA	CTTCAACTGCTTAGA---CTGAAGAGAGATGTCATATAGAGT---CAT	60696
QY	2187	GluLysValLysGluVal	AspGluLeu-----	21956
Db	6070	AAAAAAATTAATGAAT	GAACAGATGGAAGAAACAAATTGAGCCAAACTATCATGCAAG	61296
QY	2196	-----	LeuGlnHisLeuSerSerLeuLysGluGlnLeuAspGlnIleGln	22106
Db	6130	TGTGAGATGGAATAC	CTTCCAGTTGATACAGAACTTCATGAAGAACTTGAAGAAATTAAG	61896

QY	2211	MetGluLeuArg- - - AsnGluLysLeuArgAsnTyrgluLeuCysGluLysMetAspIle	222
Db	6190	ATTGTAGCTAAAGAAAGAGATGACTTAAGGAGATTAAGAAATCTCTCAAAATGGAA- - -	6244
QY	2230	MetGluLysGluIleSerValLeuArgLeuMet	2244
Db	6247	AGGGACCAATTCATGACCACTTAAGGAAATGATAGCTAGAGACCGACAGAACCA	6300
QY	2242	AsnGluProGlnGlnGlu- - - - GluSparValAlaGluArgMetAspIleLeuGlu	2255
Db	6307	GTAACACCTGAAAAAGGTTACTTAAGATGAGCAACAGCAGCTTATGGAAAGCCTGTGGA	6366
QY	2260	SerArgAsnGlnGluIleGlnGluLeuMetGluLysIleSerAlaValIleSerGluGln	2275
Db	6367	GAAAAGTGCTCAGATATAAAGAGCTTTTGAAGAGATACTCAGAGATG- - - GATGATCAT	6422
QY	2280	HisThrLeuLeuSerSerLeuSerSerGluLeuGlnLysGluThrGluAlaHisLysHis	2299
Db	6424	TATGAGTGCTGTAATGATTTGCTCTTACTTGAGAAAGGAATTTGAATTCACACAGA- - -	6488
QY	2300	CysMetLeuAsnIleLysGluSerLeuSerThrLeuSerArgSerPheGlySerLeu	2315
Db	6480	-----	6480
QY	2320	GlnThrGluHisValLysLeuAsnThrGlnLeuGlnThrLeuLeuAsnLysPheLysVal	2335
Db	6481	-----ATCATGAAGAACTGAACTGAT	6501
QY	2340	ValI- - - - - TyrArgThrAlaAlaValLysGluLysPheIleSerLeuIleLysAspIleGlu	2355
Db	6502	GTTGTTAAGCTATGTTACAAAAATAAAGAAACAAACATGAAATTCATCAATTAATTTGAA	6561
QY	2358	LysAspLeuAlaAlaGluGlnLysArgHisAspGluLeuArgLeuGlnLeuGlnCysLeu	2377
Db	6562	ATGATTTTATGATGAGAGAGTGAAGCAAGCAAAAGAAATTCGTAATTTAAATACAGACCTT	6621
QY	2378	GluGlnHisGlyArgLysTrpSerAspSerAlaSerGluGluLeuLysPheCysGluIle	2397
Db	6622	CAACAAAGAT- - - - - TGTGATGTACCATCCAGAGAAATTAAGGATCTCAAAATG	6665
QY	2398	GluPheLeuAsnGluLeuLeuPheLysAlaAsnIleIleGlnSerValGlnAspArg	2417
Db	6670	AACCGAATATGAGATCTA- - - - - CATATGAGGAATTTCTCAAGAT	6711
QY	2418	PheSerGluValGlnValPheLeuAsnGlnValGlySerThrLeuGlnGlnGluLeuGln	2437
Db	6712	TTCTCAGAAATGAG- - - - - TTCCCTAGCATTAAGACTGAATTTCAACAAGTCTAAGT	6765
QY	2438	HisLysLysGlyPheMetGlnTrpLeuGlnGluPheGluAspLeuHisValAspAlaLys	2457
Db	6766	AATAGGAAGAATAGCACAGATTTTGGAGAAAGGGTTAAATACTCGTTTGAATATGAA	6825
QY	2458	LysLeuSerGluGluMetGlnGlnGlnLysAsnArgArgIleAlaSerThrIleGlnLeuLeu	2477
Db	6826	AAGCTTAAAAATGGCATCCAGAAAGAAATGATGAGATTGTCAAGTAATACCTCTT	6885
QY	2478	ThrLysArgLeuLysAlaValAlaGlnSerLysIle- - - - - GlnArgGluIleThr	2494
Db	6886	AATAACGAAATTAATGGCATATATATGATCAACAGAGTTTGAGGAAGAAGCTGATCC	6945
QY	2495	ValTyrlsLeuAsnGlnPheGluAlaLysLeuGlnGlnLysLysGluGlnAsnLysGluLeu	2514
Db	6946	ATA- - - - - TCCAAAGAGTGGGAACAGAGACTGAAATACCTGAAAGGAAAAATGAAACCTA	7002
QY	2515	MetArgArgMetGluHisLysGlyProSerAlaSerValMetGluGlnGluAsnAlaArg	2534
Db	7003	TTTAAAAACTACCAACATTTGAAGACTTCTCTGGCATCTGGTCCAGGTTTAAT- - - - -	7056
QY	2535	LeuLeuGlyIleLeuLysThrValGlnAspGlu- - - - - SerLysLys	2548
Db	7057	-----CCTACACACAAAGCAATTAAGAACTCTATGTTCAATCAAGAGCT	7101
QY	2549	LeuGln- - - - - SerArgIleLysMetLeuGlnAsnGluLeuAsnLeuValLysAsp	2565


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QY 139 AsnLeuLeuCyAspAspArgArgLysLysProLeuGluIleArgGluAspPheAsnArg 158
Db 511 GATTACTCTGTGGCAGCTCAAAAATGAAACCTTTAATTATTCGAGAAAGATGTCATAGG 570
QY 159 AsnValTyrValAlaAspLeuThrGluGluLeuValMetValProGluHisValIleGln 178
Db 571 AATGGTATGTGGCTGATCTCCAGAGAAAGTTGTATATACATAGAAATGGCTTGGAA 630
QY 179 TrpIleLysLysGluLysLysAsnArgHisTyrGluGluThrLysMetAsnAspHisSer 198
Db 631 TGGATTCAAAAGGAGAAAGAGAGAGCATTTATGGAGAAACAAAATGATCAAGAGAGC 650
QY 199 SerArgSerHisThrIlePheArgMetIleValGluSerArgAspArgAsnProThr 218
Db 691 AGTGGTCTCATACCTCTTATAGATATTTGGAAAGCAGAGAGAGAGAGGCTGAACCTTCT 750
QY 219 AsnSerGluAsnCyAspGluValAlaValMetValSerHisLeuAsnLeuValAspLeuAla 238
Db 751 -----AATTGTGAAGATCTGTTAAGTATCCCATTTGAATTTGGTTGAATCTTGCA 801
QY 239 GlySerGluArgAlaSerGluThrGlyAlaGluGlyValArgLeuLysGluGlyCysAsn 258
Db 802 GGCAGTAAAGAGAGCTGCTCAAAAGCGCTGAGAGTGTGCGGCTCAAGAGAGGCTGTAA 861
QY 259 IleAsnArgSerLeuPheIleLeuGlyGlnValIleLysLysLeuSerAspGlyGlnAla 278
Db 862 ATTAATCGAAGCTTATTATTATTTGGGACAAAGTATCAAGAACTTGTGTGATGCAAGT 921
QY 279 GlyGlyPheIleAsnTyrArgAspSerLysLeuThrArgIleLeuGlnAsnSerLeuGly 298
Db 922 GGTGGTTTCATTAATATTCAGATAGCAAGTAAACAGAAATTTTCAGAAATCTTGGA 981
QY 299 GlyAsnAlaLysThrValIleIleCysThrIleThrProValSerPheAspGluThrLeu 318
Db 982 GGAATTCCAAAGACAGTATATCTGCACAAATTATCTCCAGTATCTTTGATGAACTCTT 1041
QY 319 SerThrLeuGlnPheAlaSerThrAlaLysHisValArgAsnThrProHisValLeuGlu 338
Db 1042 ACTGCTCTCCAGTTTGGCCACTACTGCTTAATATATAGAAATATCTCTTATGTATATG 1101
QY 339 ValLeuAspAspGluAlaLeuLeuLysArgTyrArgLysGluIleLeuAspLeuLysLys 358
Db 1102 GATATCAACTGATGAACTCTCCGAAAGGTATAGAAAGAAATATATGATCTTAAAAA 1161
QY 359 GlnLeuGluAsnLeuLysSerSerGluThrLysAlaGlnAlaMetAlaLysGluGlu 378
Db 1162 CAATTAGAG-----GAGGTTCTTTAGAGCGCGGCTCAGCAATGGAAGAAAGCA 1215
QY 379 HisThrGlnLeuLeuAlaGluIleLysGlnLeuHisLysGluArgGluAspArgIleTrp 398
Db 1216 TTGGCCCACTTTTGGAGAAAGAAAGATTGCTTCAGAAAGTACAGAAATGAGAAATTTGA 1275
QY 399 HisLeuThrAsnIleValAlaAlaSerSerGlnGluSer--GlnGlnAspGlnArgVal 417
Db 1276 AACTTAACCGAGATGCTGTGACCTCTTCTCCACGTTGCCAACAGAAATTAAGGCT 1335
QY 418 LysArgLysArgArgValThrTyrAlaProGlyLysIleGlnAsnSerLeuHisAlaSer 437
Db 1336 AAAAGAAAAGAGAGCTTACTGTGCTTGGCAAAATTAACAAAATAGAGAACTCAAC 1395
QY 438 GlyValSerAspPheAspMetLeuSerArgLeuProGlyAsnPheSerLysLeuAlaLys 457
Db 1396 TATGAGATCAATTAAAT-----ATACCAACAATATATACAAACAAAACACAT 1443
QY 458 PheSerAspMetProSerPheProGluIleAspAspSerValCysThrGluPheSerAsp 477
Db 1444 AAGCTTTCTATTAATTTTATTCAGAGAAATGATGATGCTGTCTGTCAGACTGATGAT 1503
QY 478 PheAspAspAlaLeuSerMetMetAspSerAsnGlyIleAspAlaGluThrAsnLeuAla 497
Db 1504 TTCAGTACACCTCTTGATACATTAAGT-----GAGATAGAAATGAAATCCAGCA 1551
QY 498 SerLysValThrHisArgGluLysThrSerLeuHisGlnSerMetIleAspPheGlyGln 517

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Db 1552 ACAAAGCTCTTAATAGAG----- 1572
QY 518 IleSerAspSerValGlnPheHisAspSerSerLysGluAsnGlnLeuGlnTyrLeuPro 537
Db 1572 ----- 1572
QY 538 LysAspSerGlyAspMetAlaGluCysArgLysAlaSerPheGluLysGluIleThrSer 557
Db 1572 ----- 1572
QY 558 LeuGlnGlnGlnLeuGlnSerLysGluGluGluLysLysGluLeuValGlnSerPheGlu 577
Db 1572 ----- 1572
QY 578 LeuLysIleAlaGluLeuGluGluGlnLeuSerValLysAlaLysAsnLeuGluMetVal 597
Db 1573 -----AATATGAAAGTGA 1587
QY 598 ThrAsnSerArgGluHisSerIleAsnAlaGluValGlnThrAspValGluLysGluVal 617
Db 1588 TTGAATCTA----- 1596
QY 618 ValArgLysGluMetSerValLeuGlyAspSerGlyTyrAsnAlaSerAsnSerAspLeu 637
Db 1596 ----- 1596
QY 638 GlnAspSerSerValAspGlyLysArgLeuSerSerSerHisAspGluCysIleGluHis 657
Db 1596 ----- 1596
QY 658 ArgLysMetLeuGluGlnLysIleValAspLeuGluGluPheIleGluAsnLeuAsnLys 677
Db 1596 ----- 1596
QY 678 LysSerGluAsnAspLysGlnLysSerSerGluGlnAspPheMetGluSerIleGlnLeu 697
Db 1596 ----- 1596
QY 698 CysGluAlaIleMetAlaGluLysAlaAsnAlaLeuGluGluLeuAlaLeuMetArgAsp 717
Db 1597 -----CTTCCGTCT 1605
QY 718 AsnPheAspAsnIleIleLeuGluAsnGluThrLeuLysArgGluIleAlaAspLeuGlu 737
Db 1606 GACTATGATATCTGATATAGACTATGAAACAATCGAACAAACAAAAGAAAGAAATGCA 1665
QY 738 ArgSerLeuLysGluAsnGlnGlnGluThrAsnGluPheGluIleLeuGluLysGluThrGln 757
Db 1666 TTGAATTTAAAGAAAGAAAGAAATGATTTGGATGAAATTTGAGGCTCTACAGAAAGAAACTTAA 1725
QY 758 LysGluHisGluAlaGlnLeuLeuIleHisGluIleGlySerLeuLysLysLeuValGluAsn 777
Db 1726 AAAGATCAAGAGATGCACTTAATTCATGAAATTTGCAACTTAAGAAATTTAGTTAAGCAT 1785
QY 778 AlaGluMetTyrAsnGlnAsnLeuGluGluAspLeuGluThrLysThrLysLeuLysLys 797
Db 1786 CGAAGATATATATCAAGATCTTGGAATGAACTGATCAAAAGTAGAGCTGCTTAA 1845
QY 798 GlnGlnGluIleGlnLeuAlaGluLeuArgLysArgAlaAspAsnLeuGlnLysVal 817
Db 1846 GAAAGAGAGAGACAGATTTAGAGAGCTACAGAAATCATAGACTCTCAAAAGCTTAAGAAAT 1905
QY 818 ArgAsnPheAspLeuSerValSerMetGlyAspSerGluLysLeuCysGluGluIlePhe 837
Db 1906 ATTAATAATGACTGTTCATATCATG-----GAAAGCATTTGAAGAACCCAAA 1953
QY 838 GlnLeuLysGlnSerLeuSerAspAlaGluAlaValThrArgAspAlaGlnLysGluCys 857
Db 1954 CAAATGAGCAGACTCTGTTGATGCTGAACTGTAGGCTTTGATGAGCCAAAGAGAAATCA 2013
QY 858 SerPheLeuArgSerGluAsnLeuGluLeuLysGluLysMetGluAspThrSerLysTrp 877

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OY	1541	AspAspLeuGlnGlnIleuLeuSerLeuSerLeuSerGluValIleIleLeuValGluAsn	1560
Db	4114	GAGAACCTTAAACAGATAAAGAGACCTTGAAGTTAAACAGTACAGACAGCTAAAGAAACAT	4203
OY	1551	IleAspThrThrLeuLeuSerIleHisSerAspThrGlnIleGlnLeuGlnIleThrGlnIle	1580
Db	4204	ATTGAGAAACCTTGG-----GCTAAATATCCAGAACTCCAAAGC	4242
OY	1581	GluLeuGlnLeuAlaLeuAsnLeuAlaIleAlaIleAspAspAsnGlyProIleThrGln	1600
Db	4243	AAACAGAACAGCTCTTAAATGTGAAGAAAGAAAGCAATGAAGTAACCTACCAAAATGTGAGT	4302
OY	1601	GluIlySglu-----ThrSerIleAspCysValHisProLeuGluGluIlyIleLeu	1617
Db	4303	GAGATGAGCAATTCAAACCCAAAGATTCAGACACTAAGATGAATGAATGAATGCAATGCTC	4362
OY	1618	LeuLeuThrGlnGluLeuHisGlnIlySerThrAsnGlnGlnIlyIlyLeuLeuHisGlnIlyS	1637
Db	4363	GGATTGTCCAAAGACCTTCAGAAAGTCATGATGAATGAATGAAATGTGTGACTTAAGGAATAA	4422
OY	1638	AsnGlnLeuGlnGlnAlaGlnValGluLeuIlySerCysGluValGlnIleSleuMetIlySer	1657
Db	4423	GATGACCTACAGAGCTCCAGAAAGTCTTCATCTGAAAGTACAGACTC-----	4473
OY	1658	MetIleGluSerIlySerSerLeuGlnIlySerLeuGlnIleHisGlnIlySerHisAspThrGluGln	1677
Db	4474	-----AAAGAAACATAAAGAAATTTGACCTAAACACCTGAAACCTGAAGAG	4521
OY	1678	GlnIlyu-----LeuAlaLeuIlySerGlnGlnMetGlnValIleThrGlnIlyS	1693
Db	4522	GAACTTAAAGTTCCTCATTTGTTGCTGTAAGAAAGACAGAGAACTTTAAATGAAGTTAAGA	4581
OY	1694	LysGluLeuGlnGlnIleThrHisGlnIleHisLeuThrAlaGluValAspHisSleuIlySgluAsn	1713
Db	4582	GTGAATCTTTCAGAGAAAGAA-----ACTGAATATATCAACATTCAAAACAGC	4629
OY	1714	IleGlu-----LeuGlyLeuAsnPheLeuAsnGlnAlaGlnIlySerThrThrIlySgluGln	1732
Db	4630	TTAGAAAGCAATCAATGATAAATTACAGAAACAAGATCCAAAGATTTATGAGAAAGAGAA	4689
OY	1733	CysLeuLeuAsnGlnAsnIlySgluLeuGlnIleSerGlnIleHisArgLeuGlnIlySgluIle	1752
Db	4690	CAATTT-----AATATAAACAATTAAGTAGAGTTCAGAAACAGCGAAT---GAAGTGC	4740
OY	1753	GluGlnIlyuMetClySerLeuIlyLeuAspIlySgluSerAlaLeuGlnIlyThrLeuIlySgluSer	1772
Db	4741	AAACAAATTCAAAGAGCATCGCAAAAGCCAAAGATTCAGACACTCAAAAGTATA-----	4791
OY	1773	GluGlnIlyValIleAsnIlyu-----AsnGlnGlnIlyuMetGluMet	1785
Db	4792	GAAAGTAGATGCTCGAGTTTACCAACAGACTTCAAGAAAGTCAAGAAAGAAATTAACAATT	4851
OY	1786	ValMetLeuGlnMetGluGlnIlyLeuIlyAsnSerGlnArgThrValIleAlaGluArgAsp	1805
Db	4852	ATGATTAAAGAAAAAGAGAAATGAAAAAGTACAGAGAGCCCTTCAGATAGAGAGAGAC	4911
OY	1806	GlnIlyuIleAspAspLeuArgGluSerValGlnMetSerIleGluThrGlnAspAspLeu	1825
Db	4912	CAAGCTGAAGAAAAACAATAAGAAATTGTCTAAATTAAGAAAGATTCAGAA-----	4965
OY	1826	ArgIlyValGlnGlnAlaLeuGlnGlnIleGlnIlyAspIlySgluValGlnIlyuLeuThrSerGln	1845
Db	4966	AAAGAAATATCAGTTTCTTAAGATGACAGCTGTCAATGAGACTCAGAGAAATGTGTGAA	5025
OY	1846	IleSerValIleSerGlnIlyIlySgluSerIlyu-----LeuGluAsn	1858
Db	5026	ATAGAACACTTGAAGAGAGCAATTTGAGACCCAGAAAGTTAAACCTCGGAAAAACATAGAAACG	5085
OY	1859	-----GlnMetLeuIlyr-----AsnValAlaThrValIlySgluThrIlyu	1871
Db	5086	GAGAAATTAAGGTTGACTCAGATATCTACATGAAAAACCTTGAGAAATGAGACTGTGTAAACA	5145
OY	1872	SerGluArgAspAspLeuAsnGlnIleSerIlySgluHisLeuPheSerGluIleGluThrIlyu	1891

Db	5146	AAAGAAAGAGTGCCTTAGAGAGCTGGAGAGACTCTCAAGTAGAGAGAGACCAAGCTC	5205
Oy	1892	SeuSerLeuLysGluLys--GluPheAlaLeuGluGlnAlaGluLysAspLys--	1909
Db	5206	AAGAAAGAACTTAGAGAAACTATATACAGAACCTAGAAAAACAAAGAGAGACTAAAAATT	5265
Oy	1910	-----AlaAspAlaAlaArgLysThrIleAspIleThrGluLysIleSerAsn	1925
Db	5266	GTTACATGCATCTGAGAGAGACCAAGAACTATTGAT-----AAACTAAGAGCG	5316
Oy	1926	IleGluGluGlnLeuLeuGlnGlnAlaThrAsnLeuLysGluThrLeu--TyrGluArg	1944
Db	5317	ATTGTTTCAGAGAAAAACAATGAATATCAATATATGCAAAAGGACTTAGAACATCAAT	5376
Oy	1945	GluSerLeu-----IleGlnCysLysGluGlnLeuAlaLeuAsnThrGluHis	1966
Db	5377	GATCCCTTAAAGACACAGAGATCTGAAAAATACAAAGAGAACTAAGAAATTGCTCACATGAT	5438
Oy	1961	LeuArgGluThrLeuLysSerLysAspPheAlaLeuGluLysMetGluGlnArgAsp	1980
Db	5437	CTGAAGAGCAGCAGGAACATATTGACAAACTCAGAGGAATGTTTTCGAGAACACAGAT	5496
Oy	1981	GluAlaAlaAsnLysValIleAlaLeuThrGluLysMetSerSerLeuGluGlnIle	2000
Db	5497	AAACTATCAATATGCAAAAGATTGAAATTCAAATGCTAATATTCAGAAAGAAAGATT	5556
Oy	2001	AsnGluAsnValThrThrLeuLysGluGluGluGluLysGluLysGluThrPheTyrLeuGln	2020
Db	5557	CACAGAA-----CTTAAGGCAATGACATCACTATTAGCTTAAAAAACAT	5604
Oy	2021	ArgProSerLysGlnGlnSerSerSerGlnMetGluLeuLeuArgLysLeuLysThr	2040
Db	5605	GTCATATGAGACACAGAAAAAGATGCTGAAATGAGACAACTAAGAAACAAATATTAAGAC	5664
Oy	2041	LysAspLeuGlnLeuGluGlnAlaGluLysGluLysSerGluAlaThrAsnGluLys	2060
Db	5665	CAAGCTTAACCTCGAGTAATTA-----GAAATATGAG	5697
Oy	2061	AsnLeuThrAlaLysIleSerSerLeuGluGluGlnIleLeuGlnAsnAlaSerIleLeu	2080
Db	5698	AATTTA-----AATTGGCTCCAGAACCTTCATGAAAACCTTGAGAAATG	5742
Oy	2081	AsnGluAlaValSerGluArgGluAsnLeuArgHisSerLysGlnLeuValSerGlu	2100
Db	5743	AAATCTGTAATGAAAGAAAGAAATTAATCTAAGAAAGTAAGAGGACACTCAAACTGGAG	5802
Oy	2101	LeuGluGlnLeuSerLeuThrLeu-----LysSerArgAspHisAlaPheAlaGln	2117
Db	5803	AGAGACCAACTCAAGAAAGACCTCCAGAAACCAAAAGCTAGAGATCTCGAAATATCAACAG	5862
Oy	2118	-----SerLysArgGluLys-----AspGluAlaVal	2126
Db	5863	GAACATAAAACCTGCTGATGCTATCAAAAAGAACACAAAGAAACCTGTGATTAACCTAGA	5922
Oy	2127	AsnLysIleAlaSerLeuAlaGluGlnIleLysIleLeuThrLysGluMetAspGluPhe	2146
Db	5923	GAAAAAATTCAGAAAAAGACAATTCAAATTTTCAGACACTTCAAAAGGATTTAGATAAA--	5979
Oy	2147	ArgAspSerLysGluSerLeuGlnGlnIleGlnSerSerHisLeuSerGluGluLeuCysThr	2166
Db	5980	-----TCAAAAGATGAATTAACGAAAAAAGATCCAAAGAACTTCAG-----	6018
Oy	2167	TyrLysThrGluLeuGlnMetLeuLysGlnGlnIleLysGluLysPheAsnLysLeuAla	2186
Db	6019	-----AAAAAAGAACTTCAACTGCTTAGA--GTGAAAGAAAGATGCAATATGACT--CAT	6069
Oy	2187	GluLysValLysGluValAspGluLeu-----	2195
Db	6070	AAAAAATTAATGAAATGAAACAGCTTGAAGAGCAATTTAGAGCAAACTATCTATGCAAG	6129
Oy	2196	-----LeuGlnHisLeuSerSerLeuLysGluGlnLeuAspGlnIleGln	2210

Db 6130 TGTGATGATGAATCACTTCAGTGAAGAACTTCATGAAAGCTTGGAAGAAATAGA 6189
 Qy 2211 MetGluLeuArg---AsnGluIysLeuArgAsnTyrGluLeuGlyMetLeuPhe 2229
 Db 6190 ATTGTAGCTAAAGAAAGAGATGAGCTAAGAGAGATTAAGAAATCTCTCAAAATGGA--- 6246
 Qy 2230 MetGluIysGluIleSerValLeuArgLeuMet-----Gln 2241
 Db 6247 AGGACCAATTCATTCAGCAACCTTAAGGGAATGATGACAGAACCGACAGAACCACTCA 6306
 Qy 2242 AsnGluProGlnGlnGlu-----GluAspAspValAlaGluArgMetAspIleLeuGlu 2259
 Db 6307 GTAAACCTGGAAGAAAGCTTACTAAGTATGACAAACAGCACCTTATGAAAGCCCTGAGA 6366
 Qy 2260 SerArgAsnGlnGluIleGlnGluLeuMetGluIysIleSerAlaValTyrSerGluGln 2279
 Db 6367 GAAAGAGCTCTAGAATTAAGAGCTTTGAAAGAGTACTCAGAGTGT---GATGATCAT 6423
 Qy 2280 HisThrLeuLeuSerSerLeuSerSerGluLeuGlnIysGluThrGluAlaHisIysHis 2299
 Db 6424 TATGAGTCTTGAATAGATTGTCTCTTGACCTTGAGAGAGAAATTTGAATTCACAGAC--- 6480
 Qy 2300 CysMetLeuAsnIleIysGluSerLeuSerSerThrLeuSerArgSerPheGlySerLeu 2319
 Db 6480 ----- 6480
 Qy 2320 GlnThrGluHisValIysLeuLeuAsnThrGlnLeuGlnThrLeuLeuAsnIysPheIysVal 2339
 Db 6481 -----ATCATGAGAAACTGGAAGTAT 6501
 Qy 2340 Val-----TyrArgThrAlaAlaValIysGluAspHisSerLeuIleIysAspTyrGlu 2357
 Db 6502 GTGTTAAGCTATGTTATCAAAATAAAGAGAAACACATGATGCATCAATAATTGAA 6561
 Qy 2358 LysAspLeuAlaIleGluGlnIysArgHisAspGluLeuArgLeuGlnLeuGlnIysLeu 2377
 Db 6562 ATGATTTTATGATGAAGTGAAGAAAGCAAAAGCAATTCCTAATTAAATACAGACCTT 6621
 Qy 2378 GlnGlnHisGlyArgIysTyrSerPheSerAlaSerGluGlnIysLeuPheCysGluIle 2397
 Db 6622 CAACAAAGAT-----TGATATGATCCATCCAGAGAAATTAAAGGATCTCAAAATG 6669
 Qy 2398 GluPheLeuAsnGluLeuLeuPheIysIysAlaAsnIleIleGlnSerValGlnAspArg 2417
 Db 6670 AACCAAGATATGATCTA-----CATATGAGAGAAATTTCTCAAGAT 6711
 Qy 2418 PheSerGluValGlnValPheLeuAsnGlnValGlySerThrLeuGlnGlnIysLeuGlu 2437
 Db 6712 TTCTCAGAAAGTGAAG-----TTCCCTAGCAATAAAGACTGAATTTCAACAAGTACTTAA 6765
 Qy 2438 HisIysIysGlyPheMetGlnTyrPheGluGlnIysPheGlyAspLeuHisValAspAlaIys 2457
 Db 6766 AATAGGAAGAAATGACACAGATTTTGGAGAGTGTAAATATCTGTTTGATATAGA 6825
 Qy 2458 LysLeuSerGluGluMetGlnGlnGlnIysAsnArgGluIleAlaSerThrIleGlnLeuLeu 2477
 Db 6826 AAGCTTAATAATGTCATCCAGAAAGAAATGATAGAGATTTGTCAAGTGAATAACTTCTT 6885
 Qy 2478 ThrIysArgLeuIysAlaValAlaGlnSerIysIle-----GlnArgGluIleThr 2494
 Db 6886 AATAACAGATATATGTCATATGATGAATGATCAACAGACTTTGAGAGAAAGAGTCTTACC 6945
 Qy 2495 ValTyrLeuAsnGlnPheGluAlaIysLeuGlnIysValIysGluGlnAsnIysGluLeu 2514
 Db 6946 ATA---TCCAAAGAGTGGACAGACAGCTGAATCACTGAAGAGAAATAATGAATAACTGA 7002
 Qy 2515 MetArgAspMetGluHisIleGlyProSerAlaSerValMetGluGlnGlnAsnAlaArg 2534
 Db 7003 TTTAAACCACTACCAACATTTGAAGACTTCTTGSCATCTGTGCCAGGTTAAT----- 7056
 Qy 2535 LeuLeuGlyIleLeuLeuThrValGlnAspGlu-----SerIysIys 2548
 Db 7057 -----CTTACACACAGACATAGAAATCTCTCATGTTATCATCAAGACT 7101

Qy 2549 LeuGln-----SerArgIleLeuMetLeuGluAsnGluLeuAsnLeuValIysAsp 2565
 Db 7102 ACACGTTTAACACACAGAGAAATTTGAGAGCTGGAAATTTCACTGATGAACTTAAGAA 7161
 Qy 2566 AspAlaMetHisIysGlyGluIysValAlaIleLeuGlnAspIysLeu---LeuSerArg 2584
 Db 7162 AGTCTTATGATTAAGAAAGCAAGATCTTAAGAAAGTGAAGAAAGAACTTGAGTGAATAT 7221
 Qy 2585 AsnAlaGluAlaGluLeuAsnAlaMetGlnValIysLeuThrIysIysGlnAspAsnLeu 2604
 Db 7222 GACATATATGCAAACTT-----CAAGCCAAAGTCTGATCAATCAATATATGCTT 7272
 Qy 2605 GlnAlaAlaMetIysGluIleGluLeuLeuGlnIysMetValAlaIysGluValAlaPro 2624
 Db 7273 GAAAAACAAAGAGACATTTCAAGTACTTCAGCAAAAGTTGCTTTGAGACTTAAGCCA 7332
 Qy 2625 TyrIysGluGluIleAspAsnLeuIysThrIysValAlaIysIleGluMetGluIysIle 2644
 Db 7333 TATAAAGAAAGAAATTTGAAGATCTCAAAATGAAAGCTTGGAATAATGACCTGAGAAATG 7392
 Qy 2645 LysTyrSerIysAlaThrAspGlnIleAlaTyrLeuIysSerCysLeuGluAspIys 2664
 Db 7393 AAAAATGCCAAAGAAATTTGAAAGAGAAATCACTGCTACAAAGCCACTGATGAATATCA 7452
 Qy 2665 GlnGluGluIysLeuArgArgLeuIysGluIleLeuArgArgAlaGlnAlaAspAspAspThr 2684
 Db 7453 AAGGAAGTTATAGGCTATGAGAGAAATTTCAAGAAAGTCAACAGAGCCCAAGATACC 7512
 Qy 2685 ThrValCysValProIysAspTyrGlnIysAlaSerThrPheProValThrCysGlyGly 2704
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 Qy 2705 GlySerGlyIleValGlnSerThrAlaMetLeuValLeuGlnIysSerGluIysAlaLeu 2724
 Db 7573 GCCAGCGGCAATGTTCAAACAAACAAAGCTTATTTTGAAGAAAGCAATAGAGCTA 7632
 Qy 2725 GluArgGluLeuSerHisTyrIysIysIysArgHisIleLeuSerArgThrMetSerSer 2744
 Db 7633 GAAAAAGAAATTTCTAAGCTTAAGCGCAAAATGAAACAGCTA----- 7674
 Qy 2745 SerGluAspArgIysIysThrIysAlaIysSerAspAlaHisSerSerHisThrGlySer 2764
 Db 7675 -----ATTAACAAAGATGAATGTTTAAGCAATATACAGATCTT 7716
 Qy 2765 SerHisArgIysSerProHisIysThrGluThrTyrArg-----HisGlyProVal 2781
 Db 7717 TCAATGAGTCAAAACTTGAGAGAAAGAACCTTAAGAAAGAGGCTCACAAACAGATA 7776
 Qy 2782 ThrProGluIysSerGluMetProSerLeuHisIleuGlySerProIysIysSerGluSer 2801
 Db 7777 ACTTGCTGAG-----AATTTCTCAAG----- 7797
 Qy 2802 SerThrIysArgValIysSerProAsnArgSerGluIleTyrSerGlnLeuValMetSer 2821
 Db 7798 -----TCT 7800
 Qy 2822 ProGluIysThrGlyMetHisIysHisIleLeuSerProSerIysValGlyLeuHisIys 2841
 Db 7801 CCTAAGAGTCTGGAACA-----GCTTCTTAA 7827
 Qy 2842 LysArgAlaLeuSerProAsnArgSerGluMetProThrGlnHisValIleSerProGly 2861
 Db 7828 AAGAAACAAATTAACACC----- 7845
 Qy 2862 LysThrGluLeuHisIysAsnLeuThrGluSerThrLeuPheAspAsnLeuSerSerPro 2881
 Db 7846 -----TCTCA 7851
 Qy 2882 CysIysGlnGlnIysValGlnGluAsnLeu-----AsnSerProIysGlyIysLeuPhe 2899
 Db 7852 TGCAAGGAAGCAAGAAATTTACAGATCTCTGTGCCAAAGAAATCACCAAAATCTTGTTTT 7911

QY 2900 AspValLysSerLysSerMetProTyr---CysProSerGlnPhePheAspAsnSerLys 2918
 Db 7912 GATACCCCATCAAAAGCTTTTACCATCACCCTCATCCAGTTCCTGATTTTGAATACTCAAGT 7971
 QY 2919 LeuGlyAspPheSerGluLeuAsnThrAlaGluSerAsnAspLysSerGlnAlaGluAsn 2938
 Db 7972 TTAGCCCTTTGCCAGAGGTGCMAAATGCAGAGCAGAGAGTGTGATTCACCCAGCT 8031
 QY 2939 TrpTrpTyrGluAlaLysLysGluThrAlaProGluCysLysThr 2953
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 RESULT 5
 US-09-960-253-145
 ; Sequence 145: Application US/09960253
 ; Patent No. US20020123619A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Benson, Darin R.
 ; APPLICANT: Mohamath, Michael J.
 ; APPLICANT: Lodges, Michael J.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.556
 ; CURRENT APPLICATION NUMBER: US/09/960,253
 ; NUMBER OF SEQ ID NOS: 187
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 145
 ; LENGTH: 10300
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-960-253-145

Alignment Scores:
 Pred. No.: 1.6e-63 Length: 10300
 Score: 1153.00 Matches: 675
 Percent Similarity: 39.53% Conservative: 651
 Best Local Similarity: 20.13% Mismatches: 1170
 Query Match: 7.81% Indels: 858
 DB: 10 Gaps: 138
 US-09-724-584-1 (1-2954) x US-09-960-253-145 (1-10300)

QY 110 GluValPheLysIleIleGlnGluIleProAsnArgGluPheLeuLeuArgValSerTyr 129
 Db 559 GAAATGAAAAGATTAAACATAAGCTCCAGAGAGAGAGAACTATC----- 606
 QY 130 MetGluIleTyrAsnGluThrValLysAspLeuLeuCysAspAspArgLysLysPro 149
 Db 607 -----AGCACTTTCAGAGCCAGCTTACTCAGGCAGCAGCAACAACACT 651
 QY 150 LeuGluIleArgGluLysAspPheAsnArgAsnValTyrValAlaAspLeuThrGluGluLeu 169
 Db 652 GCACAGAGTTCACAGAGATG-----GAAAGATT 681
 QY 170 ValMetValProGluHisValIleGlnTrpIleLysGlyLysAsnArgHisTyr 189
 Db 682 GTAAATGATCAACACAGCTC-----CAGGAGAAGAAAGATTCTT 723
 QY 190 GlyGluThrLysMetAsnAspHisSerSerArgSerHisThrIlePheArgMetIleVal 209
 Db 724 AGCACTTTCACAGAGCTCAGCCAGACACAGGAGAGCAAGCTGCACAGCAGAGTGTCTC 783
 QY 210 GluSerArgAspArgAsnAspProThrAsnSerGluAsnGlyAlaValMetVal 229
 Db 784 CGAGAGAAAGATGCCCGCTTGAACACACAGTTCCTTCATGAAGATGAGCTT----- 837
 QY 230 SerHisLeuAsnLeuValAspLeuAlaGlySerGluArgAlaSerGlnThrGlyAlaGlu 249
 Db 838 -----CTTCAGATTAAACCCAGCAGATGTGAGACAGAGATGCAA----- 879
 QY 250 GlyValArgLeuLysGluGlyCysAsnIleAsnArgSerLeuPheIleLeuGlyGlnVal 269

Db 880 -----CAGAAATTGAGGCTGCTCCAAAGAG 906
 QY 270 IleLysLysLeuSerAspGlyGlnAlaGlyIlePheIleAsnTyrArgAspSerLysLeu 289
 Db 907 CTGGAGAACACAGAAAGATCCTTGGTGGC-----CGTGCTCAGTTC 948
 QY 290 ThrArgIleLeuGlnAsnSerLeuGlyLysAsnAlaLysThrValIleIleCysThrIle 309
 Db 949 GTTGACTTCTGCAACAGAGCTGACTGCTGAGCAGAGA----- 990
 QY 310 ThrProValSerPheAspGluThrLeuSerThrLeuGlnPheAlaSerThrAlaLysHis 329
 Db 991 -----AACAGATTCTCTCTCAGCAGCTTACAGCAGATGGAAGCTGAGCAT 1035
 QY 330 -----ValArgAsnThrProHisValAsnGluValLeuAspArgGluAlaLeuLys 347
 Db 1036 AATACTTGGAGAACACTGTGGA-----ACAGAAAGAGAGAGTCCCAAGATTCTACTGGA 1092
 QY 348 ArgTyrArgLysGluIleLeuAspLeuLysLysGlnLeuGluAsnLeuGluSerSer 367
 Db 1093 AAGATGAACTTGAAGTGCAGAGAGAAATATCTTCCATTAATCTGCAGAAAGAAATG 1152
 QY 368 -----GluThrLysAlaGlnAlaMetAlaLysGluGluHisThr 380
 Db 1153 CATCATCTTTTGAACAGATTGAGCAAGAGCCAGCCAGCTGAAGTAAAG----- 1206
 QY 381 GlnLeuLeuAlaGluIleLysGlnLeuHisLys---GluArgGluAspArgLysThrHis 399
 Db 1207 TCTGGTATAGTCTTGGCCAGAGACACAAAGCAAGAAATGAGAGAGAGACCTTCAT 1266
 QY 400 LeuThrAsnIleValAlaLysSerGln----- 409
 Db 1267 ATTTGAGTCTTCAAAAGACTGCACAGAGCTGACGTCTGCTGATGCTTAAAGAT 1326
 QY 410 -----GluSerGlnGlnAspGlnArgValLysArgLysArgVal 423
 Db 1327 CAAAATTCAAAGCTTCTCCAGATTAAGATGAACAGCAGCTTCAGCAGCCAGACATT 1386
 QY 424 ThrTrpAlaProGluLysIleGlnAsnSerLeuHisLysSerGlyValSerAspPheAsp 443
 Db 1387 CAGCACTGGAAGATGACGCTCCAGCAAAA-----TCCAAAGAAATTGACCATT--- 1437
 QY 444 MetLeuSerArgLeuProGluLysAsnPheSerLysLysAlaLysPheSerAspMetProser 463
 Db 1438 ---CTAAATGACTGCCC-----TTGCAACAATGAAGAACACACTCTCAGACTTCT 1485
 QY 464 PheProGluIle-----AspAspSerValCysThr--- 473
 Db 1486 TTCCAGATGTTTATATGAGGACACAGGCCAGTCACTGAGGAGAAATATGCTTCTTTG 1545
 QY 474 -----GluPheSerAspPheAspAspAla-----LeuSerMetMetAsp 486
 Db 1546 CAGAAAGAGTGTGAATGATGAGATGAAGAGGAGCTTGTCTCTTATGAG 1605
 QY 487 SerAsnGlyIleAspAlaGlu---TrpAsnLeuAlaSerLysValThr----- 501
 Db 1606 CTGAGAGAGCTGAAGCTGAATGAATAAATCTGTTCTCAGATTAATCTCTCTAGAGCT 1665
 QY 502 -----HisArgGluLysThrSerLeuHisGlnSerMetIleAsp 514
 Db 1666 CAGATATGAATCGGAGAGCAGACAGAGAAAGTCAGTGAAGT-----AGCATTTGAT 1719
 QY 515 Phe-----GlyGlnIleSerAspSerValGln 523
 Db 1720 ATTGCCAACAGAGAGCTTTCTGTGAGAAAGTGAACAA-----GATGTTCTAAG 1773
 QY 524 PheHisAspSerSerLysGluAsnGlnLeuGlnTyrLeuProLysAspSerGlyLysMet 543
 Db 1774 AACACATTTTCTCAGAAACATATAAGATTATGAGTTTA-----TTG 1815
 QY 544 AlaGluCysArgLysAlaSerPheGluLysGluIleThrSerLeuGlnGlnLeuGln 563
 Db 1816 TTGAAATGAAGAGCT-----CAAGAGAAATTCATTTCTTAATTACAGTCCAG 1869

QY	564	serlyS-----	GlUGlUGlULySglULeuValGlnSerPheGluLeuLySleAla	581
Db	1870	GGAAAAAGGGCTGAGAGAAAGACATCATGATGGCTTGTGACCAGAAAGAAATGAAACAGATG	1929	
QY	582	GlULeuGluGluGlnLLeuSerValLyAlaLys-----	Asn	593
Db	1930	GAGGGTGGGGAAATGCTCCCAATTAAATGAAAGTATTTCTTGAAGATACAGGCCAAAT	1989	
QY	594	LeuGluMetValThrAsnSerArgLuhIsSerIleAlaAla-----	GlUValGlnThr	611
Db	1990	TTTCCCTTAATGCCAAAT---GAGAGAGACACTCTTCAGCAGCTTGAAAGAAACAGCGC	2046	
QY	612	AspValGluLySglULeuValArgLySglULeuSerValLeuGlyAspSerGlyTyrAsn	631	
Db	2047	AGCACTGAACATCAAAAGTAGAAGAACATCTGAGGAAATATCTTTAAATGATGCTGAGTA---	2103	
QY	632	AlaSerAsnSerAspLeuGlnAspSerValAlaGlyLyValArg-----	646	
Db	2104	-----GAATTAAATTCACAAAGCAGAGTGATGATTAATCCCTTTCGTGTA	2151	
QY	647	-----LeuSerSerSerHisAspGlySylIleGlu-----	656	
Db	2152	CCAGATATTGGTCACTGTCATGATCAGATGATTGGAAAGCTTAAAAAGTCAATTTTGGAG	2211	
QY	657	-----HisArgLySmeLeuGluGlnLys---	664	
Db	2212	CTCGAGCTAAACCTTCATTAAGGACACAAAGAAATCTATGAGAAATTTATGATGAGAAAGCT	2271	
QY	665	-----IleValAspLeuGluGluPheIleGluLeuLeuAsnLysLysSerGluAsnAsp	682	
Db	2272	AAGAAATATTAGCAACCTAAACCAGATGATTGGAGATTAAAGAAAAAGCTGACACAAC	2331	
QY	683	LySglnLys-----SerSerGluLysPheMetGluSerIleGluLeuLys	698	
Db	2332	AGCACTGCATTCACCTCTTGTGCTGAAAGAAAGACCAAGCTTCTCTC---CAGGTGAAG	2388	
QY	699	GlUAlaIleMetAlaGluLyLeuAlaAsnAla---LeuGluGluLeuAlaLeu-----	714	
Db	2389	GAACTTACATGTGTAAACAGAAATTGAGGGCTCAGGTAAAGCAACTGGAATGACCTTCCA	2448	
QY	715	-----MetArgAspAsnPheAspAsnIleIle	723	
Db	2449	GAAGCAGAAAGCAAAAGAAAGACTTATTATGAAACCAACCTGCCATGACAACTCGCTC	2508	
QY	724	LeuGluAsn-----GluThr	728	
Db	2509	ACTGAAACGATCCATAGTCTCAGCATAGAACCAATCTAAAGATGTGAAATTTGAAGTT	2568	
QY	729	LeuLysArgLuhIleAlaAspLeuLys-----Arg	738	
Db	2569	TTTACGAATGAACGTGATGATGTGCAGCTTCAGTTTCTGACAGAGTACCTGTATAGA	2628	
QY	739	SerLeuLySglULeuSngLuhThrAsnGluPheGluIleLeuGlnLysLysLuhThGlnLys	758	
Db	2629	AGCTGCGAAAGCCAGCTGCAAAATTAAGAAAGTGAAGCTTGAGGGGGCAGAAAGCTGT	2688	
QY	759	GluHisGluAlaGlnLeuIleHisGluIleGlySerLeu-----LysLyLeuValGlu	776	
Db	2689	AGGCATATCTCAAGTAAAGTAGAGAACAGTGTCCAGGCTCTTTTCCACAGAAAGAACTTGA	2748	
QY	777	AsnAlaGluMetTyrAsnGlnAsnLeuGluGlu-----AspLeuGluThThlySerThrLys	794	
Db	2749	ATTAACAAAATATGATCAGCTCTTACTTAAGAAAGAAAGAGAGATGTGAAACCTCCACAA	2808	
QY	795	LeuLeuLySglULeuGlnIleGlnLeuAlaGlu-----	805	
Db	2809	ACCATCGAGAGAGATCAACAATGACAGAAATCACACTTATGATGACTGAGAAATG	2868	
QY	805	-----	805	
Db	2869	GTTTCAGCTTAATGAGAGAAAGTTTCTCTGGGTGTGAATTAATGACCTTAAAGAACAG	2928	

QY	806	-----LeuAglvYvAglAlaAspAsnLeuGlnIlysvAlaAgnPheAspLeuSer	823
DB	2929	CTAAATTATTATTCAGAGCTGAGAGAACCAAAAAAGCGAGCTGGAAGAAATTAATGA	2988
QY	824	ValSerMetGlyAspSerGlnIlyLeuGlyGlnIlePheGlnLeuGlyGlnSer---	842
DB	2989	GTTCCTCTGGC-----CTTAAACAAATATTAT	3015
QY	843	-----LeuSerAspAlaGluAlaValThrArg--AspAlaGlnIlyGlnCysSerPhe	859
DB	3016	GATGAGATGAGCCCGACGACGACAATAAATGAAGAAACTTCAGCATGAATTGACCTT	3075
QY	860	LeuArgSerGluAsnLeuGlnLeuGlyGlnCysMet-----	871
DB	3076	CTGAAGAAAGAAATGAGCACAGAAAGAAAGAAAGCTCCAGCAGCTCTTATTACAGAAAG	3135
QY	872	-----GluAspThrSerAsnTyrValAsnGlnIly	881
DB	3136	GAGCTTCTGCAAAGAGTCATGAATTTGAGAGAAAGATTAAGCAACTTGAAGATGAATCT	3195
QY	882	GluIlyValAlaIleSerLeuPheGlnIlyS-----GlnLeuGlnThrGlnIlySerAsn	898
DB	3196	AAGAAAGAAATCCCACTCAGTGACACTGAGAGGGAGAAAGTGAAGAAAGATTAAGAAAC	3255
QY	899	TyrIlysvMetGluAlaAspLeuGlnIlyGlnLeuGlnSerAlaPheAsnGlnIleAsn	918
DB	3256	AAAGAAATCTCAGAA-----AAATGTGTCACTTCTTAAGTGCCAAGAAATAGAA	3303
QY	919	---TyrLeuAsnGlnIlyLeuAlaGlnIlyS-----ValProArgAsp	931
DB	3304	ATTATTTTAAACAGACAAATATCTGAGAAAGAGTGAATCAACATATTAAGAGAGAT	3363
QY	932	LeuLeuSerArgValGlnLeuGlnIlysvValSerGlnPheSerIlyGlnLeuGlnIlyS	951
DB	3364	TTGGAAGAAAGCTGGCAGCTGGAAGAGCAATTCAGAGCTGTGCTCAACAGATGAATCAG	3423
QY	952	AlaLeuGlnIlyIlysvAsnAlaLeuGlnAsnGlnValThrCysLeuSerGlnIlyPhe	971
DB	3424	ACCTTGCAAGATTAACAA-----	3441
QY	972	LeuProAsnGlnValGlnCysLeuIlyAsnGlnIleSerIlyS-----	985
DB	3442	-----AACCAATATGATTTGCTCCAGCAAAATCAGTGAACCAAGCAATTATCCAG	3495
QY	986	-----AlaSerGlnIlyIleMetLeuLeuIlyGln	995
DB	3496	AACTTAATCACAAATACACAGGATGCAAGTATGGGAGCTCCGTAGCATCTGTAAGGAA	3555
QY	996	GlnIlyGlnIlyIleSerAlaSerIleIleSerIlyGlnIlyIleMetGlnIlyGlnSer	1015
DB	3556	ACAGTGTGATTAAGTCCACTTGTACAGGTAGTGAACCTGAAACCAAGAACTAGAA	3615
QY	1016	GlnGlnIlyIleLeuGlnLeuThrAspGlnValThrIleThrGlnSerIlysvAlaGln-----	1033
DB	3616	GAAAGATATACGGCCCTTGAAAGAAAGAGCAACTTCAAAGAAAGCTACAGAGGCC	3675
QY	1034	-----GlnThrGlnIlyGlnIlyIlyLeu-----	1040
DB	3676	TTAACTTCCCGCAAGGCATTTCTTAAAAAGCACAGGAGAAAGAAAGACATCTCAGGGAG	3735
QY	1041	GluMetIlysvIleMetHisAspAspLeuPheGlnIlysvTyrIleArgAsnIlysvSerGlnAla	1060
DB	3736	GAGCTAAAGCAACAGAAAGATGAC-----TATATCGCTTGCAAGCAAGCTT	3783
QY	1061	GluAspLeuLeuArgGlnMetGlnAsnLeuIlysvIlyThrMetGlnSerValGlnValIlyS	1080
DB	3784	GATGAGCAAAACCAAGAAATGAGAAATATGAGAACCAAGCTTAAGCAACTCAATTCAA	3843
QY	1081	IleAlaAspThrIlysvHisGlnLeuGlnIlyThrIleArgAspIlysvGlnIleLeuHis	1100
DB	3844	GTAAGGGAATCC-----	3855
QY	1101	GluIlysvIlysvPhePheGlnAlaMetGlnIleThrIlePheProIleThrProLeuSerAsp	1120

Db	3856	-----	ATAGACCGA	3864
OY	1121	SerLeuProPserSerLeuValGluGluAenSerGlnAspProIleGluIleAsnAsp	1140	
Db	3865	AAACTCCCAAGCAGACACGAGGAAATCGTGTCTTCACCTCA-----GCT	3912	
OY	1141	TyrHisAsnLeuIleAlaLeuAlaThrGluArgAsnSerIleMetValCysLeuGluThr	1160	
Db	3913	TTAGAGAACCTTTATTTCAAACCCACAGACGATCATCACCACCTGTTTAGAGTCC	3972	
OY	1161	-----GluArgAsnSerLeuLys-----Glu	1167	
Db	3973	AACTGTGCCCGAGCTGGCTTCTCATTTCTGAAGATGGAGTGTCTCGAGGGCGGA	4032	
OY	1168	GlnValIleAspLeuAsnThrGlnLeuGlnSerLeuGlnAlaGlnSerIleGlu-----	1185	
Db	4033	TCTGTGCCACAGATTAAAGCCAGCTGAAAGAAATAGAGCTCGAAGAAATGATGATTGAA	4092	
OY	1186	-----LysSerAspLeuGlnLysProLysGlnAsp-----Leu	1196	
Db	4093	TTGAAGATTAGTCTACAAACAAGTAGAGCTTACTATAAAATCAGAGAGGTATTTCAGTTA	4152	
OY	1197	GluGluGluGluValLysLeuLeuLeuGluMetGluLeuLeuLysGlyHisLeuThrAsp	1216	
Db	4153	CAAGGCGAGATTAAATTAACAGGGTTTGAATAATCGAGACTCTTAAGACAGTATCCATGAA	4212	
OY	1217	SerGlnLeuSerIleGluLysLeuGlnLeuGlnAsnLeuGluValThrGluLysLeuGln	1236	
Db	4213	GCTGAAGTCCATGCCGAAGCCTTGAG-----CAGAAATTTGAA	4251	
OY	1237	ThrLeuGlnGluGluMetLysAsnIleThrIleGluArgAsnGluLeuGlnThrAsnAsp	1256	
Db	4252	AGACGCCAATCATCAATATTGCTGCTAGAACATCTAAGA---GAATTGCAACCTAACTG	4308	
OY	1257	GluAspLeuLysAlaGluHisAspSerLeuLysGlnAspLeuSerGlnAsnIleGluGln	1276	
Db	4309	GATGAACCTGCAMAACTCATAGCAAAAAGAGAGAGAGCTTAGCTACTTTCTGCACAA	4368	
OY	1277	SerIleGluThrGlnAspGluLeuArgAlaIaGlnGluGluLeuArgGluGlnIleGln	1296	
Db	4369	CTTAGTGGAAGAAGACGACCTCTCTCTAAATACAGACAGATATATGAAACAAGAAAT	4428	
OY	1297	LeuValAspSerPheArgGlnGlnLeuLeuAspCysSerValGlyIleSerSerProAsn	1316	
Db	4429	TTAATTAGGCTCTGCATACACAGCTA-----GAAATGCCAACCAAGAG	4473	
OY	1317	HisAspAlaValAlaAsnGlnGluLysValSerLeuGluGluValAsnSerLeuGlnSer	1336	
Db	4474	CATATGAGAGGATTAACACACTACAGCTGGAACCTTGTGAATGAGCAAAAAACGAA	4533	
OY	1337	GluMetLeuArgGlyGluArgAspGluLeuGlnThrSerCysLys-----AlaLeu	1353	
Db	4534	GAGATTGGAGAAAGAGTAGAGCAAGCAACAATCAAGAGAACTGCCAAGCTGCCCTT	4593	
OY	1354	ValSerGluLeuGluLeuLeuArgAlaHisValLysSerValGluGlyGlu-----	1370	
Db	4594	ATTTCGCCAAGAAAGACCTAAAGAAAAC---AAAAGCTCCAAAGGAATGTCTTGG	4650	
OY	1371	-----AsnLeuGlu---IleThrLysLysLeuAsnGlyLeuGluLysGlnIleLeu	1386	
Db	4651	GCCAGAGGTACATTGAACGTCTACACCAAGCTCTGGCAGATGTGGAAGCAAGTTCTT	4710	
OY	1387	GlyLysSerGluGluSerGluValLeuLysSerMetLeuGlnAsnLeuLysGlnAspAsn	1406	
Db	4711	GCTCAAAATTAAGAAAAAGATACGCTTTAGGAAGCTTAGCTCTTCTTCAAGAAAGAAAG	4770	
OY	1407	AsnLys-----LeuLysGlnGlnAlaGluGluTyrSer	1417	
Db	4771	GACAAACTCATTAACGAATGACAGGCTTATTATGAAATACAGAGCTTCACAGAGCTCC	4830	
OY	1418	SerLysGluAsnGlnPheSerLeuGlnGluValPheSerGlySerGlnLysLeuValAsp	1437	

Db	4831	TGTGAAATCTTAAAACTGAGCTCTGAGAGGCTTCTTACTGAAGCAAGAAAAGTTAGTGAAG	4890
OY	1438	GUUUGUValLeuLysValAGlnLeuLysValaGlu-----GluArg	1452
Db	4891	GAATTTGATCTTTGAAAATCTTTCT--AAGATTGCAGAAAAGTACTAGTGGCAAGAAA	4947
OY	1453	LeuGluLeuLysAspArgAspTyr-PheGluLeuValGlnThrAlaAsnThr-----	1469
Db	4948	CACAAAGAGCTACAAAAAGACTATGAAATTCTTCTGCAGTCTCTATGAGAAATGTTAGTAAT	5007
OY	1470	-----AsnLeuValGlu-----	1473
Db	5008	GAAGCAGAAAAGATTTCAGCATGTGTGGAGCTGTGAGCAAGAAAACAAGACTGAT	5067
OY	1474	GlyLysLeu-----GluThrProLeuGlnAlaAspHisGlu	1485
Db	5068	GGCAAGTTTAAAGACACAGAGGCAAAACAAGAGAGACAGAAAAGCAGTTGGCAGAAAGCT	5127
OY	1486	GluAspSerIleAspArgArgSerGluGluMet-----	1496
Db	5128	GAGCAGAGAAATGAGAGAAATGAAAGAAAAGATGAGAAAGTTTGCTAAATCTTAAACAGCAG	5187
OY	1497	-----GluLeuValLeuGly	1502
Db	5188	AAAACTCTAGCTGGAAGAAAGAGATGACCGGCTTAGGCGAAGGGGCACTCTGCAGGA	5247
OY	1503	GluLys-----LeuGluArgAsnGlnTyrLeuLeuGluArg	1514
Db	5248	GATACAGCTAAAGAGTGATAGGAAAACACTCTTTCTTCCCAATGCCAGCATGAAGAGAAAGAA	5307
OY	1515	LeuGlnGluGluLysLeuGluLeuSerAsnLysLeuGluLeuLeuGlnLysGluMetGlu	1534
Db	5308	CTTAAAAAGCGCTCAAAAATGGAG-----TATGAAACCTTTCTTAAAGATTTGAG	5355
OY	1535	ThrSerValLeuLeuLysAspAspLeuGlnGlnLysLeuLysLeu-----Leu	1551
Db	5356	TCTTTAATGTGTGAGAAAGACTCTCTAAGTGAGAGAGGTTCAAGATTTAAAGCATCAGATA	5415
OY	1552	SerGluAsnIleIleLeuLysGluAsnIleAspThrThrLeuLysHisHisSerAspThr	1571
Db	5416	GAAGATATGATGTATTAACAAGACTTAACCTAGAGGCCACGAGAAAACATGATTAACCAAAACG	5475
OY	1572	GlnIleGlnLeuGlnLysThrGlnGln-----GluLeuGlnLeuAlaLysAsnLeu	1588
Db	5476	AATGTCACTGAGGGGAGACACAGCTCTATACCAAGTGAGACTAAGAGCAAGCACTCTCG	5535
OY	1589	AlaIleAlaIleAspSerAspAsnCysProIleThrGlnGluLysGluThrSerAlaAspCys	1608
Db	5536	AGTATGAGCACAAAGACTTACATG-----TCGAATCGGTTCCATCAGCAAGAGAGT	5586
OY	1609	ValHisProLeuGlnGluLysIleLeuLeuLeuThrGluGlnLeuLysGlnLysThrAsn	1628
Db	5587	GCCAAACCTCTGTAAATGAAGATTCAGCTCAATGATGAATTAAT-----	5634
OY	1629	GluGlnGluLysLeuLeuHisGluLysAsnGlnLeuGlnIleGlnIleValGluLeuLys	1648
Db	5635	-----AACTACTTACAGACAGTTGAT---CAGCTCTCAA	5664
OY	1649	CysGluValGlnHisLeuMetLysSerMetIleGluSerLysSerSerLeuGlnSerLeu	1668
Db	5665	GAAGAAGATTCTGTGATTAGAGGAGAGCAAGACAAAGAAATTTAGCCGACCTTTA	5724
OY	1669	GlnHisGluLysHisAspThrGlnGlnGlnIleLeuAlaLeuLysGlnGlnMetGlnVal	1688
Db	5725	GAAGATAGAAAATAATCCTTACTGAGTCAATATTCACAAAGAGAGTGCTGAATTAATAAATG	5784
OY	1689	ValThrGlnGluLysLysGlnLeu-----GlnGlnThrHisGlnHisLeuThr	1704
Db	5785	CTTCAGAGAGAGTAACCAAAATGAACCTGTAAATCAGCAAAATCCAGAGAAAGATC---	5841
OY	1705	AlaGluValAlaSerHisLeuLysGluValAsnIleGluLeuGlyLeuAsnPhenylSerGlnVala	1724
Db	5842	TTCCAGATTTTCAAACTTAAAGAGACAGCAGAA-----	5874

OY	1725	glnghllyrthrthlysglucglnCysleuleuengluamlysgluLeuGlulnSer	1744
Db	5875	GAAGAGAAAGATGATTTGGAAAGAGCGCTTATGATCAATTAAGCAGAACTTAATGGAAGC	5934
OY	1745	glnhlsargleuGlnCysglulilegluIuuewelysSerleuLyAspLygluSer	1764
Db	5935	-----ATTGGGAATTACTGTCTCGAGATGTTTACAGATGCCCAATA	5973
OY	1765	AlaleuGluThrleuLygluSerGlnGlnysValileanLeuAnGlnlUmetGlu	1784
Db	5974	AAAAATGAGCTATTG---GAATCTGAATGAAG-----AACCTTAAAAAG-----	6015
OY	1785	MetValMetleuGluMetGluGluLeuLyAsnSerGlnArgThrValilealGluArg	1804
Db	6016	-----TGCTGAGTGAAATTTGAGAAAGAAAGACGAGCTTATGCAAGAAAAA	6063
OY	1805	AspGlnleuGlnAspAspLeuArgGluSerValGluMetSerlleGlu-----	1820
Db	6064	ACTAAGGTGGATCGAATAATCGAAAGAAATTTGGAGAAAAATACAGAGTCTCAGAA	6123
OY	1821	-----ThrGlnAspAspLeuArgLyAsnIleGlnuValaleuGlnGlnLyAsp	1837
Db	6124	GAACCCGGAATTAAGAGCCATGCAAGAGAACTTCGGAAGCTGTTAAAGAAAAACAACA	6183
OY	1838	LyAsValGlnGluLeuThrSerGlnIleSerValleuGlnGlnLyIleSerleuGln	1857
Db	6184	GAAGTAAAGCAGCTACAGAGAGCTGCATCAGGTATCAAGAGAAATTAAGTGCCTGGAG	6243
OY	1858	AsnGlnMetleuTyrrAsnValAlaThrValIys-----GluThrLeuSer	1872
Db	6244	AGA-----ACTGTAAAGCTCTAGAAATTTGTTCAAACTGAATCT	6282
OY	1873	GluArgAspAspLeuAsnGlnSerIlyeGlnIstleuPheSerGluIleGlu-----	1889
Db	6283	CAAAAA---GATTTGAAATATACCAAGAAATCTGCTCAAGCAGTTGAACCCGCAAA	6339
OY	1889	-----	1889
Db	6340	AAGGCACAGAGAAATTAGTACGTTCAAAGCTCTGATGATGACACTCAAGTGAAGCA	6399
OY	1890	-----ThrIleuSerleuSerleuLygluLysgluPheAlaleuGlnAlaGluLyS	1907
Db	6400	GCAAGGCTCTAGACAGACAATCTCAAGTTGAAAAAGCACTTCAAGTCAATAAAGAAATCA	6459
OY	1908	AspLyAsIaAspAlaAlaArgLyThrIleAspIleThrGluLySIlleSerAsnIleGlu	1927
Db	6460	GTTTAAAAACCAGATGAAACAAAGAGATGAAATCTTGACGCAAGATCGGAACAGCGCAGA	6519
OY	1928	GluGlnleuLeuGlnGlnAlaThrAsnleuLysgluThrleuTyrrGluArgGluSerleu	1947
Db	6520	GAGAAAGCACTCGAAAGAGAGAGACAGATATGCAAGAGAAACTG-----GATGCTTTG	6570
OY	1948	IleGlnTylysgluGlnleuAlaLeuAsnThrGlnIstleuArgGluThrLeuLySer	1967
Db	6571	CGCAGAGAAAAAGTCCACTTGGAGAGACAAATTGGAGAGATTCAGGTTACTTTGAACAG	6630
OY	1968	LyAspLeuAlaleuGlyLyMetCgluGlnGluArgAspGluAlaIAsnLyValIle	1987
Db	6631	AAAGCAAGAAAGTTCACAGCACTTCAGGAAAACTTGACACTACTGTGACCCACCTTGA	6690
OY	1988	AlaleuThrGluLyMetSerSerleuGlnGlnIleAsnGluAsnValThrThrleu	2007
Db	6691	GCTTTACTTAAGAGCAATCTTCCCTCCAGATGATCTGTCAGAGGCGATATGATGAAGCT	6750
OY	2008	LysgluGluGlu-----GlyGluLysgluThrPheTyrrleu	2019
Db	6751	AAAGAAATGGAGAGAAAGATTAGATGATCGATTCAAGCAAAAGAAAGAAATTAAGATC	6810
OY	2020	Gln-----ArgProSerlysglnGlnSerSerSerGlnMetGlu	2032
Db	6811	AAAGAGATTAATTCAGTGTCTTAAGAGATCAACTTGAACGAGATGCTCATCATTAATGAA	6870

[illegible]


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; SEQ ID NO 163
; LENGTH: 10096
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-960-253-163

Alignment Scores:
Pred. No.: 1.8e-63      Length: 10096
Score: 1152.00         Matches: 740
Percent Similarity: 37.41%      Conservative: 563
Best Local Similarity: 21.25%    Mismatches: 1160
Query Match: 7.80%             Indels: 1022
DB: 10                      Gaps: 140

US-09-724-584-1 (1-2954) x US-09-960-253-163 (1-10096)

Qy      81 PheAlaTyGlyGlnThrSerSerGlyTyThrTyThrMetMetGlyThrProAsnSer 100
Db      465 TTCAGAGAGGACACTGAACTGAGGCAAA----- 494
Qy      101 LeuGlyIleIleProGlnAlaIleGlnGluValPheIleIleGlnGluIleProAsn 120
Db      495 -----AAACAATAGAAAACCTGAAACAGGAACTTAAAGC 530
Qy      121 ArgGluPheLeuLeuArgValSerTyMetGluIleTyArgGluThrValIleAspLeu 140
Db      531 TGTAAATGTGACTTGAAAGAACCAACAGCTGGCAGCTGCGAGTCTCTCTGTAAT 590
Qy      141 LeuCyAspAspArgArgLys-----LysProLeuGluIleArgGluAspPheAsn 157
Db      591 CCATCATATACACCAAAAATTTTACAACTCCACTCAACACCAAGTCATATATATAGT 650
Qy      158 ArgAsnValIleTyValAlaAspLeuThrGluGluLeuValMetValProGlnHisValIle 177
Db      651 GGTTCCAAGTAT--GAAGATCTAAAGAAAATATATTAAGAGCTTGA----- 698
Qy      178 GlnTrpIleLysLysGlyGluLysAsnArgHisTyGlyGluThrLysMetAsnAspHis 197
Db      699 -----GAAAGAAAACATTAGGCGAGAGGCTTAAAGCCTTGCAAGCT 740
Qy      198 SerSerArgSerHisThrIlePheArgMetIleValIleGluSerArgAsp-----ArgAsn 215
Db      741 AAAAAAGAGGCAACACTCTCCACAGCCACCATGATACACGCGAGACATGCGCGGCAAT 800
Qy      216 AspProThrAsnSerGlu--AsnCyAspGlyAlaValMetValSerHisLeuAsnLeu 234
Db      801 CAGGCTTCATCATCTGTCTTCATGCGAGCAAGAGAACCCCAAGTCATCTTCA-- 857
Qy      235 ValAspLeuAlaGlySerGluArgAlaSerGlnThrGlyAlaGluGlyValArgLeuLys 254
Db      858 -----TCATATCTCAAGAACT----- 875
Qy      255 GluGlyCyAsnIleAsnArgSerLeuPheIleLeuGlyGlnValIleLysLysLeuSer 274
Db      876 -----CCAATTAGAGAGATTTCTCT 896
Qy      275 AspGlyGlnAlaGlyGlyPheIleAsnTyArgAspSerLysLeuThr----- 290
Db      897 GCATCTTACTTTTCTGGGGAACCTAGAGGTGACTCCAAAGTCATCAACTTGGCAATAGAG 956
Qy      291 ---ArgIleLeuGlnAsnSerLeuGlyLysAsnAlaLysThrValIleIleCysThrIle 309
Db      957 AAAAGAGATGCTAATAGCAAGTTCTTGGCAATCTTAC----- 995
Qy      310 ThrProValSerPheAspGluThrLeuSerThrLeuGlnPheAlaSerThrAlaLysHis 329
Db      996 AGTCTCATCTTTTGAT-----CAATTAAAGCCAGCAATCAAG 1037
Qy      330 ValArgAsnThrProHisValAsnGluValLeuAspAspGluAlaLeuLeuLysArgTy 349
Db      1038 CTAGAGAAAC-----AAGATTATATAGTTG-----GAACTACGCGCTGCAAGAGCAAT 1082
Qy      350 ArgLysGluIle-----LeuAspLeuLysLysGlnLeuGlu----- 361
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Db      1083 GAAAAAGAAATGAAGCCAGTGAATAGTTTCAAGAACTCCAACTGAGAGAA 1142
Qy      362 ---AsnLeuGluSerSerSerGluThrTyAlaGlnAlaMetAlaLysGluGluIleThr 380
Db      1143 GCAAAAGTGAATTAATTGAAAAGAGATTTTGAACAAATGTAGGATGATCACTAGT 1202
Qy      381 GlnLeuLeuAlaGluIleLysGlnLeu-----HisLysGluArgGluAspArgIle 397
Db      1203 AGAACACAGCACCAATAGCAGCGGCTGCACCAAGTATCTGCACTTGGACAAAACTG 1262
Qy      398 TrpHisLeuThrAsnIleValAlaLaseSerGlnGluSerGlnGln----- 413
Db      1263 AAAAAATTGACGGAGATTTGATGCTGCAGGACAAATGCAAGAAAGTCCAGATGTTCT 1322
Qy      414 ---AspGlnAlaGlyValLysArgLysArgValThrTrpAlaPro--GlyLysIleGln 431
Db      1323 CTGAAACAGAAAATTAAGAAAAGAAAGAGGTTTCAAGAGAGACTCTCCCGTCAACAG 1382
Qy      432 AsnSerLeuHisAlaSerGlyValSerAspPheAspMetLeuSerArgLeu--ProGlyAs 451
Db      1383 GCTTCTTCCAAACACTGACAGGAGTGCATCCAGATGAAGGCCAGACTCACCAGAG 1442
Qy      451 nPheSerLysLysAlaLysPheSerAspMetProSerPheProGluIleAspAspSerVa 471
Db      1443 TTACAGCAAG-----CCAAGAAAT 1460
Qy      471 LysThrGluPheSerAspPheAspAlaLeuSerMetCysAspSerAsnGlyIleAs 491
Db      1461 ATGCACAACGCTCTGCAGAGCTGAACCTGATTAACATCAGATCAGTAAACCAACAGCTAGAA 1520
Qy      491 PalGluThrProAsnLeuAlaSerLysValThrHisArgGluLysThrSerLeuHisGlnSe 511
Db      1521 AACAAATTGGAAGACTTAAAGCAAAAGTTGTGC--AGACTGAACAGGGCTTCCAGCGAG 1579
Qy      511 MetIleAspPheGlnIleSerAspSerValGlnPheHisAspSerSerLysGluAs 531
Db      1580 TCAGATCAAGAGAGATAGACCTGAGAGAGAACATGAG--GAAATGAAAGAGAAA 1633
Qy      531 nGlnLeuGlnIleuProLysAspSerGlyAspMetAlaGluCyAspArgLysAspSerh 551
Db      1634 CAACCTCTTAAGAGTCACTCTGCAAAAGCCAGAAAGTCTGCCACTGAGAGCGCA 1693
Qy      551 eGluLysGluIleThrSerLeuGlnGlnGlnLeuGlnSerLysGluGluLysGlu 571
Db      1694 ACTCAAGAACATCAAAACAGTGTTAATCAAGCCAGAAATTTTGCAAGAAATGAAGC 1753
Qy      571 uLeuValGlnSerPheGluLeuLysIleAlaGluLeuGluGlnLeuSerValLysAl 591
Db      1754 GAAGATACCTCTCAGAGAAACATGTTAAGATCTTCAAGAAAATTA----- 1802
Qy      591 aLysAsnLeuGluMetValThrAsnSerArgGluHisSerIle----- 605
Db      1803 -----AATCAGCAAGAAAACCTTGAATAAGAAAACCTGAA 1840
Qy      606 -----AsnAlaGluValGlnThrAspValGluLysGluValAlaArgLysG 621
Db      1841 GCTTGCTGTGCTGCTGTAAGAAAGCAGCGAGATTTGTTCAAGCCTTTTGAAAGAAAG 1900
Qy      621 uMetSerValLeuGluLysSerSerGlyTyArgAlaLaseSerAspLeuGlnAspSerSe 641
Db      1901 A-----GAACATCACTTGAACAACTTAATATAGTTAAGCAAGACAGCA 1945
Qy      641 rValAspGlyLysArgLeuSerSerSerHisAspGluCyIleGluHisArgLysMetLe 661
Db      1946 GAAAGAGTCAAAAGCCTTGCTGAGTGT-----TT 1975
Qy      661 uGluGlnLysIleValAspLeuGluGluPheIleGluAsnLeuAsnLys----- 677
Db      1976 AGAGTTAAAGAAAGAAATGAAGAAATGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2035
Qy      678 LysSerGluAsnAspLys-----GlnLysSerSerGluGlnAspPheMetGluSe 694
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Db 2036 GAAAAAGTAAACGAAAACTTTAACTCAGATGGAATCAGAAAAAGAAAACTTGACAG 2095
 QY 694 T-----11leuLeuCys----- 698
 Db 2096 TAAATTAATCACTTGGAACCTTGCTCTAAGACACAGCAATAAATAAGTCAATGAAACAA 2155
 QY 699 -----GluAla11eMetAlaGluLysAlaAsnAlaLeuGluLeuAlaLeuMe 715
 Db 2156 CGAGAGAGTAAAGAACGCTGAGATGACAGAGAAAACTTAAGTGTCCGAGATCAGAAACCT 2215
 QY 715 LArgAspAsnPhaAspAsn11e1leuGluAsnGluThrLeuLysArgGlu11eAlaAs 735
 Db 2216 TCACAGACTGTTAACAGTAAGTAAGTAGAGAGTAGAGACCAGAACTTACCTTAATATGA 2275
 QY 735 pLeuGluArgSer----- 739
 Db 2276 GCTACACACAGAAAGCTGAGTTCTCAGATCAGAAACATCAGAGAAATACAAAAATATGTC 2335
 QY 740 -LeuLysGluAsnGluLeuThrArgGluPheGlu11eLeuGluLysGluThrGlnLysGlu 759
 Db 2336 TTGGAAAGACTTCTCAGCTTACTGCGCAAGTTGAAGATCTA-----GA 2377
 QY 759 uH1sgLualag11eLeu11eH1sgL11eGlySerLeuLysLysLeuValGluAsnAlaG 779
 Db 2378 ACACAAAGCTTCAGTTACTGTCA-----AATGAAATTAATGACAAAGACCG 2422
 QY 779 uMetLysArgGluAsnLeuGluLysLeuGluThrLysThrLysLeuLysGluGlu 799
 Db 2423 GTGCTTAC--CAAGACTTGTCATGCCAAATGAGAGCCTCAGAGATCTGTCTAAATCCAA 2479
 QY 799 ngL11eGlnLeu----- 803
 Db 2480 AGATGCTCTCTCTGTGTACAAATGAATCATCAGAGAGCTTTGGCTTTTGATCAGCA 2539
 QY 803 ----- 803
 Db 2540 GCCTGCCATGATCATCTCTTGTCAATATTAATTTGAGAAACAAGAGATGCCCTTCAGA 2599
 QY 804 ----A1aGluLeuArgLysArgAlaAspAsn-----LeuGluLys 815
 Db 2600 GAGAGAGTAAATGCTGTTTAGAAGCAGACCAAGTCCGAAAAATTCGCCATCTCTCAAAA 2659
 QY 815 sLysVal1aArgAsnPhaAspLeuSerValSerMet-----GlyAspSerGlu 830
 Db 2660 TAGAGTTGATCACTCAATGATTTTCATTAAGTCTCAAAAACAGATGACATCAGACTGCA 2719
 QY 830 uLysLeuCysGluGlu11ePheGluLeuLysGluSerLeuSerAspAlaGluAlaValTh 850
 Db 2720 AAAAGCAGTGTGAAGGTTGTGCTCAATCAAGAGAGAAATAGAA-----GAAATCTCAT 2773
 QY 850 rArgAspAlaGluLysGluCysSerPheLeuArgSerGluAsnLeuGluLeuLysGluLys 870
 Db 2774 GAAACAGACAGACAGATGATCAAAAGTTTGTGCTCAAAACAGTCAAGCCATTAGTAAGTT 2833
 QY 870 sMetGluAspThrSerAsnTPPYrAsn-----Glu 880
 Db 2834 ACAGAGAAACACTTGTCTCAACAGAAATGTTGTCTGAAACCTTAAGTGCCTTGAGAA 2893
 QY 880 nLysGluLysAla11eSerLeuPheGluLysGluLeuGluThrGluLysSerAsnTPPYr 900
 Db 2894 CAAGAGAAAAAGGCTGCAACTTTTAATGATGATAGAAAGCTGAGGAGAGAGATTC 2953
 QY 900 sLysMetGlu-----AlaAspLeuGlnLysGluLeuGln----- 911
 Db 2954 AGAATTAATAAAAAAGAGACACATCTACTGGAAGACCTCTTAAGAGAGCTACCAACTTTATC 3013
 QY 912 -----SerAl 913
 Db 3014 CGAAACCTTAAGCTTGAGAAAGAAAGAAATGATTCATCTTCTTAATAAAGAGCA 3073
 QY 913 aPheAsnGlu11eAsnTPPYrLeuAsnGluLeuLeu-----AlaGlyLys 927
 Db 3074 AATTAAGAGAGCTGACCCAGAGAGATGGAGCTCTTAAGAAATTAATGATCTCTTAATCA 3133

QY 927 sValProArgAspLeuLeuSerArgVal-----GluLeuGlu 939
 Db 3134 AGAGAGATGAGAACTTAATTCAGAAAAAGTGAAGTTTGCAAACTATATAGATGAAGAGCA 3193
 QY 939 uLysLysValSerGluPheSerLeuGlnLeuGlu----- 950
 Db 3194 GAAAAACATTTCAAGATTATCTGATCAGTACAGCAAGAAAACTTATTTACTACAAAG 3253
 QY 951 -----LysAlaLeuGluGlu 955
 Db 3254 ATGTAAGAAACCGGAATGCATATGAGATCTTATGCAAAATATCAAGACGACAGCA 3313
 QY 955 uLysAsnAla-----LeuGluAsnGluValThrCysLeuSerGluTPPYrLysPh 971
 Db 3314 AAGAAATTTCTAAATTAGATCTTGCTTAAATGAATGCACTAGTCTTTGTGAAAAATAGG-- 3371
 QY 971 eLeuProAsnGluValGluCysLeuLysAsnGlu11eSerLysAlaSerGluGluLeuMe 991
 Db 3372 ----AAATATAGTTGGAACAGCTTAAGAGACATTTGCACAAAGAACACCAAGAAATTCCT 3427
 QY 991 tLeu---LeuLysGlnGluGluGluH1sSerAlaSer11e1eSerLysGlnGlu11e1 1010
 Db 3428 AACAAATTAACCAATTTGCTGAAGAAAGAAATCAGAAATCTGATGAGAGTTGAGACAGT 3487
 QY 1010 eMetGln-----GluGlnSerGlu----- 1016
 Db 3488 GCAGCAAGCTTGAGATCTGATGACAGATACCAAAACAATTTTAAGAGCGAGCTGC 3547
 QY 1017 -----Gln11eLeuGlnLeuThrAspGluValThr11eThrGlnSerLysVal 1032
 Db 3548 TGGTTTAAAGCAAAATATCATGACTTTAAAGAAAGAACAAATATGCAAAAGCAAGT 3607
 QY 1032 1-----GlnGlnThrGluGluGluGlnTPPYrLeuGluMetLysLysMetHisAsp-- 1047
 Db 3608 TAATGACTTATTAACAAGATGAAGAACGCTGATGAAGTAAAGCTTAACATGATGATG 3667
 QY 1048 ---AspLeuPheGluLysTPPYr11eArgAsnLysSerGluAlaGluAspLeuLeuArgGlu 1066
 Db 3668 TCAAATCTAGATCAACAACCAATTAAGAACTCTGTGAAGAAAGAGAGAGTGAAGAAA 3727
 QY 1066 uMetGluAsnLeuLysGluThrMetGlu----- 1075
 Db 3728 TCATGTAATTTTAAACCTCAGATGATCTTGAAGTTAAAGAAATTTCTAGATAGTTA 3787
 QY 1076 -----SerValGluValLys11eAlaAspThrLysH1sgL11eLeuGluGlu 1090
 Db 3788 TAATGCCAGTTGTGTCATTAAGATGATGCTTAAGAAATTAAGAAATTAAGAAATTCAGCA 3847
 QY 1090 uThr11eArgAspLysGluGlnLeuLeuH1sgL11eLysLysTPPYrPhePheGluAlaMetGlu 1110
 Db 3848 AAGTGAAGAGAGAGAGAGAGGCTGCGCATGAA-----TTACA 3886
 QY 1110 nThr11ePhePro11eThrProLeuSerAspSerLeuProProSerLysLeuValGluGlu 1130
 Db 3887 GACAAATTT-----AGAGCAATCTTGAACACGACAAATTTCCAAAGACAT 3928
 QY 1130 yAsnSerGlnAspPro11eGlu11eAsnAspTPPYr----- 1141
 Db 3929 GCAGTCACAAGAAATTAAGTGCCTTAAAGACGTGTAATATAGATGCGGAAGAAAGATATAT 3988
 QY 1142 -----HisAsnLeu11eAlaLeuAlaThrGluArgAsnAsn11eMetValCysLe 1158
 Db 3989 TTCAGGGCTCATGAGTTGTCAACAAGTCAAAAACGACATGACACACTTCAGTGTCTCTCT 4048
 QY 1158 uGluThrGluArgAsnSerLeuLysGluGluVal11eAspLeuAsnThrGlnLeuGlnSe 1178
 Db 4049 GCAAAACAACATGAACAAGCTGAATGAG-----CTAGCAAAATATGTGGAAT 4096
 QY 1178 rLeuGlnAlaGlnSer11eGlu-----LysSerAspLeuGlu 1190
 Db 4097 ACTGAGAGGCTGAAGATGAACCTGTAAGCTGATGATGATCAAGTCAAGATGAT 4156

Oy	1190	nlvAeprolvsglnAapleuIngluIyGlvAlvalylsleuLeuIngluMetGluLeuLe	1210
Db	4157	CACAGCAACTAGAAATATGCGAGAAAGATGAGGAAACTTAATAATGAAATAATTT	4216
Oy	1210	ulvAgly-----	1212
Db	4217	AAATGATGACAGTGGCTTCTTCATCGTGAATTAAGTGAAGACATACCAGAGGTGAATT	4276
Oy	1212	-----	1212
Db	4277	TGGTGAACACCAATGAACAGCACCCCTGTGCTTTGGCTCCATTTGACGAGATTAATTC	4336
Oy	1213	-----HisleuThraPseSerGlnLeuSerileGluylsleuIngluInleuIngl	1230
Db	4337	CTACAGACACTTGACA-----TTGTGACAGCAAAAGCTCAAAATGCACTTTGGCGA	4387
Oy	1230	uValThrGluylsleuInThrIrrleuIngluIngluMetIlyAsnIleThrIleGluAga	1250
Db	4388	ATTGCAAGAGAAATTTTATCTTTACAAAGTGAAACACAAATTTTACATGATCAGCACTG	4447
Oy	1250	ngluIngluInThraPsePheGluAapleuIlyAlaGluHisAapserLeuylsGlnAple	1270
Db	4448	TCAGATGAGCTTAATAATGTCAGACCTCAACACTTAATGATCATTAAAG-----	4499
Oy	1270	uSerGluAsnIleGluInserIleGluThrGlnApsGluLeuAAlaGlnGluI	1290
Db	4500	-GCCGAAATTTGGCTTGTC-----ACGAATCTGAGAAACTTTCAAGGTGA	4546
Oy	1290	uLeuAArgGluInlysgInleuValAapSerPheArgIngluInleuAapCySserva	1310
Db	4547	CTTGGTGAAGAGATGACAGCTG-----GGCTTGAGAGAGGGCTGCTTCATCCCTGTC	4600
Oy	1310	IGlYIleSerSerProAsnHisAapAlaValAlaAsnIngluIlyValSerLeuGlyI	1330
Db	4601	ATCCTCTGTGTGCTGCTGACAGCTCACTGACTTAAG-----AGTTGGGAGA	4645
Oy	1330	uValAsnSerleuInserGluMetLeuAArgIyGluAArgGluIngluInThraSerCy	1350
Db	4646	C---TCCTCTTTTACAGAGCTCTTTTGAA-----CAGACAGAGAGA	4684
Oy	1350	AlvalAleuValSerGluLeuGlu-----	1358
Db	4685	TATGCTCTTTTGAAGTAATTTAGAGGGGCTTTACGAAACCAAGTCAGCTAGATGA	4744
Oy	1359	-----LeuLeuAArgAlaHisValIlySservaIleGluIyGluAAsnGluI	1374
Db	4745	AGTATTTTGCAGCACTGTCAGACCTTAATGACTCATTAAGGCCCAAAATTTGGCTT	4804
Oy	1374	eThrIlyslsleuAsnGlyleuGluIyGluIleleuGlylsSerGlu-----Gl	1391
Db	4805	GTCAAACGAATGTGAAGAACTTTCAAGAGTCACTGTGTGAAGATGACAGCTGGGCTTGA	4864
Oy	1391	uSerGluValleuIySserMetLeuGluAsnleuIySgluAspAsnAsnIlysls--	1410
Db	4865	GGAGGGGCTGCTTCATCCCTGATCCTCTGTGTGCTTCAAGCACTTAAGCTTACGACG	4924
Oy	1411	-----GluGlnAlaGluIyTySer-----	1417
Db	4925	TTTGGGAGACTTCCTCTTTACAGAGCTCTTTTGAACAGACAGAGATATGCTCTTTT	4984
Oy	1418	-----SerIySgluAsnGlnPheSerleuIngluIyApe-----	1429
Db	4985	GAGTAATTTAGAAAGGCTTTGTTTTCAGCAACACAGTCAGCTGATGATGAATTTTTCGAG	5044
Oy	1430	-----SerIySerGlnIySleuA	1436
Db	5045	CAGTTCGAGAGAGAACTTGACCAAGAAAGAAACCCCTTCGGCCCAAGGAGGTGT	5104
Oy	1436	IApSpIlyLe-----GluValleuIyAlaGlnleuIySAlaIaGlnIyuar	1452
Db	5105	TGAAGAGCTTGAGTCCCTGTGAGAGGTATACCGGAGATCCCTTCAGAAAGCTTGAAGAGAA	5164
Oy	1452	gLeuIyIu-----IleIySAspAArgPtyrPheGluLeuValGlnThraIAs	1468

Db	5165	AATGGAAGTCAAGGGATTATGAAAAAATTCAAGAAATTCAAGAGCTTCAGACGTTATTAAAG	5224
Qy	1468	ntthrsnleuvalglu--glylsleugluthrproleuglnlaaaphisglu-----	1485
Db	5225	ttctgaaagcgaagacgcttgactgcctcttagaaccagatatttcacagaaatgaacactg	5284
Qy	1486	-gluapserileaspargargserglumetgluilelyvalleugllylylyle	1505
Db	5285	gcaacagaaagctgacaaagcgtgactcttgagatgagatcccaattggccgcgcaaaaagaa	5344
Qy	1505	ugluargasnltlyrleuleuglu-----argleuglnglulysleugl	1521
Db	5345	acagacggaaacactgtcacttgactggaagtagcagcagactccagctacagagctgcga	5404
Qy	1521	uleuseranysleugluileleuglnlyglumetgluthrservalileuleuylas	1541
Db	5405	cttaagttctgcg-----tctttgcttgccat	5431
Qy	1541	paapleuglnglnlylsleugluserleuleusergluasnilleuleuylgluaenil	1561
Db	5432	cgacacagaaagatgctattcaagcc-----cgaaatgagactg	5470
Qy	1561	eaapthrthreulyshishiseraerthrghlaiglnleuglnlys-----	1577
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Qy	1578	-----thrnglnglnleuglnleu-----ala	1586
Db	5531	tcagatttggatataaagatgctctgacagacactcaattacacttgagaaatattactga	5590
Qy	1586	aaunleuaillealalaseraspaenysproilethrnglnlylvgluthr-----	1604
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Qy	1613	-----gluclulyslleule	1618
Db	5711	ttctggtcttaattgcttggtaactatagatatttcctgggaatagagaaatattccatga	5770
Qy	1618	uleuthrglnleuuhisglnlyvrthrasnglulglnlyleuleuuhisglnlyvas	1638
Db	5771	ttctcaactcggggtaaaagacacatcaatagaaatttgatattacttcctgataga	5830
Qy	1638	ngluleuglulglnalaglnvalgluleuylsycgluvalglunihisleuwcetylserte	1658
Db	5831	ggaccgtgcacaga-----aaagttcaaaatttgccttaattgaaat	5869
Qy	1658	cilleugluseryserserleugluserleuglnhisgluuhynhisvaphrthrglngl	1678
Db	5870	gaagaaattgaactcgaatactc-----catttacacggagatga	5908
Qy	1678	nleuleuila-----leulysglnglnmetgluvalvalthrgl	1691
Db	5909	actaatatgacscaaaattgaacgatcatagatgaatttgaaaataattagttggcgaaacttaagaa	5968
Qy	1691	nglulysleuglueuglnglnlthrhisgluuhisleuthralagluvalasphhisleuyl	1711
Db	5969	agaaaaactcaaattttaactgaaaaaattggaaattattttcttgatcatcaccagagattact	6028
Qy	1711	agluasnilleglueu-----glyleuasnphelyaasnlylaagln--glnlysth	1728
Db	6029	ccagagactgaagaaacttgcgaagcctcaatttcgattttagaaatgcacatgaattaaatc	6088
Qy	1728	rthrysglulglnlscysleuleuaengluasnlys-----	1739
Db	6089	atcagctgaagaaatttgagagataatggcccaacagtgaaatgcacagctgaagagagatt	6148
Qy	1740	-----gluleuglulglnserglnhisvargleuglnlscysglu-----	1751

Db	6149	TCCTGATGTGGAAAATAGCTGAGTACAGATCGAGAAAGCTAGACTTGAACATGA	6208
Qy	1752	-----1legiugluleuMeLysSerLeuLysAspLysgluSeraleuGluThr	1768
Db	6209	AGCCCTTACCTCGAGGCGTGAAGTATGAGTATGTTCAACACAGAAAGCATGTTTAGAAA	6268
Qy	1768	rLeuLysgluSergluGlnLysValIle--AsnLeuasnGlnGluMetGluMetValMe	1787
Db	6269	AGACAAATAAAAATAGACAGAAAGGTATTGTCTGCTTGTAMAGAAAGAACTCTCAGTGTAC	6328
Qy	1787	rLeuGlnGluMetgluLeuLysAsnSerGlnArgThrValIleAlaGluArg-----	1804
Db	6339	AAGTAGAGAAACCGCTTCGTGGAGAAATTGATCTATGTCCAAAAAACCACGCGACT	6388
Qy	1805	-AspGlnLeuGlnAspAspLeuArgGluSerValGluMetSerIleGluThr-----	1821
Db	6389	GGATTAGCTTGTCTGAAAAATAGAGAAAAACACAA---GAGCTTGAGTCTATCAAG	6445
Qy	1822	-----GlnAspAspLeuArgLysAlaGlnGluAlaLe	1832
Db	6446	TGAGTGTCTCATTCATTCAGTGTGCGACAGGCGAGAGGTGAAGAAAAAGCGAACTCT	6505
Qy	1832	uGlnGlnGlnLysAspLysValGlnGlnLeuThrSerGlnIleSerValleuGlnGlnLys	1852
Db	6506	TCAGACTTGTCTCTCTGATGTGAGTACGTCTTAAACACAAATCTACTCTCCAGAAAA	6565
Qy	1852	sIleSerLeuLeuGlnAsnGlnMetLeuLysAsnValAlaThrValLysgluThrLeuSe	1872
Db	6566	CGTCGAGAGTTTGGAAAAAGCATCAGGCACTGCTTGGCAAATGTGAGCTGGAAAA	6625
Qy	1872	rGluArgAspAspLeuAsnGlnSerLysGlnHisLeuDbeserGluIleGluThrLeuSe	1892
Db	6626	CCAAATTGCACACACTGATTAAGAAAGAAATTCCTGTCAAGAAATCTGAAACCTGCA	6685
Qy	1892	rLeuSerLeuLysgluLysgluPhe-----AlaLeuGlnGlnAl	1905
Db	6686	GGCCGAGCTGAGTGAATCAGATTAAGAAAGCTGAATGCTTCAAGGCTTGGAGGCGCG	6745
Qy	1905	agLysAspLysAlaLeuAlaLeuAlaArgLysThrIleAspIleThrGlnLysIleSerAs	1925
Db	6746	ACTGTTGAGAGAAAGGTGAGTTCGCACTTGAGGCTGAGCTCAACACAGAGAAAGTCATCA	6805
Qy	1925	nIle-----GluGlnGlnLeuLeu	1931
Db	6806	GCTGAGAGAGGCAATCGAGAACTGAGAGTTCGCACTTGAGGCCGATGAAGAAAGACGCT	6865
Qy	1931	uGlnGlnAlaThrAsnLeuLysgluThrLeuLysrGluArggluSerLeuIleGlnCysLy	1951
Db	6866	GCACATCCGACAGAAACTGAAGAAAGGACGCGAGCGGAGAGATTCATTCACTT-----AA	6916
Qy	1951	sgLuglnLeuAlaLeuAsnThrGlnHisLeuArggluThrLeuLysSerLysAspLeuAl	1971
Db	6917	GGATTAAGTTAGAACTTGAAGGGAATTGCAAGTGTCAAGAGAAAAACGAGAGCTHGT	6976
Qy	1971	aleuGlnLysMetGlnGlnGlnArgAspGluAlaAlaAsnLysValIleAlaLeuThrGln	1991
Db	6977	GATT-----CTTGATCGCGAGAAATCCAAAGCA-----	7004
Qy	1991	uLysMetSerSerLeuGlnGlnGlnIleAsnGluAsnValThrThrLeuLysgluGlyGln	2011
Db	7005	-GAATGAGACTTCAAAAAACAAATTAAGAGAGATGCGCAGAAAGCCGAAAGTTTTTGA	7063
Qy	2011	u-----GlyGlnLysgluThrPheThrLeuGlnArgProSerLys	2024
Db	7064	ATTAGACCTTGTACGTTAAGGCTGAAAAAGAAAATGTGACAAAACAAATACAGAAAA	7123
Qy	2024	sgLInSerSerSerGlnMetGlnGlnLysLeuArggluSerLeuLysThrLysAspLeuGln	2044
Db	7124	ACAAGGTCAAGTGTGAGAACTAGACAAGATTACTCTTCAATTAAAGTCTGTTAGAGA	7183
Qy	2044	nLeuGlnGluAlaGluLysgluLysSerGluAlaThr-----	2056
Db	7184	AAAGGACGAGGAGATACAGATCAAGAAAGAAATCAATAAATCGACGTGAGAGTCTTCA	7243

QY	2057	-AsnGluIleuysanleuthrAlaVal[s]eSerLeu-----GluGluGluIleLe	2074
Db	7244	GAATCAGTAAAGAGCTTAAATGAGGACGTAGGACGCTTGtGGTGAACCAAGAAATAT	7303
QY	2074	uGln---AsnAlaSerIleIleuAnGluAlaValSerGluArgGluAnleuAArgHisSe	2093
Db	7304	GAAGGCCACAGAACAGACTCTAGACCCACCAATAGAGAGAGAGATCAGCTGAGAAATAG	7353
QY	2093	rLysGlnIleuValSerGluLeu-----GlnLeuSerLeuThrLe	2108
Db	7364	CATTGAAAGCTGAGAGCCCGCTTAGAGAGCTAGTAAAGAAAGAGAGCTGCTGCTTACA	7423
QY	2108	uLysSerArgAspHisAlaPheAlaGlnSerLeuArgGluLysAspGluAlaValAsnLy	2128
Db	7424	ACAACGTGAAG-----GAAAGGACATCATGCAGATTACTTAAAGGTAG	7468
QY	2128	sAlaSerLeuAlaGluGlnIleLysIleLeuThrLysGluMetAsp-----	2144
Db	7469	AGTGAGAGAACTTGAAAGAGAGCTTAGAGATGCCAGACAAACAGAGCATGCAGCTCT	7528
QY	2145	-GluPheArgAspSerLys-----GluSerLeuGlnGluInserSerHisLeuSe	2161
Db	7529	TGAGGCACAGAAATTCAAAGAGAGAGTAGAGACCTTAAACAAATAAGAGGAGATGC	7588
QY	2161	rGluGluLeuGlySerThrTyrLysThrGluLeuGluMetLeuGlyGlnGlnLysGluAspI	2181
Db	7589	CCAAAGCTGTGAGAGCTCTGGAATTAGATGTTGTTACTATATAAGTCACAGAAAAGAGATCT	7648
QY	2181	eAsnAsnLysLeuAlaGluLysValLysGluValAspGluLeuGlnHisLeuSerSe	2201
Db	7649	GACAAATGAATTAACAAAGAGACGACGACCAATCTCGAATTA-----	7691
QY	2201	rLeuLysGluLnuLeuAspGlnIleGlnMetGluLeuArgAsnGluLysLeuAArgAsnTy	2221
Db	7692	-----GAAATATAAATTCAATCATTTGAAAT--	7718
QY	2221	rGluLeuGlyLysMetAspIleMetGluLysGluIleSerValLeuArgLeuMetGlu	2241
Db	7719	-----ATTTTGCAAGAAAAAGA	7735
QY	2241	nasnGluProGlnGlnGluLysAspAspValAlaGluArgMetAspIleLeuGluSerAr	2261
Db	7736	GCAAGACGAATACAGATGAAAGAAAAATCAAGACATGCCACTGAGAGATGCTTCAACAC-	7793
QY	2261	gAsnGlnGluIleGlnGluLeuMetGluLysIleSerAlaValTyrSerGlnGlnHisTh	2281
Db	7794	-----CAATTAAAGAGCTCATGAGAGAGTGAGCCCTCGATATATAGCAAA-----	7841
QY	2281	rLeuLeuSerSerLeuSerSerGluLeuGlnLysGluThrGluAlaHisLysHisCysMe	2301
Db	7842	-----GAAACCCTGTAG-----	7853
QY	2301	tLeuAsnIleLysGluSerLeuSerSerThrLeuSerArgSerPheGlySerLeuGlnTh	2321
Db	7854	-----GCCAAGACGACGAATCTTAGTAGTCAAGTAGAGTCTTTGAAC	7897
QY	2321	rGluHisValLysLeuAsnThrGlnLeuGlnThrLeuLeuAsnLysPheLysValValTy	2341
Db	7898	TGAGAAAGCTCAGTTGCTACAAAGCCTTGATGAGAGCCAAATAATATATATATTTTGCA	7957
QY	2341	rArgThrAlaAlaValLysGluAspHisSerLeuIleLysAspTyrGluLysAspLeuAl	2361
Db	7958	ATCTTCAAGT-----AATGGCTCATTCAMAGAGTAGAAGTGGCAGCA	8002
QY	2361	aAlaGluLnuLysArgHisAspGlu-----LeuArgLeuGlnGlnLysLeuGln	2378
Db	8003	GAAGCTGAGAGAGAGATGGAAGAAATCAGTAGCTGAAATAATTCAAATTCAGACCAAGA	8062
QY	2378	uGlnHisGlyArgLysTrpSerAspSerAlaSerGluGluLeuLysPhe-----	2394
Db	8063	GCAGCTTGCTCTTAAAGCTGCCAGGTGGAGAGAGACCAACCTTGGAGAGACAAA	8122


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; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 365
; SOFTWARE: PERL Program
; SEQ ID NO 361
; LENGTH: 10281
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030119009A1 026662.3
US-10-084-817-361

Alignment Scores:
Pred. No.: 2,86e-63 Length: 10281
Score: 1149.00 Matches: 706
Percent Similarity: 37.53% Conservative: 550
Best Local Similarity: 21.09% Mismatches: 1030
Query Match: 7,78% Indels: 1062
DB: 14 Gaps: 141

US-09-724-584-1 (1-2954) x US-10-084-817-361 (1-10281)
QY 333 ThrProHisValAsnGluValLeuAspAspGluAlaLeuLeuLysArgTyrArgLysGlu 352
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Db 197 ACAAGAGCTCTTCAGAAAAATTCAGAGCTTGAAGGACACCTTGACAACTGAGAAAGGA 256
QY 353 IleAspLeuLysLysGlnLeuGlnLeuGlnLeuGlnLeuGlnLeuGlnLeuGlnLeuGln 372
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Db 257 AAGCAGCAAAAGCAGCTTTCAGCTGACGCTGCGCTGCGAGAGCAAAAGCAACG 316
QY 373 AlaMetAlaLysGluGlu-----HisThrGlnLeuLeuAla 384
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Db 317 AAGGTGAAAAAAGAAAAACCGAGGCTACAACTGAAAAAGGAGAAATCAAGATTGATG 376
QY 385 GlnIleLysGlnLeuHisLysGlnArgGlnAspArgGlnLeuPheHisLeuThrAsnIleVal 404
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Db 377 GAAATATGGAAGCTCTGAGAAACTTAAGCAGAAATTTCTCAT-----GACTTCA 430
QY 405 ValAlaSerSerGlnLysGlnLysGlnLysGlnLysGlnLysGlnLysGlnLysGlnLys 416
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Db 431 GTCAGAGAGTCAACAGTGAATTTCCAGAAAGCAACTGAAATTCAGGCAAAAGCAAAAT 490
QY 417 ValLysArgLysArgArgValThrTrpAlaProGlnLysIleGlnAsnSerLeuHisAla 436
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Db 491 GAAAAAAGCTGGAACAGAACTTAAGAGGTAAATCTGAGCTTGAAGAAAGCAAGCAAGCT 550
QY 437 SerGlnLysSerAspPheAspMet-----Leu 445
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Db 551 GGGCAGCTGCGAGATGCTCTCTGATCATCATGCAATACCACAAAAAATTTTACACT 610
QY 446 SerArgLeuProGlnLysAsnPheSerLysLysAlaLysPheSerAspMetProSer----- 463
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Db 611 CCACATAACCAACCAATATATATAGTGTCCAAAGTATGAAGATCTAAAGAAATAAT 670
QY 464 PheProGlnLysAspAspSer-----ValCysThrGlnPheSer 476
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Db 671 AATAAAGAGGTGAAGAAAGAAAGATTAGAGCGCAGAGTTAAAGCCCTTGAGCGCTAA 730
QY 477 AspPheAspAspAlaLeuSerMetMetAspSerAsnGlnIleAspAlaGluTrpAsnLeu 496
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Db 791 GCTTCATCATCTGTGTTCTCATGCGCAGCAAGAGAAAGACCCCAAGCATCTTTCATTAAT 850
QY 509 ----- 509
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Db 851 TCTCAAGAACTCCAAATTAGAGAGATTTCTCTGCATCTTAATTTCTGGGAGCAAGAG 910
QY 510 -----GlnSerMetIleAspPheGlnLysIleSerAspSerValGlnPheHis 525
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 911 GTGACTCCAAAGTCGATCACTTTCGCAAAATAGGAAAAAGATGCTTAATGACGATTCTTT 970

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QY 526 AspSerSerLysGlnAsnGlnLeuGlnIleuProLysAspSerGlnAspMetAlaGlu 545
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 971 GACAAATCTAGACAGCTCATCTCTTTG-----GATCAATTAATAA 1009
QY 546 CysArgLysAlaSerPheGlnLysGlnLysLeuThrSerLeuGlnGlnLeuGlnSerLys 565
   ::  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1010 GCGCAGAAATCAAGAGCTTAAGAAACAAAGATTAAATGAGTTGAGAACTAGCGCTGACAGACAT 1069
QY 566 GlnGlnGlnLysLysGlnLeuValGlnSerPheGlnLeuLysIleAlaGlnLeuGlnLys 585
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1070 GAAAAAGAAATGAAGAGCCCAAGTGAATAGTTCA-----GAATCCAACTC 1117
QY 586 GlnLeuSerValLysAlaLys-----AsnLeuGlnMetValThrAsnSer-- 600
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1118 CAACTGAGG---AAAGCAAAAGTGGAATTAATTGAAAAAGAAAGATTGGAACAAATGT 1174
QY 601 ArgGlnHisSerIleAsnAlaGlnValGlnThrAspValGlnLysGlnValAlaArgLys 620
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1175 AAGGATGAACCTAGTGAACCAACAGCACAATACGAC----- 1210
QY 621 GlnMetSerValLeuGlnLysSerGlnLysAsnAlaSerAsnSerAspLeuGlnAspSer 640
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1211 -----CAGCGCTCAACCAAGTATCTGCTGATTCGAAACAAATCTGAAAAAATTTG 1258
QY 641 SerValAspGlnLysArgLeuSerSerSerHisAspGlnCysIleGlnHisArgLysMet 660
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1259 ACGGAAAGAT-----TTGAGTTTCCAGCGACAAATGCAAGAAAGTCCAGATGTTCT 1309
QY 661 LeuGlnGlnLysIleValAspLeuGlu---GlnPheIleGlnAsnLeuAsnLysSer 679
   ::  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1310 CTGGAACGAAATAATTAAGAAAAAGAAAGAGATTCAAGAGGAGCTTCCCGT----- 1363
QY 680 GlnAsnAspLysGlnLysSerSerGlnLysAspPheMetGlnSerIleGlnLeuCysGlu 699
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1364 -----CAACGCGTCTTCCAAACACTGAGCAGCAGAGTGCATCAGATG----- 1408
QY 700 AlaIleMetAlaGlnLysAlaAsnAlaLeuGlnGlnLeuAlaLeuMetArgAspAsnPhe 719
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1409 -----AAGCCAGACTCACCCAGAGGTACAGCAAGCCAG---AATATG 1450
QY 720 AspAsnIleIle----- 1450
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1451 CACAACGCTCGCAGCGCTGAAGCTGATTAACATCATCATGTAAGCAACAGCTGAAATAC 1510
QY 727 -----GlnThrLeuLysArgGlnLysLeuAlaAspLeuGlnArgSer----- 739
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1511 AATTGGAAGAGTTTAACCAAAAGTTGACAGAGCTGAACAGCGCTTCAGGCGAGTCAG 1570
QY 740 LeuLysGlnAsnGlnLysThrAsnGlnPheGlnLysLeuGlnLysGlnLysGlnLysGln 757
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1571 ATCAAGGAGAAATGAGCTGAGAGAAAGCAATGAGAAATGAAGAAAGAAACAACTCCTT 1630
QY 758 LysGlnHisGlnAlaGlnLeuIleHisGlnLysIleGlnSerLeuLysLysLeuValGlnAsn 777
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1631 AAGAGCTCATCTGACCAAAAGCCAGAGAGTCTGCCACTGAGCGCAAACTCAAGAAC 1690
QY 778 AlaGlnMet-----TyrAsnGlnAsnLeuGlnLysAspLeuGlnThrLysThrLys 794
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1691 ATCAAAAGCTGTTTAATCAAGCCAGAGATTTTGAGAAAGAAATGAAGCAAGAAAT--- 1747
QY 795 LeuLeuLysGlnGlnLysIleGlnLeuAlaGlnLeuAlaGlnLysArgAlaAspAsnLeuGln 814
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1748 -----ACCTCTCGAGAAACCATGTATTAAGATCTTCAAGAAAAATTAATCAGCAAGAA 1801
QY 815 LysLysValArgAsnPheAspLeuSerValSerMetGlnLysAspSerGlnLysLeu----- 832
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1802 AACTCTTGACTTTAGAAAACTGAAGCTTCTGTGGCTGATCTGAGAAAGCAGCGAGAT 1861
QY 833 CysGlnGlu----- 833
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1862 TGTTCCTCAAGACCTTTTGAAGAAAAAGAGACATCATCAATTAAGAACTTAATGATTA 1921

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844 SerAepAlaGluAlaValThrArgAepAlaGluGluCysSerPheLeuArgSerGlu 863
 1922 ACCAAGACAGAGAAAGAGTCCAAA---GCCTTGCTGAGGCTTTAGAGTTAAAAA 1978
 864 AenLeuGluLeuLeuGluLeuSerGluAepThrSerAsnTyrTrsAsnGluLeuGlu 883
 1979 GAATATGAAATTAAGAAAGAACTCTGTTTCTTTGTTGAAAGAAAGTAAACGAAAA 2038
 884 AlaAserLeuPheGluLeuGluLeuGluThrGluLeuSerAsn----- 898
 2039 CTTTAACT-----CAGATGATCAGAAAAAGAAAACTTGACAGATAAATT 2086
 899 -----TyrTrsLysMet 902
 2087 AATCATTGGAACCTTGCTGTAAGACACAGCAATTAAGATCATCAATACACAGAGA 2146
 903 GluAlaAepLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGlu 922
 2147 GTAAGAACGCTGAGATGAGACAGAGAAACCTAAGTGTGAGATCAGAAACCTTCAAC 2206
 923 LeuLeuAlaGlyLys-----ValProArgAepLeuLeuSerArgValGluLeuGlu 939
 2207 GTGTATGACAGTAAGTCACTGAGTGAAGACCCAGAAACTGATTATATGAGACTACG 2266
 940 LysLysValSerGluPheSerLysGluLeuGluLysAlaLeuGluGluLysAsnAlaLeu 959
 2267 CAGAAH---GCTGAGTTCTCA-----GATCAGAAACATCAGAAAG 2302
 960 GluAenGluValThrCysLeuSerGluTyrLysPheLeuProAsnGluValGluCysLeu 979
 2303 GAATATGAAATATATGTTTGAAGACTTCTCAG---CTTACTGGGCAAGTTGAAATCTA 2359
 980 LysAsnGluLeuSerLysAlaSerGluLeuMet----- 991
 2360 GAACACAGCTTCACTACTGCTCAATGAAATATGAGCAAGACCGGTGTTACCAAGAC 2419
 992 -----LeuLeuLysGluGluGly----- 997
 2420 TTGCATGCCGAATATGAGAGCTCAGAGGATCTGCTAAATCCAAAAGTCTTCTGCGG 2479
 998 -----GluHis 999
 2480 ACAATGAAAGATCATCAGAGAGCTTTTGGCTTTTATGATCAGAGCGTGCATGATCAT 2539
 1000 Ser---AlaSerIleLeuSerLysGluIleIle----- 1010
 2540 TCTTTGCAATATATATGAGAACAGAGACATGCTTTCAGAGAGAGTGAATGTCGT 2599
 1010 ----- 1010
 2600 TTAGAGACAGACCAAGTCCGAAAAATTCGCCATCTCAAAAATATAGATTGATTCATT 2659
 1011 -----MetGluGluGluSerGluGlu 1017
 2660 GAATTTTCATTAGACTCAAAAACAGATGAATCAGAGCTCAAAAGAGGTGAAGAG 2719
 1018 IleLeuGluLeuThrAspGluValThrHisThrGlnSerLysValGlnGluThrGlu 1037
 2720 TTGGTGAATTAAGAGAAATATGAGAAATTCATGTAAGACAGAGATGATGATCA 2779
 1038 GlnTyrLeu-----GluMetLysMetHisAspAsp----- 1048
 2780 AGTTTGTGGCTGAAACAGTACGCGCATTAAGTTACAGAAAGACATTTGCTCTAC 2839
 1048 ----- 1048
 2840 CAGAAATGTTGCTGTAACCTTAAGTGCCTTGAGAACAGAAAAAGAGCTGCAACT 2899
 1049 LeuPheGluLysTyrIleArgAsnLysSerGlu----- 1059
 2900 TTAATATTAAGTGAAGAACTGAGCAGAGATTCAGAAATTAAGAAAGACACCAT 2959
 1060 ---AlaGluAepLeuLeuArgGluMetGluAenLeuLysGlyThrMetGluSerValGlu 1078

2960 CTACTTGAAGACTCTTAAGAGAGCTACAACTTTATCCGAACCTTA---AGCTTGGAG 3016
 1079 ValLys-----IleAlaAepThrLysLeuGluLeuGluThrIleArg 1093
 3017 AAGAAAGAAATGAGTTCATCTCAATCTTAATTAAGGAAATGAAAGAGCTGACCCAA 3076
 1094 Asp-----LysGlu-----GlnLeuLeuHisGluLysLysTyrPhePhe 1106
 3077 GAGAAATGGAGCTTTAAGGAAATTAATGATCTTTAAATCAAGAGAAAGTGAACCTTAATC 3136
 1107 GlnAlaMetGlnThrIlePhe-----ProIleThrProLeu 1118
 3137 CAGAAAGTGAAGATTTTGCAAACTATATAGTGAAGAGAGAAAAAGATTCAGAGTTA 3196
 1119 SerAepSerLeuProProSerLysLeuVal-----GluLysAsn 1131
 3197 TCTGATCAGTACAGAACAGAAACCTTATTTACTACAAGATGTGAAGAAACCGGAAT 3256
 1132 SerGlnAepProIle----- 1136
 3257 GCATATGAGATCTTATGCAAAAAATACAAAGCAGACAGAAAAAGAAATTTAAATTAGAA 3316
 1136 ----- 1136
 3317 TGCTTGTAATGAATGACACTAGTCTTTGTGAATATAGGAAAAATGAGTTGAGACAGCTA 3376
 1137 -----GluIleAsnAepTyrHisAsnLeuIleAlaLeuAlaThrGlu 1150
 3377 AAGGAAGATTTTGCAAGAAACACCCAGAAATCTTAAACAAATTTAGCATTTGCTGAGAA 3436
 1151 ArgAsn---AsnIleMetValCysLeuGluThr----- 1160
 3437 AGAAATCAGAAATCTAGCTAGAGTTGAGAGACAGTGCAGCAAGCTCTGAGATCTGAGATG 3496
 1160 ----- 1160
 3497 ACAGATTAACCAAAACATTTCTAAGAGCAGAGCTGTGTTTAAACGAAATCATGACT 3556
 1161 -----GluArgAsnSerLeuLysGluGluValIleAepLeu-----AsnThr 1174
 3557 TTAAGGAAGAAACAAACAAATGCAAAAGAAAGTTATGACTTATTAACAGAGATGAA 3616
 1175 GlnLeu-----GlnSerLeuGlnAlaGlnSerIle 1184
 3617 CAGCTGATGAAGTAAAGACTAAGACTAAGATGCTCAAAATCTAAGATCAGAACCAATT 3676
 1185 GluLysSerAepLeuGln-----LysProLysGln 1194
 3677 AGGAATCTGTGAAGAAAGAAAGAGAGTGAAGAAATCAATGTAATTTTAAACCTCAGATG 3736
 1195 AepLeuGluGluGlyGluValLysLeu-----LeuLeuGluMetGlu 1208
 3737 GATCTTGAAGTTAAAGAAATTTCTAGATAGTTAATGAGCGAGTGTGCAATTAAGAA 3796
 1209 LeuLeuLysGlyHisLeuThrAspSerGluLeuSerIleGluLysLeuGluLeuGluLeu 1228
 3797 GCTATG-----CTAAGAAATTAAGAAATTTAACTTCAGAAAGTGAAGAGAGAAAG 3847
 1229 LeuGluValThrGluLysLeuGlnThrLeuGluGluGluMetLysAsnIleThrIleGlu 1248
 3848 -----GAGTGCCTGACAGCATGAATTAACAGAAATTT----- 3877
 1249 ArgAenGluLeuGlnThr---AsnPheGluAepLeuLysAlaGluHisAspSer---Leu 1266
 3878 AGAGAGATCTTGAACACAGAAATTTGCAAGACATGACAGTCAAGAAATTAAGTGGCTCT 3937
 1267 Lys-----GlnAepLeuSerGlu 1272
 3938 AAAGACTGTGAATAGATGCGAAAGAAAGATATTTTCAGGAGCTCATGAGTTGTCAAACA 3997
 1273 AsnIleGluGlnSerIleGluThrGlnAepGluLeuArgAlaIleGluGluLeuArg 1292

Db 3998 AGTCAAAAGCAGATGCACACCTTCCTGCTCTGCAAAACAAATGAAAGCTGAAAT 4057
 QY 1293 GUGLNLySGlNLyValAspSerPheArgInGlnLeuAspCysSerValGlyIle 1312
 Db 4058 GAGCTAGAGAAAATGTGAAATAGTACGAGCTGAAAGAAAGTAACTGTAAGTACGAGCTG 4117
 QY 1313 SerSerProAsnHisAspAlaValAlaAsnGlnGluValSer 1327
 Db 4118 AATGATCTCAAGTCAAGATGTAATCTACAGCAACTAGGAAATGCGACAGAGAGTGGAGAA 4177
 QY 1328 ---LeuGlyGluValAsnSerLeu---GlnSerGlnMetLeuArgGlyGluArgAsp 1344
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 QY 1345 Gln 1345
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 QY 1345 1345
 Db 4298 GCTCATTTGACAGAGATTAATTCACAGCACTTGCACTTGCAAGAAAGTTCAA 4357
 QY 1346 1346
 Db 4358 ATGCACTTTGCCGAATTCAGAGAAATCTTATCTTTACAAAGTGAACAAATTTTA 4417
 QY 1354 1354
 Db 4418 CATGATCAGACTGTCAGATGAGCTTAAATGTCAGAGCTCAGACCTATGTAATCA 4477
 QY 1367 ValGlnGluValAsnLeuGlnLeuThyLysLeuAsnGlyLeuGlnGluLeu 1386
 Db 4478 TTAAAGCCGAAATTTGTCTGTTCACGAATCTGAGAACTTTCAAGTGAATGGTG 4537
 QY 1387 GlyLysSerGlu---GlnSerGluValLeuLysSerMetLeuGlnAsnLeuLys 1403
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 QY 1404 GluAspAsnAsnLysLeuLysGlnGlnAlaGlu 1414
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 QY 1415 1415
 Db 4658 CAGACAGAGATATCTCTTTTGAATTAATTAAGAGGGCTGTTACGAACAACAGTGC 4717
 QY 1424 SerLeuGlnGluValPhe 1429
 Db 4718 AGTGAATGAAGTATTTTGCAGAGCTGCGAGAGAGAACTGACCGAAGAAACC 4777
 QY 1430 ---SerGlySerGlnLysLeuValAspGluIle---GluValLeuLysAla 1444
 Db 4778 CCTTGGGCCCCAGCAAGGCTGTGAAGAGCTTGCCTCTGTGAGCTGTACCGGAG 4837
 QY 1445 GlnLeuLysAlaAlaGlnGluArgLeuGlu---IleLysAspArgAspArg 1460
 Db 4838 TCCTCTGAGAGCTGAGAGAGAAATGAAAGTCAAGGATTAAGAAATTAAGAAATT 4897
 QY 1461 PheGlnLeuValGlnThrAlaAsnThrAsnLeuValGlu---GlyLysLeuGlnThrPro 1479
 Db 4898 CAAGAGCTGAGACGTTATTAAGTCTGAAAGCAAGAGCTTGACCTTGAGAGAGAG 4957
 QY 1480 LeuGlnAlaAspHisGlu---GluAspSerIleAspArgArgSerGlnGlnMetGlu 1497
 Db 4958 TATTGTGAGAAAGAAAGCAAGTGCAGACGAGCTGACCAAGCTCACTTGAGATGAG 5017
 QY 1498 IleLysValLeuGlyGluLysLeuGluArgAsnGlnThrLeuLeuGlu 1513
 Db 5018 TCCAAAGTGGCGCGCAAGAAAGCAAGAGCAAGCAAGCTGCACTTGAGGTGAAGTGA 5077
 QY 1514 ArgLeuGlnGlnGluLysLeuGlnLeuSerAsnLysLeuGlnIleLeuGlnLysGlnMet 1533
 Db 5078 AGACTCCAGGCTACAAAGGTCTGAGCTTAAGTCTCGG 5113

QY 1514 GlnThrSerValLeuLeuLysAspLeuGlnGlnLysLeuGlnSerLeuLeuSerGlu 1553
 Db 5114 ---TCCTTGTGGGATCGACACAGAAAGTCAATTCAGAGC 5152
 QY 1554 AsnIleIleLeuLysGluAsnIleAspThrThrLeuLysHisSerAspThrGlnAla 1573
 Db 5153 ---CGAATGAGAGCTGTGACATATCAAAAAGAACATCTTCTGAAACTACAGAA 5203
 QY 1574 GlnLeuGlnLys 1583
 Db 5204 AGAACACCAAGACATGATGTTTCATCATGATTTGTGTAAGATGCTCAGACAGACTCAAT 5263
 QY 1584 Leu 1598
 Db 5264 CTAGACATTTGAGAAATTAAGTGAAGCTGTGCTGATGAAACCCACAGAGAGTCTGGG 5323
 QY 1599 ThrGlnGlnLysGlnThr 1606
 Db 5324 GAACGCTCCAGATACCAATTAATGAGCTCCAGGGAGAAATMAAACCCAGAGCTTTCA 5383
 QY 1607 AspCysValHisProLeu 1612
 Db 5384 GAATCATTTGCAATTTGCTATTTCTGCTCTAATGCTTTGTGATGATTTCTCG 5443
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 QY 1651 ValGlnHisLeuMetLysSerMetIleGlnSerLysSerLeuGlnSerLeuGlnHis 1670
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 QY 1671 GlnLysHisAspThrGlnGlnLeuLeuAla 1683
 Db 5588 ---CATTTACAGAGAGTACCACTAAATGACCAAAATTAAGACATGATGAATGGAA 5641
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 QY 1704 ThrAlaGlnValAspHisLeuLysGlnAsnIleGlnLeu---GlyLeuAsnPheLys 1721
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 QY 1722 AsnGlnValGln---GlnLysThrThrLysGlnGlnGlnLysLeuLeuAsnGlnAsnLys 1739
 Db 5762 TTGAAGATGATGAGATTAATCAATCAAGTGAAGATTAATGAGATGAGTGCAGAGGTG 5821
 QY 1740 1740
 Db 5822 AATGACAGCTGGAAGAGAGATTTCTTGATGTGAGAAATGAGCTGAGATGATGATGAG 5881
 QY 1751 Gln 1760
 Db 5882 GAGAAAGCTACATGAGCATGAAGCCCTTACCTGAGGAGCTGACTTAAGAGTGAATCAA 5941
 QY 1761 AspLysGlnSerAlaLeuGlnThrLeuLysGlnSerGlnGlnValIle---AsnLeu 1779
 Db 5942 ACAGAGAAAGCTATGTTTGAAGAAAGACAAATTAATTAAGCAAGGTTATGCTGCTCT 6001
 QY 1780 AsnGlnGlnMetGlnMetValMetLeuGlnMetGlnGlnLysLysAsnSerGlnArgThr 1799
 Db 6002 GAAGAAGACTCTGATGCTGATCAAGTGAAGAAACACAGCTTCTGAGAGATTTAGATGCT 6061
 QY 1800 ValIleAlaGlnArg---AspGlnLeuGlnAspAspLeuArgGlnSerValGln 1816
 Db 6062 ATGCAAAAACCAAGAGCTGATGATGCTGTAAGAAATGAAGAGAGAAACACAA 6121

1817 MetSerIleGluThr-----GlnAspAsp 1824
1822 ---GAGCTTGAGTCTCAAAAGTAGTGTCATTCATTCAGGTGGCAGAGCGCAG 6178
1825 LeuArgIleAlaGlnAlaLeuGlnGlnIleValAspIleValGlnIleuThrSer 1844
6179 GTGAAGGAAAGAACGAGACCTCTTCAGACTTTGTCCTGATGTGAGTGAAGCTTTAAA 6238
1845 GlnIleSerValLeuGlnIleuValIleSerLeuLeuGlnIleuMetLeuIleVal 1864
6239 GACAAAACATCTCCAGGAAAAGCTGCAGAGTTGGAAAAGACATCACAGCAGCTGCT 6298
1865 AlaThrValIleGluThrLeuSerGluArgAspAspLeuAsnIleSerGlnIleu 1884
6299 TTGACAAATGTGAGCTGGAAAACCAATTCGACCACTGAATTAAGAAAAGAAATGCTT 6358
1885 PheSerGluIleGluThrLeuSerLeuSerLeuValGluIleGluPhe----- 1900
6359 GTCAAGAACTCGAAAGCCTGCAGCGCCAGACTGAGTAATCAATTAAGAAAAGCTGAAT 6418
1901 -----AlaLeuGlnIleAlaGluValAspIleValAlaAspIleValArgIle 1917
6419 GTCTCCAAAGCCTTGAGGCGCAGCTGTGAGAAAAGTGAAGTTCGATTCAGGCTGAGC 6478
1918 AspIleThrGluValIleSerAsnIle----- 1926
6479 TCAACACAGAGGAAGTGCATCAGCTGAGAAAGGATCGAAGAACTGAGATTCGAT 6538
1937 -----GluGluGlnLeuGlnGlnAlaThrAsnLeuValGluThrLeuIleu 1943
6539 GAGCGGATGAAAAGAGCAGCTGCATCGCAGAGAACTGAAGAACCGCAGCGGAG 6598
1944 ArgGluSerLeuIleGlnCysIleGluIleuAlaLeuAsnThrGlnIleuArgIle 1963
6599 AATGTAATCTT-----AAGATAAAGTTGAGAACCTTGAAAGGAAATTCGAGAG 6649
1964 ThrLeuValSerLeuAspLeuAlaLeuGluIleuMetGluGlnIleuArgGlnAla 1983
6650 TCAGAGAAAACAGAGAGCTAGTGAT-----CTTGATCCGAGAAATTCAGAGCA--- 6700
1984 AsnIleValIleAlaLeuThrGluIleuMetSerLeuGluGlnIleuAsnIleu 2003
6701 -----GAGTAGAGACTTAAACCAATTAAGAGAGAG 6736
2004 ValThrThrLeuValGluIleu-----GlyIleuGluThr 2016
6737 GCCAAGACCTTGAGTTTGAATTAGACCTTGTCAGCTTAAGGTCGAAAAAGAAAT 6796
2017 PheThrLeuGlnArgProSerLeuGlnIleuSerSerSerGlnMetGluGlnLeuArgIle 2036
6797 CTGACAAAACAAATTCAGAAAACAGGTCAGTGTCAAGCTGACCAAGTACTCTCT 6856
2037 SerLeuValThrValAspLeuGlnIleuGlnAlaGluValIleSerGlnIleu 2056
6857 TCATTAAAGCTCTTAGAAGAAAAGGAGCAGAGATACAGATCAAAAGAAATCT 6916
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6917 AAAACTCAGATGAGATGCTTCAGAAATCACTTAAGAGAGCTTAAGAGCAGTACAGCC 6976
2069 Leu-----GluGluGlnIleuGln-----AsnAlaSerIleLeuAsnGlnAlaValSer 2085
6977 TTGTGTGTCGACCAAGAAATTAAGAGCCACAGAACAGAGCTTGAACCCACCAATTAAG 7036
2086 GluArgGlnLeuValAspIleSerLeuGlnIleuValIleSerGluLeuIleu----- 2102
7037 GAAAGCATCAGCTGAGAAATGATGAAAAAGCTGAGAGCCCGCTGAAGCTAATGAA 7096
2103 -----GlnLeuSerLeuThrLeuValSerArgAspIleAlaPheAlaGlnSerIleuArg 2120
7097 AAGAGCAGCTCTGTCTTACCAACTGAAG-----GAAAGTGAAGCAT 7141
2121 GluValSerGlnAlaValAsnIleValIleSerLeuAlaGluGlnIleuValIleuThr 2140

7142 CATGCAATTTACTTAAGGGTAGAGGAGAACTTGAAGAGAGAGCTAAGATACCGCAG 7201
2141 LysGluMetAsp-----GluPheAlaAspSerIle-----GluSerLeu 2153
7202 ACAAAACCAAGCATGACAGCTTGTAGCGCAGAAATTCAAAAGAGAGGTAGAACCTTA 7261
2154 GlnGluGlnSerSerIleuSerGlnIleuValCysThrTyThrThrGluLeuGlnMet 2173
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2194 GluLeuLeuGlnIleuSerSerLeuValGluIleuValAspGlnIleGlnMetGluLeu 2213
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2214 ArgAsnGluValLeuValArgAsnThrGluLeuValGluValMetAspIleMetGluValGlu 2233
7394 ATAAATTCATCTTGAATA----- 7414
2234 IleSerValLeuArgLeuMetGlnAsnGluProGlnGlnIleuValAspValAlaGlu 2253
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2254 ArgMetAspIleLeuGluSerArgAsnGlnIleGlnIleuMetGluValIleSer 2273
7469 GCCATGAGATGCTTCAACA-----CAATTAAAGAGCTCAATGAGAGAGCGCA 7519
2274 AlaValTySerGluGlnIleThrLeuLeuSerSerLeuSerGlnIleuValGlu 2293
7520 GCCCTGCAATAGACCA----- 7537
2294 ThrGlnAlaIleValIleCysMetLeuAsnIleValGluSerLeuSerThrLeuSer 2313
7538 ---GAGCCTGAAG-----GCCAAGACAGAAATCTTACT 7570
2314 ArgSerPheGlySerLeuGlnThrGlnIleValIleValLeuAsnThrGlnIleuGlnThrLeu 2333
7571 AGTCAGTAGAGATGCTTGAAGCTTGAAGAGCTGATGACAGGCTTATGATGAGCC 7630
2334 LeuAsnIlePheValValIleValArgThrAlaValIleValGluAspIleSerIle 2353
7631 AAAAATAATTAATGTTGTTGCAATCTTCAGT-----AATGCTCAT 7675
2354 LysAspTyArgIleValAspLeuAlaIleGluGlnIleValAspIleValIleu-----Leu 2370
7676 CAGAGTAGAGATGAGCAGACAGAACTGAGAGAGAGATGAAGAAATCATGATGACTG 7735
2371 ArgLeuGlnIleuGlnCysLeuGlnIleIleGlyArgIleTrpSerAspSerIleSerGlu 2390
7736 AAAATCAATTCAGACAGCAGAGCAGCTGCTTAACGTCCAGGTGAAGCAGAG 7795
2391 GluLeuValPhe-----CysGluIleGluPheLeuAsnGluLeuPheVal 2406
7796 CACCAACTTGGAGAGCAGCAAACTTGAAGCTGAGAAATTCGACAGCTGAATTTGAGAGAG 7855
2407 LysAlaAsnIleIleGlnSerValGlnAspPheSerGluValAlaValPheLeuVal 2426
7856 AAGATCAAGTGTCAATTCAGAAAATCCCTTTGACAGACACTTGAAGTCTGAG 7915
2427 GlnValGlySerThrLeuGlnIleuGlnIleu-----HisValGluValPheMetGlnTrp 2445
7916 AGTTCTTCAAGAAATCTGAGAAATGAGCTTGAATTAAGCAAAAATGCAAAAATGCTCTT 7975
2446 LeuGluGluPheGly-----AspLeuHisVal 2454
7976 GTTGAAGAAAGTAAACAAATGACTGCAAGAGAACTGACAGAGGAAATGATGAG 8035
2455 AspAlaValVal-----LeuSerGluIleuMetGlnIleuValAsnArgIleAla 2471

DB: 12 Gaps: 139
 US-09-724-584-1 (1-2954) x US-10-240-965-201 (1-10281)
 333 ThrPcHleValaenGluValLeuAAspAArgLualaleuLeuLysergLyArgLyGlu 352
 197 ACAAGAGCTCTCAGAAAATTCAAGAGCTGAAGGACAGCTTGACAAATGAGAAAGAA 256
 353 IleuAAspLeuLyserGluLeuGluAenLeuGluSerSerSerGluThrLyalaGln 372
 257 AAGCAGCAAGGCGACTTCAGCTTCAGAGCTCGCGCTGAGAGGCAAGCAAAACAG 316
 373 AlaMetAlaLyserGluGlu-----HisThrGlnLeuLeuAla 384
 317 AAGGTTGAAAATGAAAAAAGCGAGGTACAACTGAAAAAGGAGAAATTAAGATTGATG 376
 385 GluIleLyserGlnLeuHisLeuLyserGluArgLyuaArgLyIleThrPHisLeuThrAsnIleVal 404
 377 GAAATATGTGAAGCTCGAGAAACTAAGCAAGATTTCTCAT-----GAAGCTCA 430
 405 ValAlaSerSerGlnLyserGlnLyserGlnLyser-----GlnArg 416
 421 GTCAAGAGAGTCAAGAGTGAATTTCCAGAGAGACAACTGAATTCAGGCAAAAGCAAAATA 490
 417 ValLyserArgLyArgArgValThrThrPalaProGlyLyserIleGlnAsnSerLeuHisAla 436
 491 GAAAAAAGCTGAAACAGAACTTAAAGGTGAATCTGAGCTTGAAGAAAGCAACAGCT 550
 437 SerGlyValSerAAspPheAAspMet-----Leu 445
 551 GCGAGCTGCGAGAGTCTCTCTGAAATCCATGCAATACACCAAAAAATTTTACAAT 610
 446 SerArgLeuProGlyAAspPheSerLyserLyserLyserLyserAAspPheProSer----- 463
 611 CCACATACACCAAGTCAATATATATATAGTGCTCCAGATGATGATTAAGAAATAAT 670
 464 PheProGluIleAAspAAspSer-----ValCysThrGlnLeuPheSer 476
 671 AATAAAGAGGTGAAGAAAGAAAGATTAGAGGAGAGGTTAAAGCTTGAGAGCTAAA 730
 477 AAspPheAAspAlaLeuSerMetAAspSerAsnGlyIleAAspAlaGluThrAsnLeu 496
 731 AAAGCAAGCCAGACTCTTCCACAGCCACCATGAAATCACCGGACATTCGCCGATCAG 790
 497 AlaSerLyserValThr-----HisArgGlyLyserThrSerLeuHis----- 509
 791 GCTTATCATCTGTGTTCTCATGCGACAGAAAGAAAGACCCCAAGCATCTTTCATCTAAT 850
 509 ----- 509
 851 TCTCAAGAACTCCAATTAGAGAGATTTCTGCACTTACTTTCTGGGAAACAAGAG 910
 510 -----GlnSerMetIleAAspPheGlnIleSerAAspSerValGlnPheHis 525
 911 GTGACTCCAAGTCGATCAACTTTGCAAAATAGGAAAGAGATGCTTAATGCACTTTCTTT 970
 526 AAspSerSerLyserGluAAsnGlnLeuGlnIleuProLyserAAspSerGlyAAspMetAlaGlu 545
 971 GACATTTCTAGACAGCTCATCTTTG-----GATCAATTAAAA 1009
 546 CysAArgLyserAlaSerPheGlnLyserGluIleThrSerLeuGlnGlnIleuGlnIleuGlnIleu 565
 1010 GCGCGAATCAAGACTTAAGAAACAAAGATTAATGAGTTGAACTACGCTGCAAGACAT 1069
 566 GlnGlnGlnLyserLyserGluLeuValGlnSerPheGlnLyserIleAlaGluLeuGlnGlu 585
 1070 GAAAAAGAAATGAAAGGCCAAGTGAATTAAGTTCAA-----GAAGTCCCAATC 1117
 586 GlnLeuSerValLyserAlaLyser-----AsnLeuGlnMetValThrAsnSer----- 600
 1118 CAAGCTGGAG-----AAAGCAAAAGTGAATTAATGAAAAAGAGAAAGTTTGAACAAATGT 1174
 601 ArgGlnHisSerIleAAsnAlaGluValGlnThrAAspValGlnLyserGluValAlaArgLyser 620

DB 1175 AGGATGAAGTACTGTGAGAAACACAGCAATATCGAC----- 1210
 621 GlnMetSerValLeuGlyAAspSerGlyTyrrAsnAlaSerAAspSerAAspLeuGlnAAspSer 640
 1211 -----CAGCGCTCAACCAAGATATATGCTATGGAACAAAAAATCTGAAAAATTTG 1258
 641 SerValAAspGlyLyserArgLyserSerSerHisAAspGluCysIleGlnHisArgLyserMet 660
 1259 ACGGAAGAT-----TTGAGTTGTACAGCAGCAAAATGCAGAAAGTCCAGATGTTT 1309
 661 LeuGlnGlnLyserIleValAAspLeuGlu-----GluPheIleGluAAsnLeuAAsnLyserSer 679
 1310 CTGGAACAGCAAAATTAAGGAAAAAGAAAGAGTTTCAAGAGAGACTCTCCCGT----- 1363
 680 GluAAspLyserGlnLyserSerSerGluIleAAspPheMetGluSerIleGlnLeuCysGlu 699
 1364 -----CAACAGCGTCTTTCCAAACACTGACAGCAGAGAGTGCATCCAGATG----- 1408
 700 AlaIleMetAlaGluLyserAlaAsnAlaLeuGlnGluLeuAlaLeuMetArgAAspPhe 719
 1409 -----AAGCCAGACTCACCCAGAGTTACAGAACCAAG-----AATATG 1450
 720 AAspAsnIleIle----- 1450
 1451 CACAACTCTCTGAGAGCTGAACTGATTAATCATCATCATGATTAAGCAACAGCTAGAAAC 1510
 727 -----GluThrLeuLyserArgGluIleAlaAAspLeuGluArgSer----- 739
 1511 AATTGGAAGAGATTAAAGCAAAAGTTGTGACAGCTGAACAGAGCTTCCAGCGAGTCAAG 1570
 740 LeuLyserGluAAsnGlnIleuThrAsnGluPheGluIleLeuGlnLyserGluIleuThrGln----- 757
 1571 ATCAAGAGAAAGAGACTGAGAGAAAGCATGAGGAATGAAAGAAAGAAACAACTCTCTT 1630
 758 LyserGluIleGluAlaGlnLeuIleHisGluIleGlySerLeuLyserLeuValGluAAsn 777
 1631 AAGAGTCACTGTAGCAAAAGCCAGAGAAAGTCTGCCACTTGAGAGCAAGACTCAAGAAC 1690
 778 AlaGluMet-----TyrrAsnGlnAAsnLeuGlnGluAAspLeuGluIleuThrLyserThrLyser 794
 1691 ATCAAAAGAGTGTTAATACAGCCAGATTTTGCGAAGAAATGAAGCAAGCAAGAT--- 1747
 795 LeuLeuLyserGluGlnGluIleGlnLeuAlaGluLeuAArgLyserArgAlaAAspAAsnLeuGln 814
 1748 -----ACCTTCAGAGAAACCATGTTAAGAGATCTTCAAGAAATAATATACAGCAAGAA 1801
 815 LyserLyserValArgAAspPheAAspLeuSerValSerMetGlyAAspSerGluLyserLeu----- 832
 1802 AACTCTTGACTTTAGAAAAAAGTGAAGCTGTGCTGTGCTGATCTGGAAGCAAGCAAGAT 1861
 833 CysGlnGlu-----IlePheGlnLeuLyserGlnSerLeu 843
 1862 TGTTCCTCAAGACTTTTGAAGAAAGAGAAATCATCATCATTAATGAATTAATGAATTA 1921
 844 SerAAspAlaGluAlaValThrArgAAspAlaGlnLyserGluCysSerPheLeuArgSerGlu 863
 1922 AGCAAGACAGAGAAAGAGCTCAAA--GCTTGTGAGAGCTTTTGAAGTTAAAAA 1978
 864 AAsnLeuGlnLyserGluLyserMetGluAAspThrSerAAsnThrTyrrAsnGlnLyserGluLyser 883
 1979 GAATATGAATTTGAAGAAAGAGAAACCTGTTTCTTTGTTGAAAAAGTGAACGAAAC 2038
 884 AlaAlaSerLeuPheGluLyserGlnLeuGlnIleuThrArgLyserAAsn----- 898
 2039 CTTTAATCT-----CAGATGGAATCAGAAAAAGAAAGCTTGACAGATTAATTT 2086
 899 -----TyrrLyserMet 902
 2087 AATCACTTGAAACTGTGTGAAAGACAGCAAAATTAAGTCAATGAAATACAGACAGAGA 2146
 903 GluAlaAAspLeuGlnLyserGluLeuGlnIleuThrAlaPheAAsnGluIleAAsnTyrrLeuAAsnGly 922

Db 2147 GTAAGACCGCTGAGATGAGACAGAGAAAACCTAAGTGTGAGATCGAAGAACTTCACAAAC 2206
 Qy 923 LeuLeuAlaGlyLys-----ValProArgAspLeuLeuSerArgValGluLeuGlu 939
 Db 2207 GTGTAGACAGATGACAGTGTGAGAGAGACCCAGAAACTAGCTTATATGAGCTACAG 2266
 Qy 940 LysIleValSerGlnLeuSerLysGlnLeuGluLysAlaLeuGluLysAsnAlaLeu 959
 Db 2267 CAGAAA---GCTGAGTTCTCA-----GATCGAACAACATCGAAG 2302
 Qy 960 GUAAGGluValThrCysLeuSerGluIleLysPheLeuProAsnGluValGluCysLeu 979
 Db 2303 GAAATAGAAATATATGCTTTGAAGACTTCTCAG---CTTACGGGCAATTTGAAGTCTA 2359
 Qy 980 LysAsnGlnIleSerLysAlaSerGluIleMet----- 991
 Db 2360 GAACACAGCCTCAGTTACTGTCAATGAATATATGACAAAGACCGGTGTACCAAGAC 2419
 Qy 992 -----LeuLeuLysGlnGluLys----- 997
 Db 2420 TTGCATGCCGAATATGAGAGCCTCAGGATCTGTAAATCCAAAGATCTTCTGTGTG 2479
 Qy 998 -----GluHis 999
 Db 2480 ACAATGAGATCATCAGAGAAAGCTTTGGCTTTGATCAGCAGCTGCATGATCAT 2539
 Qy 1000 Ser---AlaSerIleIleSerLysGlnIleIle----- 1010
 Db 2540 TCCCTTGCAATATATATGAGAACAGAGAGCATCTTCAGAGAGAGTGAATGTCTGT 2599
 Qy 1010 ----- 1010
 Db 2600 TTAGAGACAGCAAGTCCGAAAAATTCGCCATCTCAAAATAGATTACACTT 2659
 Qy 1011 -----MetGlnGlnGlnSerGlnGln 1017
 Db 2660 GAATTTCTTACAGCTCAAAAAACGATGAACCTCAGCTCAAAAGAGTGTGAAGG 2719
 Qy 1018 IleLeuGlnLeuThrAspGluValThrHisThrGlnSerLysValGlnGlnThrGluGln 1037
 Db 2720 TTGGTGCAATATCAAGAGAAATATAGAAAGAAATCTCATGAAGACAGAACAGATGCATCA 2779
 Qy 1038 GlnIleLeu-----GluMetLysLysMetHisAspAsp----- 1048
 Db 2780 AGTTTGTGGCTGAACAAGTCAGCGCATTAAGTTACAGGAAGACCTTCTGTCTAC 2839
 Qy 1048 ----- 1048
 Db 2840 CAGATGTGTTGCTGGAACCTTAAGTGCCTTGAGAACAGAGAAAGAGCTGCACATT 2899
 Qy 1049 LeuPheGlnLysTyrIleArgAsnLysSerGlu----- 1059
 Db 2900 TTAATGATTAAGTGAAGAACTGAGCAGCAGAGATTCAAGATTAAGAAAGAGCAACCAT 2959
 Qy 1060 ---AlaGluAspLeuLeuArgLysMetGluAsnLeuLysGlyThrMetGlnSerValGlu 1078
 Db 2960 CTACTTGAAGACTCTTAAGAGAGCTACAACTTTATTCGAAACCTTA---AGCTTGGAG 3016
 Qy 1079 ValLys-----IleAlaSerThrLysHisGlnLeuGlnGluThrIleArg 1093
 Db 3017 AAGAAAGAAATGATGCTTCATTTCTTAATTAAGAGAAATGAGAGAGCTGACCCAA 3076
 Qy 1094 Asp-----LysGlu-----GlnLeuLeuHisGlnLysLysTyrPhePhe 1106
 Db 3077 GAGATGGGACTCTTAAGGAAATTAATGATCTTAATCAAGAGAGATGAACCTTAATC 3136
 Qy 1107 GlnAlaMetGlnThrIlePhe-----ProIleThrProLeu 1118
 Db 3137 CAGAAAGTGAAGATTGTCAAACTATATATAGATGAAGAGAGAAAGCAATTCACAGTTA 3196
 Qy 1119 SerAspSerLeuProSerLysLeuVal-----GluGlyAsn 1131
 Db 3197 JCTGATCAGTACAGCAAGAAACCTATATTTACTACAAAGATGTGAAGAAACCGGAAT 3256

Qy 1132 SerGlnAspProIle----- 1136
 Db 3257 GCATATGAGGATCTTAGTCAAAAATACAAAGCAGACAGAAAGAAATTTCTAATTAGAA 1136
 Qy 1136 ----- 1136
 Db 3317 TGCTTGCTAATGAATGACATAGCTTTGTGAAAAATAGAAAAATGAGTTGGAACAGCTA 3376
 Qy 1137 -----GluIleAsnAspTyrHisAsnLeuIleAlaLeuAlaThrGlu 1150
 Db 3377 AAGAGAGATTTGCAAGAGAACCAAGAAATTTCTTAACAAATATGACATTTGCTGAGAA 3436
 Qy 1151 ArgAsn---AsnIleMetValCysLeuGlnThr----- 1160
 Db 3437 AGAAATCAGAAATCTGATCTGAGAGTTGAGACAGTGCAGCAAGCTTGAGATCTGAGATG 3496
 Qy 1160 ----- 1160
 Db 3497 ACAGATTAACCAAAACATTTCAAGAGCGAGCTGTGTTAAAGCAAGAAATCTGACT 3556
 Qy 1161 -----GluArgAsnSerLeuLysGlnGlnValIleAspLeu-----AsnThr 1174
 Db 3557 TTAAGAGAGAAACAAACAAATGCAAAAGAGATTAATGACTTATTAAGAGAGATGA 3616
 Qy 1175 GlnLeu-----GlnSerLeuGlnAlaGlnSerIle 1184
 Db 3617 CAGCTGATGAAGTATATGAGATCAATCAATGATGTCAAAATCTGAATTCGAAACCAAT 3676
 Qy 1185 GluLysSerAspLeuGln-----LysProLysGln 1194
 Db 3677 AGCAACTCTGTGAAGAAAGAGAGAGTGAAGAAATCAATGATTTAACTCAGATG 3736
 Qy 1195 AspLeuGlnGlnGlyGluValLysLeu-----LeuLeuGluMetGlu 1208
 Db 3737 GATCTTGAAGTAAAGAAATTTCTAGATAGTTATATGCGCAGTGTGCAATTAGAA 3796
 Qy 1209 LeuLeuLysGlyHisLeuThrAspSerGlnLeuSerIleGluLysLeuGlnLeuGln 1228
 Db 3797 GCTATG-----CTAAGAAATGAAGAAATTAACCTTCGAGAAAGTGAAGAGAGAG 3847
 Qy 1229 LeuGluValThrGluLysLeuGlnThrLeuGlnGlnGluMetLysAsnIleThrIleGlu 1248
 Db 3848 -----GAGTGCCTGCAGCTGATTAACAGACAAAT----- 3877
 Qy 1249 ArgAsnGlnLeuGlnThr---AsnPheGlnAspLeuLysAlaGluHisAspSer---Leu 1266
 Db 3878 AGAGAGATCTTGAACAACAGCAATTTGCAAGACATGACAGTCAACAAAGAAATTAGTGCCTT 3937
 Qy 1267 Lys-----GlnAspLeuSerGlu 1272
 Db 3938 AAAAGCTGTGAATATGATCGGAGAAAGATATATTCAGGGCCTCATGATTTGTCAACA 3997
 Qy 1273 AsnIleGlnGlnSerIleGluThrGlnAspGlnLeuArgAlaIleGlnGluLeuArg 1292
 Db 3998 AGTCAAAAGCAATGACACACCTTCAGTCTCTGCAAAACAAATGAACAAAGCTGAT 4057
 Qy 1293 GlnGlnLysGlnLeuValAspSerPheArgGlnLeuLeuAspCysSerValGlyIle 1312
 Db 4058 GAGCTAGAGAAATATGATGGAATATCTGACAGCTGAAAAGTGAACCTGTAACAGCTG 4117
 Qy 1313 SerSerProAsnHisAspAlaValAlaAsnGlnGlnLysValSer----- 1327
 Db 4118 AATGATTCAGGTCAGAAATGTATACACAGCAACTAGAGAAATGGCAGAGAGATGAGGAAA 4177
 Qy 1328 ---LeuGlyGluValAsnSerLeu-----GlnSerGluMetLeuArgGlyGluArgAsp 1344
 Db 4178 CTACTAATATGAAGTTAAATATTTAAATGATACAGTGTCTTCTTCATGAGTGAAGT 4237
 Qy 1345 Glu----- 1345
 Db 4238 GAAGCATACAGAGAGGTGAATTTGTGTAACAACAAATGAACAGACACCTGTGTCTTTG 4297

QY 1345 ----- 1345
 Db 4298 GGTCCATTGGAGAGATTAATTCCTACAGCACTTGACATGTGCAGACAAAGATTCA 4357
 QY 1346 ----- LeuGlnThrsCysValAlaLeu 1353
 Db 4358 ATGACATTGGCCGAATTGCAAGAAATTCCTATCTTACAAAGTGCAACAAATTTTA 4417
 QY 1354 ----- ValSerGluLeuGluLeuAlaHisValIysSer 1366
 Db 4418 CATGATCAGCACTGCATGAGCTCTTAAATGTCAGACCTGCAGACCTATGTACTCA 4477
 QY 1367 ValGluGluAlaSerLeuGluIleThrIleValSerGluLeuGluIleValLeu 1386
 Db 4478 TTTAAAGCCGAAATTTGGTCTGTTCACGAATCTGAGAACTTTCAGAGTACCTGGG 4537
 QY 1397 GlyIysSerGlu-----GluSerGluValLeuIysSerMetLeuGluAlaHis 1403
 Db 4538 AAGGAGATGCAGCTGGCTGGAGAGGGGCTCGTTCCATCCCTGCATCTCTGTGTG 4597
 QY 1404 GluAlaSerAlaSerLeuIleValGluAlaGlu----- 1414
 Db 4598 CCTGACACCTGATCTTAGCAGATTGGAGACTCCTCTTTACAGACTTTTAGAA 4657
 QY 1415 ----- GluIysSerSerIleGluAlaSerPhe 1423
 Db 4658 CAGACAGAGATATGCTCTTTGAGTAATTAGAAAGGGCTGTTTCAGCAAAACAGTGC 4717
 QY 1424 SerLeuGluGluValPhe----- 1429
 Db 4718 AGTGAAGATGAAGTATTTTGCAGCAGTGCAGAGAGAAATCTGACCAAGAAACC 4777
 QY 1430 ---SerGlySerGluLeuValAlaSerGluIle-----GluValLeuValAla 1444
 Db 4778 CCTTCGGCCCGCAGCAAGAGTGTGAAGCTTGAAGCTTCTGTGAGGTGACCGGAG 4837
 QY 1445 GlnLeuIysValAlaGluGluAlaSerGlu-----IleIysAlaSerPhe 1460
 Db 4838 TCCCTCGAAGACTTGAAGAAATGGAAGTCAAGGATTTATGAAATTAAGAAATT 4897
 QY 1461 PheGluLeuValGlnThrAlaSerPheValGlu-----GlyIleSerIleThrPro 1479
 Db 4898 CAAAGCTCGAGCACTTATTAAGTCTGAAGCAAGACTGACTGCTTGAAGACG 4957
 QY 1480 LeuGlnAlaSerPheGlu-----GluAlaSerIleAlaSerGluIleMetGlu 1497
 Db 4958 TATTTGTCAGAAATGAACAGTGCACAGAGCTGACAAAGCTGACTCTGAGATGAG 5017
 QY 1498 IleIysValLeuGluIleValSerGluAlaSerGluIle----- 1513
 Db 5018 TCCAAAGTGGCGGCGAAGAAACAGACGGAACACTGCTCAGCTGAGCTGAAAGTCA 5077
 QY 1514 ArgLeuGlnGluIleValSerAlaSerIleValLeuIleGluIleGluMet 1533
 Db 5078 CGACTCCAGCTACAAAGCTGTGACTTAAGTCTCG----- 5113
 QY 1534 GluThrSerValLeuLeuIysAlaSerPheGluIleValSerIleLeuSerGlu 1553
 Db 5114 -----TCTTGTCTGGCATCGACACAGAAATGCTATTCAGGC----- 5152
 QY 1554 AsnIleIleLeuIysGluAlaSerPheThrIleValSerPheHisSerPheGlnAla 1573
 Db 5153 -----CGAAATGAGAGCTGATCATATCAAAAGAACATATCTTCAAACTTACAGAA 5203
 QY 1574 GlnLeuGlnIys-----ThrGlnGlnLeuGln 1583
 Db 5204 AGAAGACCAAGAGCATGATTCATCAGATTCTGTATAAGATGCTCAGCAGAGACTCAAT 5263
 QY 1584 Leu-----AlaIysAlaSerValAlaIleAlaSerAlaSerPheProIle 1598
 Db 5264 CTAGACATTGAGAAATATAGTACGTGTGATTTGAACCAACAGAGAGTGTCTGG 5323
 QY 1599 ThrGlnIleValGluThr-----SerAla 1606

Db 5324 GAACAGTCCCGGAGATACCAATTAATGAGCTCCAGGGGAAGATAAACCAGGCTCTTCA 5383
 QY 1607 AspCysValHisProLeu----- 1612
 Db 5384 GAATCATTTCTGAATGTGCATTTTGTGCTCAATGCTTTGGTACTATGATTTCTCG 5443
 QY 1613 -----GluGluIleIleLeuLeuIleThrGluIleGluHisGlnIleThrAlaGln 1630
 Db 5444 GGGATTCAGGAAGATATCCATATATCTTCACTGCGGGTAAAGACATCAATAGGAAT 5503
 QY 1631 GluIysLeuLeuHisGluIysAlaSerGluGluGlnAlaGlnValAlaIleLeuIleCysGlu 1650
 Db 5504 TTGACATTAATCTCATGTGATAGAGACCGTGACAA-----AA 5542
 QY 1651 ValGluHisLeuMetIysSerMetIleGluSerIysSerSerLeuGluSerLeuGlnHis 1670
 Db 5543 GTTGAAGTTTGTCTTAAATGAATGAAGAAATTAGACTCAAAATC----- 5587
 QY 1671 GluIysHisAlaSerPheGluGlnGlnIleLeuAla-----LeuIys 1683
 Db 5588 -----CATTTACAGAGGTACACTTAATGACCAAAATTTGAAGCATGCATGAATTTGA 5641
 QY 1684 GlnGlnMetGlnValValThrGlnGluIleValSerGluLeuGlnIleThrHisGlnIleVal 1703
 Db 5642 AAATAGTTGGGAGATTAAGAAAGAAAGAAATCAGATTTAAGTGAAGAAATTTGAAATTTT 5701
 QY 1704 ThrAlaGluValAlaSerPheIleValSerGluIleGluLeu-----GlyLeuAlaSerPhe 1721
 Db 5702 TCTTGATACACAGAGATTACTCCAGAGATGAAGAAATTTGAAAGCTTCAATCTGAT 5761
 QY 1722 AsnGluAlaGln-----GlnIleThrIleValSerGluIleValSerGluIleValSer 1739
 Db 5762 TTGAATGATGCATGAGATTAATCATCAGCTGAGATGAATGATGAGATTTGGCCAGGTG 5821
 QY 1740 -----GluLeuGlnGlnSerGlnHisAlaSerGluIleCys 1750
 Db 5822 AATGACACTGGAAGAGATTTTGTGATGTGGAAGAAATGAGTACAGTACATGATCAGATG 5881
 QY 1751 Glu-----IleGluIleLeuMetIysSerLeuIys 1760
 Db 5882 GAGAAAGCTAGCATGACATGAAAGCTTCACTGAGAGAGTGAAGTATGAGTATTTCA 5941
 QY 1761 AspIysGluSerAlaLeuGluThrIleValSerGluIleValSerGluIleValSer 1779
 Db 5942 ACAGAGAACTATGTTTGAAGAAACAAATGAAGAAATGACAGAGTATGTCTGCTT 6001
 QY 1780 AsnGlnIleMetGluMetValMetLeuGluMetGluIleValSerGluIleValSer 1799
 Db 6002 GAGAGAACTCTCTGCTGTCACAGTGAAGAAACAGCTTCTGTGAGAAATTAGATCT 6061
 QY 1800 ValIleAlaGluArg-----AspGlnLeuGlnAlaSerPheValArgGluSerValGlu 1816
 Db 6062 ATGTCAAAAAAACACAGCACTGATCATGTTGTGTGAAAAATGAGAGAAAAACACA 6121
 QY 1817 MetSerIleGluThr-----GlnAlaSerPhe 1824
 Db 6122 ---GAGCTTGATGCTCATCAAGTGAAGTGTCTCATTCATTCAGTGCAGAGCAAG 6178
 QY 1825 LeuArgValAlaGlnAlaLeuGlnGlnIleValSerPheValGlnGlnIleThrSer 1844
 Db 6179 GTGAAGAAAGACGGAAGCTCTTCAAGCTTTGCTCTGTGATGAGTGAAGCTTTAAA 6238
 QY 1845 GlnIleSerValLeuGlnIleValIleSerLeuLeuGlnAlaGlnIleMetLeuIleVal 1864
 Db 6239 GACAAACTATCTCCAGAAAGAGTGCAGAGTTTGAAGAAAGACTCAGAGCACTGTCT 6298
 QY 1865 AlaThrValIysGluThrLeuSerGluIleValSerPheValSerGlnIleValSer 1884
 Db 6299 TTGACAAATGTGAGCTGGAAGAACCAATTGACAACTGAAATTAAGAGAAAGATTGCTT 6358
 QY 1885 PheSerGluIleGluThrLeuSerLeuSerLeuIysGluIleValSerPhe----- 1900

Db 6359 GTCAAGATCTGAAAGCTCAGGCCAGCTGATGATGATTATGAAAGCTGAAT 6418
Qy 1901 -----AlaLeuGlnGlnAlaGlnLysAspLysAlaAspAlaAlaArgLysThrIle 1917
Db 6419 GTCTCAAGAGGCTTGAGAGCGCGACCTGGTGAGAAAGTAGTTCGATTGAGGCTGAGC 6478
Qy 1918 AspIleThrGlnLysIleSerAsnIle----- 1926
Db 6479 TCAACACAGGAGTGCCATCAGTGAAGAGGACATCGAAGAACTGAGAGTTCCGATT 6538
Qy 1927 -----GlnGlnGlnLeuGlnGlnAlaThrAsnLeuLysGlnThrLeuLysGln 1943
Db 6539 GAGGCCGATGAAAGAGCAGCTGCACATGCGAGAACTGAAAGAAAGCCGAGCGGAG 6598
Qy 1944 ArgGlnSerLeuIleGlnCysLysGlnGlnLeuAlaLeuAsnThrGlnIleAsnArgGln 1963
Db 6599 AATGATTCACCT-----AAGGATAAAGTTGAGAACTTGAAGAGGAAATTGCAAGAG 6649
Qy 1964 ThrLeuLysSerLysAspLeuAlaLeuGlyLysMetGlnGlnGlnArgAspGlnAlaAla 1983
Db 6650 TCAGAGAGAAACCGAGAGCTAGTCATT-----CTTGATCCGAGAAATTCGAAAGCA-- 6700
Qy 1984 AsnLysValIleAlaLeuThrGlnLysMetSerSerLeuGlnGlnIleAsnGlnAsn 2003
Db 6701 -----GAAGTAGAGACTTAAACACAAATGAAAGAGATG 6736
Qy 2004 ValThrThrLeuLysGlnGlnGln-----GlnLysLysGlnThr 2016
Db 6737 GCCAGAGGCTGAAAGTTTGTGATTAGACCTTGTGACGTTTAAAGCTGTAAGAAAGAAAT 6796
Qy 2017 PheThrLeuGlnArgProSerLysGlnGlnSerSerSerGlnMetGlnLeuLeuArgGln 2036
Db 6797 CTGACAAAACAATACAGAAAAACAAGGTCAGCTGTGCAACTGACATACAAAGTACTCTCT 6856
Qy 2037 SerLeuLysThrLysAspLeuGlnLeuGlnGlnAlaGlnLysGlnIleSerGlnAlaThr 2056
Db 6857 TCATTAAAGTCTGTAGAGAAAGAGCAAGCAGAGATACAGTCAAGAGAGATCT 6916
Qy 2057 -----AsnGlnIleLysAsnLeuThrAlaLysIleSerSer 2068
Db 6917 AAAACGTCAGTGAAGTCTTCAAGATCAGTTAAAGAGCTTAAATGAGGACGATACAGCC 6976
Qy 2069 Leu-----GlnGlnGlnIleLeuGln-----AsnAlaSerIleLeuAsnIleAlaLys 2085
Db 6977 TTGTGCTGACCAAGAAATTTAGAGCCACAGAACAGATCTAGACCCCAATAGAG 7036
Qy 2086 GlnArgGlnAsnLeuArgHiserLysGlnGlnLeuValSerGlnLeuGln----- 2102
Db 7037 GAAGAGCATCAGCTGAGAAATAGCATTTGAAAGCTGAGAGCCGCTAGAGCTTAATGAA 7096
Qy 2103 -----GlnLeuSerLeuThrLeuLysSerArgAspHisAlaPheAlaGlnSerLysArg 2120
Db 7097 AAGAGCAGCTCTGTCTTACACAACTGAAG-----GAAAGTAGCAT 7141
Qy 2121 GlnLysAspGlnAlaValAlaAsnLysIleAlaSerLeuAlaGlnGlnIleLysIleLeuThr 2140
Db 7142 CATGCAAGATTACTTAAGGGTAGAGTGAAGAACTTTGAAAGAGAGCTAGAGTGGCCAG 7201
Qy 2141 LysGlnMetAsp-----GlnPheArgAspSerLys-----GlnSerLeu 2153
Db 7202 ACAAAACAAGCAGATCAGCTCTTAGGACAGAAATTTCCAAAGAGAGTGAAGACCTTA 7261
Qy 2154 GlnGlnGlnSerSerHisLeuSerGlnGlnLeuLysCysThrLysThrGlnLeuGlnMet 2173
Db 7262 AAAGCAAAATATGAAAGGATGACCCAAAGCTGAGAGGCTGGAATTTGATGTTGTTACT 7321
Qy 2174 LeuLysGlnGlnLysGlnAspIleAsnAsnLysLeuAlaGlnLysValLysGlnValAsp 2193
Db 7322 ATAAAGGTGAGAAAAGAGATCTGCAAAATGATTAACAAAAGAGCAAGAGCAATATCT 7381
Qy 2194 GlnLeuLeuGlnHisLeuSerSerLeuLysGlnGlnLeuAspGlnIleGlnMetGlnLeu 2213
Db 7382-GAATT-----GAAATA 7393

Qy 2214 ArgAsnGlnLysLeuLeuArgAsnThrGlnLeuLysCysGlnLysMetAspIleMetGlnLysGln 2233
Db 7394 ATTAATTCATCTTTGAAAT----- 7414
Qy 2234 IleSerValLeuArgLeuMetGlnAsnGlnProGlnGlnGlnGlnAspValAlaGln 2253
Db 7415 -----ATTTCAGAAAAGAGCAGAGGAAAGATGACAGATGAAAGAAATCAAGCACT 7468
Qy 2254 ArgMetAspIleLeuGlnSerLysArgAsnGlnGlnIleGlnGlnLeuMetGlnLysIleSer 2273
Db 7469 GCCATGAGATGCTTCAACA-----CAATTAAAGAGCTTCAATGAGAGAGTGGCA 7519
Qy 2274 AlaValLysSerGlnGlnHisThrLeuLeuSerSerLeuSerSerGlnLeuGlnLysGln 2293
Db 7520 GCCCTGCATATGACCA----- 7537
Qy 2294 ThrGlnAlaHisLysHisCysMetLeuAsnIleLysGlnSerLeuSerThrLeuSer 2313
Db 7538 --GAGCCTGTAG-----GCCAAAGACAGAACTTAACT 7570
Qy 2314 ArgSerPheGlnSerLeuGlnThrGlnHisValLysLeuAsnThrGlnLeuGlnThrLeu 2333
Db 7571 AGTCAAGTAGAGTCTTGAACCTTGAGAGGCTCAGTTGTCACAGGCTTGATGAGGCC 7630
Qy 2334 LeuAsnLysPheLysValValLysArgThrAlaAlaValLysGlnAspHisSerLeuIle 2353
Db 7631 AAAATATATATATTGTTTTCATCTTCAGT-----ATGGCTCATTT 7675
Qy 2354 LysAspThrGlnLysAspLeuAlaAlaGlnGlnLysArgHisAspGln-----Leu 2370
Db 7676 CAAGAGTAGAAGATGCGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 7735
Qy 2371 ArgLeuGlnLeuGlnCysLeuGlnGlnHisGlyArgLysThrPheArgAspSerAlaSerGln 2390
Db 7736 AAAATCAAAATTCAGACCAAGACAGCTTGTCTTAACTGTGCCAGGTGAGAGGAG 7795
Qy 2391 GlnLeuLysPhe-----CysGlnIleGlnPheLeuAsnGlnLeuLeuPheLys 2406
Db 7796 CACCAACTTTGAGAGAGCAAAACTTAGAACTGAGAAATGTGACAGTGAATTTGAGACAG 7855
Qy 2407 LysAlaAsnIleIleGlnSerValGlnAspAspPheSerGlnValGlnAlaPheLeuAsn 2426
Db 7856 AAGATCCAAAGTCTACATCAAAATGCTCTTTGACAGACATTAGAAGTGTGCGAG 7915
Qy 2427 GlnValGlySerThrLeuGlnGlnGlnGlnGln-----HisLysLysGlnPheMetGlnThr 2445
Db 7916 AGTCTTACAAAGATCTAGAGAAATGAGCTTGAATTTGACAAATAATGACAAATAATGCTCTTT 7975
Qy 2446 LeuGlnGlnPheGly-----AspLeuHisVal 2454
Db 7976 GTTGAAAAGTAAACAAATGACTGCAAGAAAGAACTGAGCTGAGAGGAAATGATGAG 8035
Qy 2455 AspAlaLysLys-----LeuSerGlnGlnLysMetGlnGlnLysAsnArgGlnIleAla 2471
Db 8036 ATGGCACAGAAAACAGCAGAGCTGCAAGAAAGAACTGAGTGAAGAAATAGGCTAGCT 8095
Qy 2472 SerThrIleGlnLeuLeuThrLysArgLeuLysAlaValAlaGlnSerLysIleGlnArg 2491
Db 8096 GAGAGTTGCACTTACTGTTGGAAAGAAATAAAGAGC-----AGCAAGATCA-- 8143
Qy 2492 GlnIleThrValLysLeuAsnGlnPheGlnAlaLysLeuGlnGlnLysLysGlnGlnAsn 2511
Db 8144 -----TTGAAAGAGCTCACTAGCAAAAT 8167
Qy 2512 LysGlnLeuMetArgArgMetGlnHisGlyProSerAlaSerValMetGlnGlnGln 2531
Db 8168 AGTGATTTAAGAG-----AGCTTGATTTGATGACAAAGAGC 8206
Qy 2532 AsnAlaArgLeuLeuGlnLysLeuLysThrValGlnAspGlnSerLysLysLeuGlnSer 2551
Db 8207 CAGGTGAAAAGAGAGG-----AAAGTGAAGAGAGAAATAGCTGAATATACAGCTA 8257

Oy	385	GlulileuysglnleuNiileuysgluyluysbragllletrphilsleuthAsnIleVal	404
Db	292	GAATATGTGAATAGTCTGGAGAAACTAAAGCAAGATTCTCAT	345
Oy	405	ValAlaserSerGlnIuSerGlnIuAsp	416
Db	346	GTCAAGAGAGTCSAAGTGAATTTCCAGAAAGGACAACTGAATTCAGCAAAAACAAATA	405
Oy	417	ValIySalgIyValgATgValThrTrrAlarProGlyIysIleGlnAsnSerLeuHisAla	436
Db	406	GAATAAAGTGAACACAGAACTTAAAGAGTGAATCTGATGCTTGAAGAAGCAACAAAGCT	465
Oy	437	SerGlyValSerAspPheAspMet	445
Db	466	GCGCAGTGTGCAGATGTCTCTTGAAATCCATGCAATACACCAAAAAATTTTAACACT	525
Oy	446	SerArgLeuProGlyAsnPheSerIyLysAlaIysPheSerAspMetProSer	463
Db	526	CCACTAACACCAAGTCATATATATATGTGTCTCCAAAGTATGAAGATCTAAAGAAATAAT	585
Oy	464	PheProGluIleAspAspSer	476
Db	586	AATAAAGAGGTGAAGAAAGAAAGATTAGAGCAGAGGTAAAGCCTTGACAGCTAA	645
Oy	477	AspPheAspAlaIleuSerMetMetAspSerAsnGlyIleAspAlaGluTrrAsnIu	496
Db	646	AAAGCAAGCCACAGCTCTTCCACAGCCACCATGAATACCCGACATTTGCCCGCATAG	705
Oy	497	AlaSerIyValThr	509
Db	706	GCTTCATCATCTGTGTCTTCATGGCAGAGAAAGAAACCCCAAGTCATCTTCACTAAT	765
Oy	509		509
Db	766	TCTCAAGAACTCCAAATTAGAGAGATTCTCTGCATCTTACTTTTGGGGAACAAG	825
Oy	510	-----GlnSerMetIleAspPheGlyGlnIleSerAspSerValGlnPheHis	525
Db	826	GTGACTCCAAAGTCATCAACTTTTGCAAATAGGAAAGAAAGATGCTAAATAGCAATTTCTTT	885
Oy	526	AspSerSerIyGluAsnGlnIuLeuIrrIleuProIyAspSerGlyAspMetAlaGlu	545
Db	886	GACAAATTTACACAGCTCATCTTTTG	924
Oy	546	CysArgIySalaserPheGluIySerIuIleThrSerLeuGlnGlnIleuGlnSerIy	565
Db	925	GCGCAGAAATCAAGAGCTAAGAAACAAGATTAAATGAGTTGGAAGCTACGCTCCAAAGACAT	984
Oy	566	GlulGlnGluIyLysGlnIleValGlnSerPheGluIeulysIleAlaGluIleuGlnIu	585
Db	985	GAATAAGAAATGAAGAAAGCCAGTGAATAAGTTTCA	1032
Oy	586	GlnIuSerValIySalAlys	600
Db	1033	CAACTGGAG-----AAAGCAAAAGTGAATTAAATTGAAAGAAAGTTTGAACAAATGT	1089
Oy	601	ArgGlnHisSerIleAsnAlaGluValGlnIrrAspValGluIyGlnIuValAlaGly	620
Db	1090	AGGAGTGAAGTAGTAGAACAACAGCAAAATTCGAC	1125
Oy	621	GluMetSerValIleuGlyAspSerGlyTyrAsnAlaSerAsnSerAspLeuGlnAspSer	640
Db	1126	-----CAGCGCTCAACCAAGATATCTGCATGTGGAAACAAATACTGAAAAAATTG	1173
Oy	641	SerValAspGlyIySalArgLeuSerSerSerHisAspGluCysIleGlnHisArgIyMet	660
Db	1174	ACCGAAGAT-----TTGAGTTGTACAGGACCAAAATGCAGAAAGTCCAGATGTCTT	1224
Oy	661	LeuGlnGlnIyIleValAspLeuGlu-----GluPheIleGluAsnLeuAsnIyLysSer	679
Db	1225	CTGGAACAGAAATTAAGCAAAAAAGAAAGAGATTTCAGAGAGAGACTCTCCGT-----	1278

QY	660	GIUsnAspLysGlnLysSerSerGluInAspPheMetGluSerLscIleuNeuGlu	699
Db	1219	-----CAACACGCTCTTTCCAAACACTGGACCCAGAGTGCATCCAGTg-----	1322
QY	700	AlaIleMetAlaGluValAsnAlaLeuGluGluLeuAlaLeuMetArgSpAsnPe	719
Db	1324	-----AAGCCAGACTACCCGAGAGTTTACAGCAAGCCAAg---AATATG	1366
QY	720	AspAsnIlelle-----LeuGluAsn	726
Db	1366	CACAACTCTCCGACAGCTGAACCTGATAACTCATCATGTAAGCAACAGCTAGAAAC	1422
QY	727	-----GluThrLeuLysArgGluIleAlaAspLeuGluArgSer-----	739
Db	1426	AATTGGAAAGACTTTAAAGCAAAAAGTTGGCAGAGCTGAACAGGCTTCCAGCCAGTCA	1486
QY	740	LeuLysGluAsnGlnGluThrAsnGluPheGluIleLeuGluLysGluThrGln-----	757
Db	1466	ATCAAGAGGAAATGAGCTGAGGAGAAAGCATGAGGAAATGAAGAAGAAACAACTCCCT	1541
QY	758	LysGluHisGluAlaGlnLeuIleHisGluIleGlySerLeuLysLeuValGluAsn	777
Db	1546	AAGAGTCACTCTGAGCAAAAGCCAGAAAGCTCCACCTGGAGGCAAACTCAAGAAC	1601
QY	778	AlaGluMet-----TyrAsnGlnAsnLeuGluLysAspLeuGluThrLysThrLys	794
Db	1606	ATCAAAACGCTGTTAAATCATAGAGCCAGAAATTTTGCAGAAAGATTAAGAACCGAAGAT--	1667
QY	795	LeuLeuLysGlnGlnGluIleGlnLeuAlaGluLeuArgLysArgAlaAspAsnLeuGln	814
Db	1663	-----ACCTCTCAGAAACCATGTTAAGAGATCTTCAAGAAAAATAATAGCAGAGA	1711
QY	815	LysLysValArgAsnPheAspLeuSerValSerMetGlyAspSerGluLysLeu-----	832
Db	1717	AACTCCTTGACTTTAGAAAAACTGAAGCTTGCTGGCTGATCTCGAAAAACAGCGAGAT	1771
QY	833	CysGluGlu-----IlePheGlnLeuLysIleSerLeu	843
Db	1777	TGTTCTCAAGACCTTTGAGAAAAAGACATCATGTAACAACCTTAATGATTAAGTTA	1831
QY	844	SerAspAlaGluAlaValThrArgAspAlaGlnLysGluCysSerPheLeuArgSerGlu	863
Db	1837	AGCAAGACAGAGAAAGAGTCCAAA---GCCTTGCGAGTGCCTTAAGAGTTAAAAAGAAA	1891
QY	864	AsnLeuGlnLeuLysGluLysMetGluAspThrSerAsnTyrPyrAsnGlnLysGluLys	883
Db	1894	GAATATGATTTGAAAAGAGAGAAAACTCTGTTTCTTGTTGAAAAGTCAAAAAACGAAAA	1951
QY	884	AlaAlaSerLeuPheGluLysGlnLeuGluThrGlyLysSerAsn-----	898
Db	1954	CTTTTAACt-----CAGATGAAATCAGAAAAAGAAAACCTTCAGAGTAAATT	2007
QY	899	-----TyrLysLysMet	902
Db	2002	AATCACTTGAAACTTGTTCTGAGACACACAGCAAAATAAAAGTCATGATACACAGCAGA	2066
QY	903	GluAlaAspLeuGlnLysGluLeuGlnSerAlaPheAsnGluIleAsnTyrLeuAsnGly	922
Db	2062	GTAGAAACCGCTGGAGATGACACAGAAACCTTAAGTGCAGATCAGAAACCTTCAACAAC	2122
QY	923	LeuLeuAlaGlyLys-----ValProArgAspLeuLeuSerArgValGluLeuGlu	939
Db	2122	GTGTTAGACAGACTAAGTCACTGAGAGGTAGAGCCAGAAAACCTTAATAGAGCGCTACAG	2188
QY	940	LysLysValSerGluPheSerLysGlnLeuGluLysAlaLeuGluGluLysAsnAlaLeu	959
Db	2182	CAGAAA---GCTGAGTTCTCA-----GATCAGAAACATCATCAAG	2211
QY	960	GluAsnGluValThrCysLeuSerGluTyrLysPheLeuProAsnGluValGluCysLeu	979
Db	2218	GAAATAGAAATATCTGTTTGAAGCTTCTCAG---CTTACTGGCGCAAGTTAAAGATCTA	2277
QY	980	LysAsnGlnLysSerLysAlaSerGluIleMet-----	991

Db 2275 GAACCAAGCTTCACTTACTGTCTCAATATGAAATATGACAAAGACCGGTGTACCAAGC 2334
QY 992 -----LeuLeuLyvGlnGluLy----- 997
Db 2335 TTGCATGCCGAATATAGAGCCTCAGGGATCTGTATAAATCCAAAGATCTTCTGTGG 2394
QY 998 -----GluHis 999
Db 2395 ACAAAATGAATCATCAGAGAACTCTTTGGCTTTTATCAGCAGCCTGCCATGCATCAT 2454
QY 1000 Ser---AlaSerIleIleSerLyvGlnGluIleIle----- 1010
Db 2455 TCCTTGCATAATATATTTGAGACACAGAGACATGCCCTTCAGAGAGATGAATGTGCT 2514
QY 1010 ----- 1010
Db 2515 TTAGACGACACCAAAAGTCCGAAAATTCTGCCATCTTACAAATATAGATTGATTCAC 2574
QY 1011 -----MetGlnGlnGlnSerGlnGln 1017
Db 2575 GAATTTTCATTAGAGCTTCAAAACAGATGAATCAGACCTGCAAAAGCAGGTGAAGAG 2634
QY 1018 IleLeuGlnLeuThrAspGlnValThrHisThrGlnSerLyvAlaGlnGlnThrGlnGlu 1037
Db 2635 TTGGTCGAATATCAAAAGGAAATAGAGAAAATTCATGAAAGCAGAACAGATGCATCA 2694
QY 1038 GlnTyLeu-----GluMetLyvLysMetHisAspAsp----- 1048
Db 2695 AGTTTGTGGGTGAACAAGTCAGCGCATTTAGTAAGTTACAGAGACACTTCTGTGAC 2754
QY 1048 ----- 1048
Db 2755 CAGATGTGTGTGCTGAAACCTTAAGTGCCTTGAAACAGAAAAGAGCTGCACTT 2814
QY 1049 LeuPheGlnLyvTyIleArgAsnLyvSerGlu----- 1059
Db 2815 TTAAATGATTAAGTGAAGTAAGTACGACGACAGAGATTCAGAATTTAAAAAGCAGACCAT 2874
QY 1060 ---AlaGluAspLeuLeuArgGluMetGluAsnLeuLyvGlyThrMetGlnSerValGlu 1078
Db 2875 CTACTTGAAGACTCTTAAGAGGCTACAACTTTATCCGAAACCTTA---AGCTTGGAG 2931
QY 1079 ValLyv-----IleAlaAspThrLyvHisGlnLeuGlnGluThrIleArg 1093
Db 2932 AAGAAAGAAATGAGTTCATCTTCTTAATTAAGGAAATGAGAGCTGACCCAA 2991
QY 1094 Asp-----LysGlu-----GlnLeuLeuHisGlnLyvLysTyvPhePhe 1106
Db 2992 GAGAAATGGGACTCTTAAGGAAATTAATGCATCTTAAATCAAGAGAGATGAATTAATC 3051
QY 1107 GlnAlaMetGlnThrIlePhe-----ProIleThrProLeu 1118
Db 3052 CAGAAAACTGAGAGGTTTGCAAAACTATATAGTGAAGGAGAAAGCAATTCACAGTTA 3111
QY 1119 SerAspSerLeuProProSerLyvLeuVal-----GluGlyAsn 1131
Db 3112 TCTGATCAGTACAGCAAGAAAACCTTATTTACTACAAAGATGTGAAGAAACCGGAAT 3171
QY 1132 SerGlnAspProIle----- 1136
Db 3172 GCATGTAGAGATCTTAGTCAAAAATACAAAGCAGACAGAAAAGAAATTTAAATTAAGA 3231
QY 1136 ----- 1136
Db 3232 TGCTTGTAATGATGACTAGTCTTGTGAAAATAGGAAAATAGAGTTGGAACAGCTA 3291
QY 1137 -----GluIleAsnSerTyvHisAsnLeuIleAlaLeuAlaThrGlu 1150
Db 3292 AAGGAAGCATTTGCAAGAGAACACCAAGAAATCTTAACAAAATTTAGCATTTGCTGAAGA 3351
QY 1151 ArgAsn---AsnIleMetValCysLeuGlnUthr----- 1160

Db 3352 AGAAATCAGAAATCTGATGCTAGAGTTGGAGACAGTCAGCAAGCTGTGAGATCTGAGATG 3411
QY 1160 ----- 1160
Db 3412 ACAGATTAACAAACAAATTTTAAGAGCGAGCGTGTGTTAAACGAAGAAATCATGACT 3471
QY 1161 -----GluArgAsnSerLeuLyvGlnGlnValIleAspLeu-----AsnThr 1174
Db 3472 TTAAGGAAGAACAAACAAATGCAAAAGAGATTAATGACTTTTACAGAGAAATGAA 3531
QY 1175 GlnLeu-----GlnSerLeuGlnAlaGlnSerIle 1184
Db 3532 CAGCTGATGAAGATTAATGAGACTTAACATGATGATCAAAATCTGATGACAAACCAAT 3591
QY 1185 GlnLyvSerAspLeuGln-----LysProLyvGln 1194
Db 3592 AGGAACCTGTGAAAGAAAGAGAGAGTGAAGAAATCAATGTAATTTAACTCTAGATG 3651
QY 1195 AspLeuGlnGlnGlnGlnValLyvLeu-----LeuLeuGlnMetGlu 1208
Db 3652 GATCTTGAAGTTAAAGAAATTTCTTACATAGTTAATGCGCAGCTGTGCTGAATTAAGA 3711
QY 1209 LeuLeuLyvGlnHisLeuThrAspSerGlnLeuSerIleGlnLyvLeuGlnLeuGlnAsn 1228
Db 3712 GCTATG-----CTAAGAAATTAAGGAATTAATACTTCAGAAAGTGAGAAAGAGAAAG 3762
QY 1229 LeuGlnValThrGlnLyvLeuGlnThrLeuGlnGlnGlnMetLyvAsnIleThrIleGlu 1248
Db 3763 -----GAGTGCCTGCAGCATGAAATTACACACAAAT----- 3792
QY 1249 ArgAsnGlnLeuGlnThr---AsnPheGlnAspLeuLyvAlaGlnHisAspSer---Leu 1266
Db 3793 AGAGAGATCTTGAACACAGCAATTTGCAAGACATGACAGTACAGAAATTAAGTGCTT 3852
QY 1267 Lys-----GlnAspLeuSerGlu 1272
Db 3853 AAAGACTGAATAGATGCGGAGAAAGAAATGATATTTCAGGGCTCATGAGTTGTCAACA 3912
QY 1273 AsnIleGlnGlnSerIleGlnThrGlnAspGlnLeuAlaGlnGlnGlnLeuArg 1292
Db 3913 AGTCAAAAAGCAAAATGACACACCTTCAGTCTCTGCAAAACAAATGAAACAGCTGAAT 3972
QY 1293 GlnGlnLyvGlnLeuValAspSerPheArgGlnGlnLeuLeuAspCysSerValGlyIle 1312
Db 3973 GAGCTAGGAAATATGTGAATTAAGTACAGAGCTGAAAAGCTGAATCTGAATCAGCTG 4032
QY 1313 SerSerProAsnHisAspAlaValAlaAsnGlnLyvAlaSer----- 1327
Db 4033 AATGATTAAGGTCAAGATGATATCAGCAACTAGAAATAGCGAAGAGTAGAGAA 4092
QY 1328 ---LeuGlnGlnValAsnSerLeu-----GlnSerGlnMetLeuArgGlyCysIleArgAsp 1344
Db 4093 CTACTAATTAAGATTAATTAATTAATGATGACAGTGTCTTCCATGATGAGTTAGTG 4152
QY 1345 Gln----- 1345
Db 4153 GAAAGCATTAACAAGAGTGAATTTGGTGAACAACCAATGAACAGACCCCTGTGCTTTG 4212
QY 1345 ----- 1345
Db 4213 GCTCATTGAGAGAGATTAATCTTAGAGGACTTGACATTTGTGACAGAAAGATTCAA 4272
QY 1346 -----LeuGlnThrSerCysLeuValLeu 1353
Db 4273 ATGCACTTGCCGAATTCAGAGAAATTTCTTATCTTTAACAAGTGAACACAAATTTTAA 4332
QY 1354 -----ValSerGlnLeuGlnLeuLeuValArgAlaHisValLysSer 1366
Db 4333 CATGATCAGCACTGTACATAGACTTAATAATGTCAGAGCTGCGACAACTTGTGACTCA 4392
QY 1367 ValGlnGlnGlnLeuGlnGlnIleThrLyvLyvLeuAsnGlnLyvLeuGlnLyvGlnIleLeu 1386
Db 4393 TTAAGGCCGAAATTTGTGCTTGTTCACAGAAATCTGAAGAACTTTCAAGGTGACTTGGTG 4452

QY 1387 GlyLysSerGlu-----GluSerGluValLeuLysSerMetLeuGluSerLeuLys 1403
DB : : : : :
DB 4453 AAGGAGATCGACTGGGCTTGAGAGAGGAGGCTGCTTCATCCCTGCATCCCTGCTGTG 4512
QY 1404 GluAspAsnAsnLysLeuLysGluGlnAlaGlu----- 1414
DB : : : : :
DB 4513 CCTGACAGCTTAGCTTAGACAGTTGGAGACTCCTCTTTACAGACTCTTTAGAA 4572
QY 1415 -----GluTyrSerSerLysGluAsnGlnPhe 1423
DB : : : : :
DB 4573 CAGACAGAGATATGCTCTTTGAGTATTTAGAAAGGCGCTGTTACACAAACAGTGC 4632
QY 1424 SerLeuGluGluValPhe----- 1429
DB : : : : :
DB 4633 AGTGTAGATGAAGTATTTTTCAGACAGTCTGACAGAGAAATCTGACAGAAAGAAC 4692
QY 1430 ---SerGlySerGlnLysLeuValAspGluLe-----GluValLeuLysAla 1444
DB : : : : :
DB 4693 CCTTGGGCCCCAGCGAAGGGGTGTGAAAGCTTGAAGTCCCTCTGTGAGGTGACCGGAG 4752
QY 1445 GlnLeuLysAlaAlaGluGluValArgLeuGlu-----IleLysAspArgAspTyr 1460
DB : : : : :
DB 4753 TCCCTCGAAGACTGAGAGAAAGAAATGAAAGTCAAGGATTTATGAAATAAAGAAATT 4812
QY 1461 PheGluLeuValGlnThrAlaAsnThrAsnLeuValGlu--GlyLysLeuGluThrPro 1479
DB : : : : :
DB 4813 CAAGAGCTCGACAGCTTATTAGTTCTGAAAGGCAAGACTTGACTGCTTAGAGAACAG 4872
QY 1480 LeuGlnAlaAspHisGlu-----GluAspSerIleAspArgArgSerGlnGluMetGlu 1497
DB : : : : :
DB 4873 TATTTGTCAAGAAATGAACAGTGGCAACAGAGCTGCAAGCGGTGCTGTGAGATGAG 4932
QY 1498 IleLysValLeuGlyLysLeuGluValArgAsnGlnTyrLeuLeuGlu----- 1513
DB : : : : :
DB 4933 TCCAACTGGCGCGGCAAAAGAAACAGACAGCAAACTGCTCACTGAGCTGGAAGTACGA 4992
QY 1514 ArgLeuGlnGluGluLysLeuGluLeuSerAsnLysLeuGluIleLeuGlnLysGluMet 1533
DB : : : : :
DB 4993 GCATCCAGCTCAAGAGTCTGAGCTTAAAGTTCTCGG----- 5028
QY 1534 GluThrSerValLeuLysAspArgLeuGlnGlnLysLeuGluSerLeuLeuSerGlu 1553
DB : : : : :
DB 5029 -----TCTTGTGTCATCGACACAGAAAGATGATTCAAGGC----- 5067
QY 1554 AsnIleIleLeuLysGlnAsnIleAspThrThrLeuLysHisHisSerAspThrGlnAla 1573
DB : : : : :
DB 5068 -----CGAAATGAGAGCTGTGACATATCAAAAGAACATATCTCAAAACTACAGAA 5118
QY 1574 GlnLeuGlnLys-----ThrGlnGlnLysLeuGln 1583
DB : : : : :
DB 5119 AGAAACCAACCAATGATGTCATGATGATGATGATGATGATGATGATGATGATGAT 5178
QY 1584 Leu-----AlaLysAsnLeuAlaIleAlaIleSerAspAsnProIle 1598
DB : : : : :
DB 5179 CTAGACATTGAGAAATTAAGTACTGTGCTGATTTGAAACCAAGAGAGAGTGTCTGGG 5238
QY 1599 ThrGlnGluLysGluThr-----SerAla 1606
DB : : : : :
DB 5239 GAACAGTCCCGGAGATACCAATTAATGAGCTCCAGAGGAGATTAACCAAGGCGCTTTCA 5298
QY 1607 AspCysValHisProLeu----- 1612
DB : : : : :
DB 5299 GAATGCATTTTGAATTTGATTTTCTGCTCTTAATGCTTTGGTACTTGAATTTCTG 5358
QY 1613 -----GluGluLysLeuLeuLeuLeuThrGluGluLysHisGlnLysThrAsnGluGln 1630
DB : : : : :
DB 5359 GGGAAATCAGGAAGATATTCATTAATCTTCAACTGGGGGTAAAGAGACATCAATGAAAT 5418
QY 1631 GluLysLeuLeuHisGluLysAsnGluLeuGlnAlaGlnValGluLeuLysCysGlu 1650
DB : : : : :
DB 5419 TTGAGATTACTTCACTGTGTATAGAGAGCGGTGACAG-----AAA 5457

QY 1651 ValGluHisLeuMetLysSerMetIleGluSerLysSerSerLeuGluSerLeuHis 1670
DB : : : : :
DB 5458 GTTGAAAGTTGCTTAATGAATAAGAAATTAAGACTCAAAACTC----- 5502
QY 1671 GluLysHisAspThrGluGlnGlnLeuLeuAla-----LeuLys 1683
DB : : : : :
DB 5503 -----CATTTACAGAGAGTACACTAATGACCCAAATTTGAAGCATGCTAGAAATTGGA 5556
QY 1684 GlnGlnMetGlnValValThrGlnLysLysGluLeuGlnGlnThrHisGlnHisLeu 1703
DB : : : : :
DB 5557 AAAATAGTTGGGAACTTAAGAAAGAAACTCAGATTTAAGTAAAGAAATTTGAAATATTT 5616
QY 1704 ThrAlaGluValAspHisLeuLysGluAsnIleGluLeu-----GlyLeuAsnPheLys 1721
DB : : : : :
DB 5617 TCTTGTGATCACACAGAGTTACTCCAGAGAGTAAAGTCTTGAAAGGCTCAATTTGAT 5676
QY 1722 AsnGluValAlaGln--GlnLysThrThrLysGluGlnCysLeuLeuAsnLysLys-- 1739
DB : : : : :
DB 5677 TTAGAAATCGATCGAGATTAATCATCAGCTGAAGATATTGAGATATGTGGCCAAAGTG 5736
QY 1740 -----GluLeuGlnGlnSerGlnHisArgLeuGlnCys 1750
DB : : : : :
DB 5737 AATGACGTGAGAGAGAGATTTCTGTATGTGAAATGAGCTGATGAGATTCAGATCG 5796
QY 1751 Glu-----IleGluGluLeuMetLysSerLeuLys 1760
DB : : : : :
DB 5797 GAGAAAGCTAGCATGACATGAAGCCCTTACTCTGAGGGCTGACTTACAGGTATCTTAA 5856
QY 1761 AspLysGlnSerAlaLeuGluThrThrLeuLysGlnSerGlnLysValIle--AsnLeu 1779
DB : : : : :
DB 5857 ACAGAGAACTATGTTTGAAGAAAGAAACAAATGAATAAGCAAGAGTTATGTGCTGCT 5916
QY 1780 AsnGlnGlnMetGluMetValMetLeuGlnMetGluLysLysAsnSerGlnArgThr 1799
DB : : : : :
DB 5917 GAAGAGAACTCTCACTGCTGTCACAAAGTGAAGAAACCGCTTCGTGGAGAAATTAGATCT 5976
QY 1800 ValIleAlaGluArg-----AspGlnLeuGlnAspArgLeuArgGluSerValGlu 1816
DB : : : : :
DB 5977 ATGTCAAAAAAACCAGCGCACTGATGATGATGCTGTAATAAATGAAGAGAAACACAA 6036
QY 1817 MetSerIleGluThr-----GlnAspAsp 1824
DB : : : : :
DB 6037 ---GAGCTTGAGTCTCATCAAAAGTACGTCTCCATTCGATTCAGGTGGCAGAGCAGAG 6093
QY 1825 LeuArgLysAlaGlnValLeuGlnGlnLysAspLysValGlnGluLeuThrSer 1844
DB : : : : :
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QY 1845 GlnIleSerValLeuGlnGluLysIleSerLeuLeuGlnAsnGlnMetLeuTyrAsnAl 1864
DB : : : : :
DB 6154 GACAAAGCTCATCTCCAGAAAGAGCTGCAAGTTTGGAAAGAGACTCACAGGCACTGTCT 6213
QY 1865 AlaThrValLysGluThrLeuSerGlnLysArgAspLeuAsnGlnSerLysGlnHisLeu 1884
DB : : : : :
DB 6214 TTGACAAATGAGAGCTGGAAGAACCAATTCGACACACTGATTAAGAAAGAAATGTGCT 6273
QY 1885 PheSerGluIleGluThrLeuSerLeuSerLeuLysGluLysGluPhe----- 1900
DB : : : : :
DB 6274 GTCAAGGAATCTGAAGGCTCGAGGCTGAGTGAATGATGATTAAGAAAGCTGAAT 6333
QY 1901 -----AlaLeuGlnGlnAlaGluLysAspLysAlaAspAlaAlaArgLysThrIle 1917
DB : : : : :
DB 6334 GTTCCAAAGGCTTGAGAGCCGACGTGAGTGAAGAAAGGTGAGTTGCAATGAGCTGAGC 6393
QY 1918 AspIleThrGluLysIleSerAsnIle----- 1926
DB : : : : :
DB 6394 TCAACACAGAGAGAGTGCATCAGCTGAGAGAGGATTCGAAAGTTCGATTC 6453
QY 1927 -----GluGlnGlnLeuLeuGlnGlnAlaThrAsnLeuLysGluThrLeuTyrGlu 1943
DB : : : : :
DB 6454 GAGGCGATGAAGAAAGACAGCTGCATCCAGAGAAACTGAAAGAACGCGACGCGGAG 6513
QY 1944 ArgGluSerLeuIleGlnCysLysGluGlnLeuAlaLeuAsnThrGlnHisLeuArgGlu 1963


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Db 6514 AATGATTCCT- - - - - AAGATAAAGTTGAGAACCTTGAAGGGAATTCGAGATG 6564
Qy 1964 ThrLeuValSerLeuAspLeuAlaLeuGlyValMetGluGlnGluValArgAspGluAla 1983
Db 6565 TCAGAGAAACACAGAGAGCTAGTGA- - - - - CTTGATGCCGAGATTCCAAAGA- - - 6615
Qy 1984 AsnLysValIleAlaLeuThrGluLysMetSerSerLeuGluGlnGlnIleAsnGluAsn 2003
Db 6616 - - - - - GAACTAGAGACTTAAACACAAATAGAACAGATG 6651
Qy 2004 ValThrThrLeuLysGluGlyGlu- - - - - GlyGluLysGluThr 2016
Db 6652 GCCAGAGAGCTGAAGTTTGAATTAGACCTTTCACGCTTAAGGCTGAAGGCTGAAGAAAT 6711
Qy 2017 PheTyrLeuGlnArgProSerLysGlnGlnSerSerSerGlnMetGluLysLeuArgGlu 2036
Db 6712 CTGACAAAACAAATACAGAAAAACAGAGCTCAGTTCTCAGAACTAGACAACTAGTCTCT 6771
Qy 2037 SerLeuLysThrLysAspLeuGlnLeuGluGluAlaGluLysGluIleSerGluAlaThr 2056
Db 6772 TCATTAAAGTCTGTTAGAGAAAAAGAGCAAGAGATACAGATCAAGATCAAGAGATCT 6831
Qy 2057 - - - - - AsnGluIleLysAsnLeuThrAlaLysIleSerSer 2068
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Qy 2069 Leu- - - - - GluGluGluIleLeuGln- - - - - AsnAlaSerIleLeuAsnGluAlaValSer 2085
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Qy 2086 GluArgGluAsnLeuArgHisSerLysGlnIleuValSerGluLeuGlu- - - - - 2102
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Qy 2121 GluLysAspGluAlaValAsnLysIleAlaSerLeuAlaGluGluIleLysIleLeuThr 2140
Db 7057 CATGACAGATTACTTAAGGGTAGAGTGAAGAACTTGAAGAGAGAGCTAGAGTACCAGG 7116
Qy 2141 LysGluMetAsp- - - - - GluPheArgAspSerLys- - - - - GluSerLeu 2153
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Db 7297 GAATTA- - - - - GAAATA 7308
Qy 2214 ArgAsnGlnLysLeuArgAsnTyrGluLeuCySerGluLysMetAspIleMetGluLysGlu 2233
Db 7309 ATAAATTCATCTTTGAAAT- - - - - 7329
Qy 2234 ILeSerValLeuArgLeuMetGlnAsnGluProGlnGlnGlnGluAspArgValAlaGlu 2253
Db 7330 - - - - - ATTTGCAAGAAAAAGACAGAGAAAGTACGATGAAGAAATAATCAAGACT 7383
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Qy 2334 LeuAsnLysPheLysValValTyrArgThrAlaAlaValLysGluAspHisSerLeuIle 2353
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Qy 2354 LysAspTyrGluLysAspLeuAlaAlaGluGlnLysArgHisAspGlu- - - - - Leu 2370
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Qy 2472 SerThrIleGlnLeuLeuThrLysArgLeuLysValValGlnSerLysIleGlnArg 2491
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Qy 2492 GluIleThrValTyrLeuAsnGlnPheGluAlaLysLeuGlnGluLysLysGluGlnAsn 2511
Db 8059 - - - - - TTGAAGAGAGCTCACACTAGAAAT 8082
Qy 2512 LysGluLeuMetArgArgMetGluHisIleGlyProSerAlaSerValMetGluGlu 2531
Db 8083 AGTGAATTAAGAGAG- - - - - ACCCTAGATTGATGACACAAAGAC 8121
Qy 2532 AsnAlaArgLeuLeuGlyIleLeuLysThrValGlnAspGlnSerLysLysLeuGlnSer 2551
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Db 8173 CGG- - - - - CTTCAATGAACT 8187
Qy 2572 GluLys- - - - - ValAlaIleLeuGlnAspLysLeuLeuSerArgAsnAlaGluAlaGlu 2589
Db 8188 GAAAAGAAACACAGAGCTTGTCTTTGGAC- - - - - ACAACAAACACTATCAAGATAGAA 8241
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Db 8242 ATCCAGACATACCGAGAGAAATTAATGCTTAAAGAAAGATGTCTCAGTTCAACAGAGCTG 8301
Qy 2610 GluIleGluAsnLeuGlnLysMetValAlaLysGluAlaValProTyrLysGluGluIle 2629
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QY 2643 LyslleLysTyr-----SerLysAlaThrAspGlnGlu 2654
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      8398 AATCTAAATATGTAATCATGTTGAAAGAAAGAAATGAACGCGCCAGGGGAAATGAAG 8457
QY 2655 AlaTyrLeuLysSerCys-----LeuGluAspLysGluGluGlyLeuArgArgLeuLys 2672
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      8458 TTGTTGATCAAAATTCCTGTAACAGCGTGGAAGAGAAAGAAAGATCTGCAAGAAAGACCC 8517
QY 2673 GluGluLeuArgArgAlaGlnAlaAspAsnAspThrThlValCysValProLysAspTyr 2692
      :::::
      8518 TCTCAACTTCAAGCTGCACAGAGAAAGCAAAACA----- 8553
QY 2693 GlnLysAlaSerThrPheProValThrCysGlyGlyGlySerGlyTyrLeuAlaGlnSerThr 2712
      :::::
      8554 -----GGTACTGTTATGATAC 8571
QY 2713 AlaMetLeuValLeuGlnSerGlu-----LysAlaAlaLeuGlu----- 2725
      :::::
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QY 2726 ArgGluLeuSerHisTyrLysLysLysTyrHisHisLeuSerArgThrMetSerSer 2745
      :::::
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QY 2822 ---ProGlyLys----- 2824
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      8965 CACCTGCAAGAGACAGAGAGTACTGAGTTTGAAGCCAGAGGACTTCCAGAGTTGA 9024
QY 2825 -----ThrGlyMetHisLys-HisIle----- 2831
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QY 2832 -----LeuSerProSerLysValGlyLeuHisLysLysArgAlaLeuSerPro-- 2847
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QY 2848 ----- 2850
      :::::
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QY 2868 nLeuThrGluSerThrLeuPheAspAsnLeuSerSerProCysLysGlnGlnLysValIle 2888
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RESULT 10
US-09-954-456-1153
; Sequence 1153, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1153
; LENGTH: 10211
; TYPE: DNA
; ORGANISM: Homo sapiens
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Score: 1139.00 Matches: 703
Percent Similarity: 37.36% Conservative: 556
Best Local Similarity: 20.86% Mismatches: 1052
Query Match: 7.71% Indels: 1060
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QY 353 lLeuAspLeuLysLysGlnLeuGlnAsnLeuGlnLysSerSerSerGluThrLysAlaGln 372
      :::::
      172 AAGCAGCAAGAGCAAGTTTCAGCTTGCAGCTCTGAGGCTGCGCTCAGAAACCAACAG 231
Db 373 AlaMetAlaLysGluGlu-----HisThrGlnLeuLeuAla 384
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QY 385 GluLeuLysGlnLeuHisLysGluArgGluAspArgGlnIleThrHisLeuThrAsnIleVal 404
      :::::
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QY 385 GluLeuLysGlnLeuHisLysGluArgGluAspArgGlnIleThrHisLeuThrAsnIleVal 404
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Db 2335 TTGCATGCCGAATATAGAGCCTCAGGGATCTGTAATAATCCAAAGATGCTTCTGTG 2394
 QY 998 -----GluHis 999
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 QY 1010 ----- 1010
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 QY 1011 -----MetGlnGlnSerGlnGln 1017
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1430 ---SerGlySerGluLeuValAspGluLe-----GluValLeuVal 1444
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5068 -----CGAAATGAGAGCTGTACATATCAAAAGAACATATCTCAGAACTACAGAA 5118
1574 GluLeuGluVal-----ThrGluGluGluGlu 1583
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1584 Leu-----AlaValAsnLeuAlaIleAlaSerAspAsnProIle 1598
5179 CTAGACATTGAGAAATTAAGTGAAGCTGTGATGAAACCCACAGAGAGTCTTGGG 5238
1599 ThrGluGluValGluThr-----SerAla 1606
5239 GACAGCTCCCAAGATTAACATTAATAGCTCCAGGGAGAAATTAACAGGAGCTTCTCA 5298
1607 AspCysValHisProLeu----- 1612
5299 GAATCATTTTGCATTTCTGCTCTAATGCTTGGTACATGATTTCTCG 5358
1613 -----GluGluValIleLeuLeuValThrGluGluValHisGluValThrAsnGluGlu 1630
5359 GCGAATCGAAGAAATCATTAATCTTCAACTGCGGTAAAGAGACATCAATAGAGAT 5418
1631 GluValSerLeuHisGluValAsnGluLeuGluGluAlaGluValGluLeuValCysGlu 1650
5419 TTGAATTAATCTTCAATGATGAGAGCCGTGACAG-----AAA 5457
1651 ValGluHisLeuMetLeuSerMetIleGluSerLeuValSerSerLeuGluSerLeuGluHis 1670
5458 GTTGAAGTGTCTTAATGAATGAAGATTAAGACTCAAACTC----- 5502
1671 GluValHisAspThrGluGluGluValLeuVal-----LeuVal 1683

5503 -----CATTTACAGAGGTACACTAATGACCAAAATTGAGCATGCTAGATTTGGA 5556
1684 GluGluMetGluValValThrGluGluValGluLeuGluGluThrHisGluHisLeu 1703
5557 AAAATAGTGGGAAATTAAGAAAGAACTCAGATTTTGAAGTGAAGAAATTTGAAATTTT 5616
1704 ThrAlaGluValAspHisLeuValSerLeuValGluLeu-----GlyLeuAsnProIle 1721
5617 TCTTGTGATCAGCAGAGGTACTCCAGAGAGTGAAGAACTTGAAGGCTCAATTTCTGAT 5676
1722 AsnGluAlaGlu---GluValThrThrGluGluGluValLeuValAsnGluValHis 1739
5677 TTGAAGAAATGATGATGATTAATCATCATCAGTGAAGATTTGAGATTAATGCGCAAGCTG 5736
1740 -----GluLeuGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1750
5737 AATGACAGCTGGAAGAGAGATTTCTGATGATGGAAGAAATGAGCTGATGATGATGATG 5796
1751 Glu-----IleGluGluLeuMetLeuSerLeuVal 1760
5797 GAGAAAGCTAGCATTTGACATGAGAGCCCTTACCTGAGAGCTGATTAAGGTAGTCA 5856
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1800 ValIleAlaGluVal-----AspGluGluGluGluGluGluGluGluGluGluGluGlu 1816
5977 ATGTCAAAAGAAACAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 6036
1817 MetSerIleGluThr-----GluAspAsp 1824
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6094 GTGAAGAAAG 6153
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1901 -----AlaLeuGluGluAlaGluValAspValAlaAspAlaAlaArgValThrIle 1917
6334 GTCTCAAGAGCTTGAAG 6393
1918 AspIleThrGluValIleSerAsnIle----- 1926
6394 TCACACAG 6453
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RESULT 11
US-09-967-768A-186
Sequence 186, Application US/09967768A
Patent No. US20020150877A1
GENERAL INFORMATION:
APPLICANT: Augustus, Meena
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
FILE REFERENCE: 689290-72
CURRENT APPLICATION NUMBER: US/09/967,768A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/60/236,109
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,034
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,111
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 325
SOFTWARE: PatentIn version 3.0
SEQ ID NO 186
LENGTH: 10211
TYPE: DNA
ORGANISM: Homo sapiens
US-09-967-768A-186
Alignment Scores:
Pred. No.: 1,236-62 Length: 10211
Score: 1139.00 Matches: 703
Percent Similarity: 37.36% Conservative: 556
Best Local Similarity: 20.86% Mismatches: 1052
Query Match: 7,71% Indels: 1060
Gaps: 139
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 QY 998 -----GluHis 999
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D6	2695	AGTTTGTGGCTGAACAACAGTCACGGCATTTAGTAAGTAACAGAAAGACACTTCGCTCAC	2754
QY	1048	-----	1048
D6	2755	CAGAAATGTTGTGCTGAACCTTAAGTCCTTGAGAAACAAGAAAAAGAGCTCAACTT	2814
QY	1049	LeupheGluysrYrIleArgAsnLysSerGlu-----	1059
D6	2815	TTAAATGATTAAGTAGAGAAACTGACGAGCGACAGATTCAAGATTAAAAAGACCAACCAT	2874
QY	1060	--AlaGluAspLeuLeuArgGluMetGluAsnLeuysgIlyThrMetGluSerValGlu	1078
D6	2875	CTACTGTAAGACTCTCTTAAGAGACTACACTTTATTCGAAACCCTA--AGCTTGAG	2931
QY	1079	ValIys-----IleAlaAspThrLysHisGluLeuGluIuThrIleArg	1093
D6	2992	AAGAAAGAAATGAGTTCATCATTTCTCTTAATTAAGGAAATTTGAAGAGCTGACCCAA	2991
QY	1094	Asp-----LysGlu-----GluLeuLeuHisGluLysLysrPhePhe	1106
D6	2992	GAGATGGACTCTTAAGAAATTAATGCATCTTAATCAAGAGAGATGAACCTAATC	3051
QY	1107	GlnAlaMetGlnThrIlePhe-----ProIleThrPheLeu	1118
D6	3052	CAGAAAGTAGAGAGTTTGCAAACTATATAGATGAAGGAGAAAGCAATTCAGAGTTA	3111
QY	1119	SerAspSerLeuProProSerLysLeuVal-----GluGlyAsn	1131
D6	3112	TCTGATCAGTACAGACAGAAAACTTATTTTACTACAAAGATGGAAGAAACGGAAAT	3171
QY	1132	SerGlnAspProIle-----	1136
D6	3172	GCATATGAGAGTCTTAGTCAAAAAATACAAAGCAGACAGAAAAGAATCTTAATTAGAA	3231
QY	1136	-----	1136
D6	3232	TGCTTGCTAAATGAATGCATGATCTTTGTGAATAATGAAAAATGAGTTGGAACAGCTA	3291
QY	1137	-----GluIleAsnAspTryHisAsnLeuIleAlaLeuAlaThrGlu	1150
D6	3292	AAGAGAGACTTTGCAGAGAACACACCAAGAATTTCTTAACAAAATTATGACTTTGCTGAAGAA	3351
QY	1151	ArgAsn--AsnIleMetValCysLeuGluThr-----	1160
D6	3352	AGAATACAGATCTGATCTGATGAGTGGAGACAGTCAGCAAGCTGTGAGATCTGAATG	3411
QY	1160	-----	1160
D6	3412	ACAGATAACAAAACAATTTCTAAGACGAGCGTGTGTTAAAGCAAGAAATCATGACT	3471
QY	1161	-----GluArgAsnSerLeuysGluIuValIleAspLeu-----AsnThr	1174
D6	3472	TTAAAGAGAGAACAAAAACAAATGCAGAAAGAGTTAATGACTTTTACAGAGAAATGAA	3531
QY	1175	GlnLeu-----GlnSerLeuGlnAlaGlnSerIle	1184
D6	3532	CAGCTGATGAGTAGTAATGAGACTTAACATGATGTCAAATCTTAGATCAGAACCAATT	3591
QY	1185	GluLysSerAspLeuGln-----LysProLysGln	1194
D6	3592	AGGAATCTTGTAAGAAAGAGAGAGTAGAGAAATCAATGTAAATTTAAACCTCAAGATG	3651
QY	1195	AspLeuGlnGluGluGluValLysLeu-----LeuLeuGluMetGlu	1208
D6	3652	GATCTTGAAGTTAAAGAAATTTCTCTAGATAGTTAATGCGCAGCTTGCTCAATTGAA	3711
QY	1209	LeuLeuLysGlyHisLeuThrAspSerGlnLeuSerIleGluLysLeuGlnLeuGlnAsn	1228

Db	3712	GCTATG-----CTAAGAAATTAAGAAATTAATACTTCAGGAAAGTGCAGACGACAG	3762
Qy	1229	LeuGIuValIThrGIuLysLeuGIuInThrLeuGIuInGIuInuLysAsnIleThrIleGIu	1248
Db	3763	-----GAGTGCCTGCAGCATGAATTAACAGACAAATT-----	3792
Qy	1249	ArgAsnGIuLeuGIuInThr---AspPheGIuAspLeuValAsnIleValAspSer---Leu	1266
Db	3793	AGAGAGAGATTGTGAACCCAGCAATTTGCGAAGACATGCACACAAAGAAATTTAGTGGCCTT	3852
Qy	1267	Lys-----GlnAspLeuSerGIu	1272
Db	3853	AAAGACTGTGAATTAAGATGCGGAAAGAAAGTAATTTTCAGGGCCTCATGACTTGTCAACA	3912
Qy	1273	AsnIleGIuInserIleGIuInThrGlnAspGIuLeuValAsnIleValAsnIleGIuLeuArg	1292
Db	3913	AGTCAAAACGACAAATGCACACCTTCAGTGCCTCTCGCAACCAACAAATGAAACAGCTGAAAT	3972
Qy	1293	GIuInLysGIuLeuValAspSerPheArgGlnGIuLeuAspCysSerValGIlyle	1312
Db	3973	GAGCTAGAGAAATATGTGAATACTCGCAGGCTGAAAAGATGATGAACTCGTAACTGACCTG	4032
Qy	1313	SerSerProAsnHISAspAlaValAlaAsnIleGIuLysValSer-----	1327
Db	4033	AATGATTTAAGGTCAGATGTATGATACAGCAACTGAGAAATGGGAGAGAGCTAGCGAAA	4092
Qy	1328	--LeuGIuGIuValAsnSerLeu-----GlnSerGIuLeuValArgGIuValAsp	1344
Db	4093	CTACTTAATGAAGTTAAATTTAAATGATGACAGTGTGCTTCCTCAATGGTGAATTAGTG	4152
Qy	1345	GIu-----	1345
Db	4153	GAAGCATACCGAGAGTGAAATTTGTGAACCAACCAATGAAACAGACCCCTGTCTTTTG	4212
Qy	1345	-----	1345
Db	4213	GCTCCATTGACGAGAGTAATTCTTACGACACTTGACATTGTGCACAAAGAAATTCAA	4272
Qy	1346	-----LeuGIuInThrSerCysValAsnLeu	1353
Db	4273	ATGCACCTTGGCCGAATTCGAAGAAATAATCTTATCTTTACAAAGTGAACACAAATAATTTA	4332
Qy	1354	-----ValSerGIuLeuGIuLeuValAsnIleValAsnIleSer	1366
Db	4333	CATGATCAGCACTGTGAGATGAGCTTAAATATGCAGAGCTGCAGACCTATGTTGACTCA	4392
Qy	1367	ValGIuGIuGIuAsnLeuGIuInleThrLysValAsnGIuLeuAsnGIuLysGIuLysLeu	1386
Db	4393	TTAAAGGCCGAAATTTGGTCTTGTCTCAACGAATTCGAGAACTTTCAAGGTGACTTGGTG	4452
Qy	1387	GIuLysSerGIu-----GlnSerGIuValLeuLysSerMetLeuGIuAsnLeuLys	1403
Db	4453	AAGAGATGCAGCTGGGCTTGGAGAGAGGGCTCTTCATCTCTGTATCTCTTGTGTG	4512
Qy	1404	GIuAspAsnLeuLysLeuLysGIuGIuAlaGIu-----	1414
Db	4513	CCTGACAGCTCTTAGCTTAGACAGTTTGGAGACCTCTCTTTTACAGAGCTTTTAGAA	4572
Qy	1415	-----GluTyrSerSerLysGIuAsnGIuPhe	1423
Db	4573	CAGACAGAGATATGTCTCTTTTGAATTAATTTAGMAAGGGCTGTTTCAGCAAAACAGATGC	4632
Qy	1424	SerLeuGIuGIuValAspPhe-----	1429
Db	4633	AGGTAGATGAAGATTTTTCGACAGAGCTGCAGAGAGAGAAATCTGACAGAGAAAGAAAC	4692
Qy	1430	--SerGIuSerGIuLysLeuValAspGIuIle-----GIuValLeuLysVala	1444
Db	4693	CCTTTCGGCCCCAGGAAAGGCTGTGAAGAGAGTGAAGTCCCTGTGTGAGGTGACCGGACG	4752
Qy	1445	GlnLeuLysValaIleGIuGIuValAsnGIu-----IleLysAspArgAspTyr	1460
Db	4753	TCCCTCGAAGAGCTTAGAAGAAAGAAATGTCMAAGGATTAAGAAATTAAGAAATTT	4812

Oy	1461	FheglIuLeuValGlnThrAlaAsnThrAsnLeuValGlu--GlyLysLeuGluThrPro	1479
Db	4813	CAAGAGCTTCGAGCAGATTATTAAGTTCTAAMAGCAAGCTTGACTGCTTACGAAACAG	4872
Oy	1480	LeuGlnAlaAspHisGlu-----GluAspSerIleAspArgSerGluIleuGlu	1497
Db	4873	TATTTCGAGAAATCGAACACAGTGGCAACAGAACTGCACAGAGTCACTCTGGAGATGGAG	4932
Oy	1498	IleLysValLeuGlyLysLeuGluArgAsnGlnTyLLeuLeuGlu-----	1513
Db	4933	TCCAAAGTTGGCGCGCAAAAGAAACAGACCGAAACAACCTGCACCTTGAACTGAAAGTACA	4992
Oy	1514	ArgLeuGlnGluGlyLysLeuGluLysSerAsnLysLeuGluIleLeuGlnLysIleuMet	1533
Db	4993	CGACTCCAGCTACAAAGCTCTGGACTTAAAGTTCTCGG-----	5028
Oy	1534	GluThrSerValLeuLeuLysAspAspLeuGlnGlyLysLeuGluSerLeuLeuSerGlu	1553
Db	5029	-----TCTTCTCTGGACTGCACACAGAAAGATGCTATTCAAGGC-----	5067
Oy	1554	AsnIleIleLeuLysGluLysAsnIleAspThrLysLysHisHisSerAspThrGlnAla	1573
Db	5068	-----CGAATGAGAGCTGTACATATCAAAAAGACATCTTCAGAAACTACAGAA	5118
Oy	1574	GlnLeuGlnLys-----ThrGlnGlnLeuGln	1583
Db	5119	AGAACACCAAAAGCATGATGTTTCATGAGTTTGTGATAAAGATGCTCACACAGACTCAT	5178
Oy	1584	Leu-----AlaLysAsnLeuAlaIleAlaAspAspAspCysProIle	1598
Db	5179	CTAGACATTGAGAAATAAAGTAACTGAGCTGTGTGTTGAAACCCACAGAGAGTGTCTGGC	5238
Oy	1599	ThrGlnLysGluThr-----SerIa	1606
Db	5239	GAAACAGTCCCAAGATACCAATTTATAGCTCCAGGGAAAGATAAACCCAGGGCTTTCA	5298
Oy	1607	AspCysValHisProLeu-----	1612
Db	5299	GAATGCATTTCTGAATTTGTCATTTTCTGCTCTTAATGCTTTGTACTATGATTTCTCTG	5358
Oy	1613	-----GluGlnLysIleLeuLeuLeuThrGlnGluLysHisGlnLysThrAsnGluGln	1630
Db	5359	GCGAATACGGAAGATATCCATTAATTTTCACTCGCGGTAAAGAAAGACATCAAAATGAGAT	5418
Oy	1631	GluLysLeuLeuHisGlnLysAsnGlnLysLeuGlnGlnAlaGlnValGluLeuLysCysGlu	1650
Db	5419	TTGAGATTACTTCAATGATGATGAGGACCGGTACACA-----AAA	5457
Oy	1651	ValGlnHisLeuMetLysSerMetIleGluSerLysSerSerLeuGluSerLeuGlnHis	1670
Db	5458	GTTGAAAGTTGTCTTAATGAATGAATAAATTAAGACTCAAAATCTG-----	5502
Oy	1671	GluLysHisAspThrGlnGlnGlnLeuLeuAla-----LeuLys	1683
Db	5503	-----CATTTACAGAGAGGTACAAATTAATGACCAAAATTTGAAGCTGCATAGATTGGAA	5556
Oy	1684	GlnGlnMetGlnValValThrGlnGlnLysLysLeuGlnGlnThrHisGlnHisLeu	1703
Db	5557	AAAATAGTGTGGGAACTTACAGAAACAACTCAGACTTTTAAGTAAAAATTTGGAAATATTTT	5616
Oy	1704	ThrAlaGlnValAspHisLeuLysGlnLysAsnIleGluLeu-----GlyLeuAsnProLys	1721
Db	5617	TCTTGTGTATCACCAGAGTTACTCCAGAGAGTGAAGAACTTTGAAAGGCTCAATTTCTGAT	5676
Oy	1722	AsnGlnAlaGln-----GlnLysThrThrLysGlnGlnCysLeuLeuAsnGlnLysLys--	1739
Db	5677	TTAGAAATGATCATGATTAATCATCAGGTGAAGATTTGGAGATTAATGTGGCAAGGTG	5736
Oy	1740	-----GluLeuGlnGlnSerGlnHisArgLeuGlnCys	1750
Db	5737	AATGACAGCTGGAAGAGAGATTTCTTATGTGGAAATTAAGACTGATAGGATGATCAGATCG	5796

QY	1751	GlU-----	-----	llegluileuMeLysSerLeuLys	1760
Db	5797	GAGAAAGCTACCATTTAGACATGAAGCCCTTACCTGGAGGCTGA	CTTAAAGATGATTTCA	5856	
QY	1761	AspYsgIuSerAlaLeuGluThrLeuLysGluSerGluLysValIle--	AsnLeu	1779	
Db	5857	ACAGAGAAAGCTATGTTTATGAAAAAGACATGATAATGAACGAAGGTTATTTGTCGCTT		5916	
QY	1780	AsnGluGluMetGluMetValMetLeuGluMetGluGluLeuLysAsnSerGluArgThr		1799	
Db	5917	GAGAGAAAGCTCTCAGTGTGCACAAGTGAGAGAAACACAGCTTCTGTGGAGATTGATTA	CT	5976	
QY	1800	ValIleAlaGluArg-----	AspGluLeuGluAsnSerLeuArgGluSerValGlu	1816	
Db	5977	ATGTCAAAAAAACCCACGGCAGCTGGATTCAGTTGCTGAAAAAATGAAGAGAAAAACAA		6036	
QY	1817	MetSerIleGluThr-----	-----	GlnAspAsp	1824
Db	6037	---GAGCTTGAGTCTCATCAAAAGTACGTCTCATTTGACCTTACGGTGGCAGAGGCAAG		6093	
QY	1825	LeuArgLysAlaGluGluAlaLeuGluGlnGlnLysAspLysValGlnGluLeuThrSer		1844	
Db	6094	GTGAAGAGAAAGACGGAACCTCTTCAAGCTTTGCTCCTCATGTGAGTGAAGCTTTAAA		6153	
QY	1845	GlnIleSerValLeuGluGluLysIleSerLeuLeuGluAsnGlnMetLeuTyAsnVal		1864	
Db	6154	GACAAACCTCATCTCCAGAAAAACCTGCAGAGTTTGGAAAAAGCATCACAGGCACTGCT		6213	
QY	1865	AlaThrValLysGluThrLeuSerGluArgAspSerLeuAsnGlnSerLysGlnHISLeu		1884	
Db	6214	TTGCAAAATGTGAGCTGGAAAAACCAATTTGCACAATGAATTAAGAGAAAGATTGCTT		6273	
QY	1885	PheserGluIleGluThrLeuSerLeuSerLeuLysGluLysGluPhe-----		1900	
Db	6274	GTCAAGAAATGTGAAGCGCTGCAGCCAGATGTAGTGAATTCAGATTATGAAGACTGAT		6333	
QY	1901	-----AlaLeuGluGlnAlaGluLysAspLysAlaAspAlaAlaArgLysThrIle		1917	
Db	6334	GTCTCCAAGCGCTTGGAGCGCGCATCTGTGAGAAAGTGAGTTGCGATTGAGCGCTGAC		6393	
QY	1918	AspIleThrGluLysIleSerAsnIle-----		1926	
Db	6394	TCAACACAGAGGAGGTGCATCACTGACAGAAAGAGCATCGAGAACTGAGAGTTGCAATT		6453	
QY	1927	-----GluGluGlnLeuLeuGlnGlnAlaThrAsnLeuLysGluThrLeuTyGlu		1943	
Db	6454	GAGGCCGATGAAAAAGAACGACGCTGCACATCGCAAGAACTGAAGAAACGGACGGGAG		6513	
QY	1944	ArgGluSerLeuIleGlnCysLysGluGlnLeuAlaLeuAsnThrGluHISLeuArgGlu		1963	
Db	6514	AATGATTCACCTT-----AAGATTAAGTTGAGAACTTGAAGAGGAATTCACATG		6564	
QY	1964	ThrLeuLysSerLysAspLeuAlaLeuGluLysMetGluGlnGluArgSerGluAlaAla		1983	
Db	6565	TCAAGAGAAAAACGAGAGCTAGTATT-----CTTATGCCGAGAAATTCCAAGACA--		6615	
QY	1984	AsnLysValIleAlaLeuThrGluLysMetSerSerLeuGluGlnGlnIleAsnGluAsn		2003	
Db	6616	-----GAAGTAGAGCTTAAAAAACAAATATGAAGAGATG		6651	
QY	2004	ValThrThrLeuLysGluGluGlu-----	GlyGluLysGluThr	2016	
Db	6652	GCCAGAAAGCGTGAAGTTTGAATTGACCTTGTCACGTTAAGCTGAAAAAGAAAT		6711	
QY	2017	PheThrLeuGlnArgProSerLysGlnGlnSerSerSerGlnMetGluGluLeuArgGlu		2036	
Db	6712	CTGACAAACCAATATACAGAAAAACAAGTCACTTGACAACTACGACAAATTA	CTCT	6771	
QY	2037	SerLeuLysThrLysAspLeuGlnGluGlnGlnAlaGluLysGluLysSerGluAlaThr		2056	
Db	6772	TCAATTAATCTCTGTTAAGAAAGAAAGACGACAGATACGATCAAAAGAAATCT		6831	
QY	2057	-----AsnGluIleLysAsnLeuThrAlaLysIleSerSer		2068	

Db	6832	AAACTGCAGTGGAGATCTTCAGATCAGTAAAGGAGCTTAAATGAGGCAGTACACCC	6891
Oy	2069	Leu-----GluGluGluIleuGln---AsnIleSerIleLeuasnGluAlaValSer	2085
Db	6892	TTGTGTGGTACCAAGAAATTATTAAGAGCCACAGAAACAGAGCTTACAGCCCAATAAG	6951
Oy	2086	GluArgGluasnLeuArgHisSerIlysglnLeuValSerGluLeu-----	2102
Db	6952	GAAGAGCATCAGCTGAGAAATAGCATTTGAAAAAGCTGAGAGCCCGCTGAAGCTGATGAA	7011
Oy	2103	-----GlnLeuSerLeuThrLeuIlySerArgAspHisAlaPheAlaGlnSerIlyArg	2120
Db	7012	AAGAAAGCGCTCTGTCTTATCCAAACCTGAAG-----GAAAGTAGCAT	7056
Oy	2121	GluIlySerAspGluAlaValAsnIlySerIleLeuAlaGluIlyIleValIleuThr	2140
Db	7057	CATCGACGTTTACTTAAAGCGTAGAGTGGAGAACCTTGAAGAAGAGCTACAGATTACCG	7116
Oy	2141	LysGluMetAsp-----GluPheArgAspSerIly-----GluSerLeu	2153
Db	7117	ACAAACCAAGAGCATGCGACTTGTAGCGACAGAAATTCCAAAGGAGAGTAGAGACCTTA	7176
Oy	2154	GlnGluGlnSerSerHisIleuSerGlnIleuGlySerTrpIlyIlyThrGluLeuGlnMet	2173
Db	7177	AAAGCAAAATAGAAAGGATAGACCCAAAGCTGAGAGGCTTGAAATTGAGTGTGTAAT	7236
Oy	2174	LeuIlySerGlnIlySerGluAspIleAsnAsnIlySerIleAlaGluIlyValIleAsp	2193
Db	7237	ATTAAGCTACAAAAGAAATATCTGCAAAATGAATTACAAAAGACCAAGACGAATATCT	7296
Oy	2194	GluLeuLeuGlnHisIleuSerSerLeuIlysglnLeuAspGlnIleGlnMetGluLeu	2213
Db	7297	GAATTA-----GAAATTA	7308
Oy	2214	ArgAsnGluIlyIleuArgAsnTrpGluLeuGlySerGluIlySerMetAspIleMetGluIlyGlu	2233
Db	7309	ATTAATTCATCATTTGAAAT-----	7329
Oy	2234	IleSerValIleuArgLeuMetGlnAsnGluProGlnGlnGluAspAspValAlaGlu	2253
Db	7330	-----ATTGTGCAAGAAAAAGACAGACAGAAAGTACAGTAAAGAAATCAAGCACT	7383
Oy	2254	ArgMetAspIleLeuGlnSerArgAsnGlnIlyleGlnIlyLeuMetGluIlyIleSer	2273
Db	7384	GCATGAGAGATGCTTCACAAAC-----CAATTAAAGAGCTCAATGACAGAGTGGCA	7434
Oy	2274	AlaValIlyTrSerGluGlnHisThrLeuLeuSerSerLeuSerSerGluIlyGlu	2293
Db	7435	GCCTGCTAATGACCAA-----	7452
Oy	2294	ThrGluAlaHisIlyValHisCysMetLeuAsnIleIlyGluSerLeuSerSerThrLeuSer	2313
Db	7453	---GAGCGCTGTAG-----GCCAAAGACAGAACTTTAGT	7485
Oy	2314	ArgSerPheGlySerLeuGlnThrGluHisValIlyIlyLeuAsnThrGlnLeuGlnThrLeu	2333
Db	7486	AGTCAAGTAGAGCTGCTTGAAGCTTGAAGAGCTCAGTTCACAAAGCCTTGATGAGGCC	7545
Oy	2334	LeuAsnIlyPheIlyValIlyTrpArgThrAlaAlaValIlyGluAspHisSerLeuIle	2353
Db	7546	AAAAATATATTTATTTGTTTCCAACTCTTCAGTG-----AATGCGCTCATTT	7590
Oy	2354	LysAspTrpArgIlyIlyAspLeuAlaAlaGluGlnIlyAspArgHisAspGlu-----Leu	2370
Db	7591	CAGAGAGTAGAAGATGGCAGACAGAAATCGAGAGAAAGAGATGAAGAAATCAGTAGATG	7650
Oy	2371	ArgLeuGlnLeuGlnCysLeuGlnGlnHisGlyIlyArgIlyTrpSerAspSerAlaSerGlu	2390
Db	7651	AAAATATCAATTCACAAAGACAGAGAGCTTGTCTTAAACGTCCCAAGCTGGAAGAGAG	7710
Oy	2391	GluLeuIlyPhe-----CysGluIleGluPheLeuAsnGluLeuLeuPheIly	2406

Db	7711	CACCAACTTTGGAGGACCAAAACTTGAAGTACAGTGAATCTGCAGAGTGCATTTGGACAG	7770
Qy	2407	LYSALAENILEIIEGINSERVALGNAPRAPHESERGLUVALGINVALPHELUAN	2426
Db	7771	AAGATCCAAAGTGTCAATCCAAAAATCCCTCTTTGCAGACACATTTAGAGTCTGCAG	7830
Qy	2427	GLINVALGYSERTHRLLEUGINGLUINUENLU---HISLYBYLVGILYRHEMECTLRP	2445
Db	7831	AGTTCTTACAAAGAACTTAGAGAAATGAGCTTAAATTGACAAAATGACAAAATGTCCTTT	7890
Qy	2446	LEUGINGLUINPHELY-----ASPLENHIVAL	2454
Db	7891	GTTGAAAAGTAACAAACAAATGACTGCAAAAGAACTGAGCTGCAGAGGAAATGCAATAG	7955
Qy	2455	ASPAIALYLYS-----LEUSERGLUIMETCINGLINGUASPARGARGILEAL	2471
Db	7951	ATGGCACAGAAAACAGCAGAGCTGCAGAGAACTGAGAGAAAATAATAGCTAGCTACT	8010
Qy	2472	SERTHRIIEGINSLEUTHLYEARGLEULYALVALVALGINSERLYIEGINARG	2491
Db	8011	GGAGAGTTGCGAGTTACTGTTGGAAAGAAATMAAGAGC-----AGCAAAAGATCA---	8058
Qy	2492	GLUIETHRVALTYRLEUANGILNPHEDULALYLSLEUGINGLUINYLYVLEUGLUNPN	2511
Db	8059	-----TTGAAAGAGCTCAGACTGAAAT	8082
Qy	2512	LYVEGLUEMEARGARGMETGLUHIENIEGLYPROSERALASERVALMECGLUICLU	2531
Db	8083	AGTGAAATTTGAAGAG-----AGCCTAGATTGCTAGCTCACAAGAC	8121
Qy	2532	ASPAIALARGLEULGLYILEULYETHYVALGLINPARGIUSERLYVLYSLEUGLINSER	2551
Db	8122	CAGGTGGAAAAGGAAGG-----AAAGCTGAGAGGAAATAGCTGAATATCAGCTA	8172
Qy	2552	ARGILEYMECUELEUGLUAENGLULEUASNULEUVALLYSAPRPAALAMETHISLYGLY	2571
Db	8173	CGG-----CTTCAATGAAGCT	8187
Qy	2572	GLUIYLS-----VALAIAILEUGLINAAPRYLEUUSERARGSPALAGLUALGLIU	2589
Db	8188	GAAAAGAAACACCCAGAGCTTTGCTTTTGAC-----ACAAACAAACAGTAAAGATGAA	8241
Qy	2590	LEUASNALAMETGLINVALYSLUETHRYLYSLYSGLINAPRAPHENLEUGNALIALAMECLY	2609
Db	8242	ATCCAGACATCCGAGAGAAATTTGACTTTCTTAAAGAAAGATGCTCAGTTCCACAGACTG	8301
Qy	2610	GLUILEGUANELEUGLINYMECVALALALYSELVALVALPROTYRLYVLEUGLUNILE	2629
Db	8302	GAGATAGACCTTTTAAAGCTTAGT-----AAAGAAAGACTG	8337
Qy	2630	ASPRAN-----LEUYETHRYVALVALYSLIEGLIMECGLU	2642
Db	8338	AATAATTCATTGAAGAAGCTACTACTCAGATTTTGGAGAAATTTGAAGAAAACCAATGAC	8397
Qy	2643	LYSILELYLYR-----SERLYSALATHRAPRGINGLUILE	2654
Db	8398	AATCTAAAAATATGTAAATCAGTTGAGAGAAATGAACGTGCCAGGGGAAATGAG	8457
Qy	2655	ALATRYLEULYSERCY-----LEUGLUAAPRYSELGLUINGLYLEUARGARGLEULY	2672
Db	8458	TTGTGTGATCAATCTCTGTAAACAGCTGGAAAGAAAAGGATATCTGCAGAAAAGAACTC	8517
Qy	2673	GLUGLUEUARGARGALAGLIALASPRANAPRTHRYVALCYVALPROLYDAAPTRY	2692
Db	8518	TCTCAACTTCAAGCTGCACAGAGAGACAGAAAACA-----	8553
Qy	2693	GLINLYSALASERTHRHPEPROVALTHRCYSELGYLYGYSERGLYILEVALGINSERTHR	2712
Db	8554	-----GGTACTGTTATGATATCC	8571
Qy	2713	ALAMETLEUVALLEUGINSERGLU-----LYSALAIALEUGLU-----	2725
Db	8572	AAGGTGATGAATTTAACACATCGAGATCAAGAACTGAAGAACTTTGAAGAAAACCC	8631

[illegible]

QY 546 CysArgLysAlaSerPheGluLysGluIleThrSerLeuGlnGlnLeuGlnSerLys 565
 Db 925 CGCGAATCAAGACTAAGAAACAAGATTAAATGAGTTCGAACTACGCTGCAAGACAT 984
 QY 566 GluGluGluLysLysGluLeuValGlnSerPheGluLeuLysIleAlaGluLeuGlu 585
 Db 985 GAAAGAAAGATGAAGCCCAAGTGAATAGTTTCAA-----GAACTCCAACTC 1032
 QY 586 GlnLeuSerValLysAlaLys-----AsnLeuGlnMetValThrAsnSer--- 600
 Db 1033 CAACTGGAG---AAAGCAAAAGTGAATTAAATGAAAAAGAAAGTTTGAACAAATGT 1089
 QY 601 ArgGlnHisSerIleAsnAlaGluValGlnThrAspValGluLysValValArgLys 620
 Db 1090 AGGGATGAAGTACTAGTACAGAACACACACATACGC----- 1125
 QY 621 GluMetSerValLeuGluAspSerGlyTyrAsnAlaSerAsnSerAspLeuGlnAspSer 640
 Db 1126 -----CAGGCGTCAACCAAGTATCTGATTCGAAACAAAACTGAAAAAATTG 1173
 QY 641 SerValAspGlyLysArgLeuSerSerSerHisAspGluCysIleGluHisArgLysMet 660
 Db 1174 ACGGAAAGT-----TTGAGTGTCAAGCCACAAATGCAAAAGTCCCGATGTTCT 1224
 QY 661 LeuGluGlnLysIleValAspLeuGlu---GluPheIleGluAsnLeuAsnLysSer 679
 Db 1225 CTGGACAGAAATTAAGAAAGAAAGAGAGTTTCAAGAGAGACTCTCCCT----- 1278
 QY 680 GluAsnAspLysGlnLysSerSerGluGlnAspPheMetGluSerIleGlnLeuGlu 699
 Db 1279 -----CAACAGCGTCTTCCAAACACTGCAGCCAGAGTGCATCAGATG----- 1323
 QY 700 AlaIleMetAlaGluLysAlaAsnAlaLeuGluGluLeuAlaLeuMetArgAspAsnPhe 719
 Db 1324 -----AAGGCCAGACTCACCCAGAGATTACAGCAAGCAAG---AATATG 1365
 QY 720 AspAsnIleIle----- 1365
 Db 1366 CACAAACGCTCTGCAGCGCTGAACCTGATTAACCTCAGATCACTGAAACCAAGTACAAAC 1425
 QY 727 -----GluThrLeuLysArgGluIleAlaAspLeuGluArgSer----- 739
 Db 1426 AATTGGAAAGATTAAACCAAAAGTTGTGCAGAGCTGAAACAGGCTTCCAGCCAGTCAAG 1485
 QY 740 LeuLysGluAsnGlnIleThrAsnGluPheGluIleLeuGluLysGluThrGln----- 757
 Db 1486 ATCAAGAGAGATGAGCTGAGAGAGCATGAGAAATGAAGAAAGAAACAACTCTCT 1545
 QY 758 LysGluHisGluAlaGlnLeuIleHisGluIleGlySerLeuLysLysLeuValGluAsn 777
 Db 1546 AAGAGTCACTCTGAGCAAAAGCCAGAGAGCTCCACCTGAGCAAGAACTCAAGAAC 1605
 QY 778 AlaGluMet-----TyrAsnGlnAsnLeuGlnGluAspLeuGluThrLysThrLys 794
 Db 1606 ATCAAAAGCTGTTTAAATCAAGACCAAGATTTCAGAGAGAAATGAAGCCAGAGAT--- 1662
 QY 795 LeuLeuLysGluGlnGluIleGlnLeuAlaGluLeuArgLysArgAlaAspAsnLeuGln 814
 Db 1663 -----ACCTCTCAGGAACCAATCTTAAGAGATCTTCAAGAAAAAATTAATCAGCAAGAA 1716
 QY 815 LysLysValArgAsnPheAspLeuSerValSerMetGlyAspSerGluLysLeu----- 832
 Db 1717 AACTCTCTGACTTTAGAAAACTGAAGCTTGCTGTGCTGATCTGAAAAAGCAGAGAT 1776
 QY 833 CysGluGlu-----IlePheGlnLeuIleGlnSerLeu 843
 Db 1777 TGTTCACAGACCTTTGAGAAAAAGAGAACATCACTTGAACACCTTAATGATATAGTTA 1836
 QY 844 SerAspAlaGluAlaValThrArgAspAlaGlnLysGluCysSerPheLeuArgSerGlu 863
 Db 1837 AGCAAGACAGAGAAAGAGTCCAAA---GCCTTGCTGAGAGCTTTAGAGTTAAAAAAGAAA 1893

QY 864 AsnLeuGluLeuLysGluLysMetGluAspThrSerAsnTyrTyrAsnGlnLysGluLys 883
 Db 1894 GAATATGATTGAAGAAAGAGAGAACTCTGTTTCTTCTGTGAAAAACGAAAA 1953
 QY 884 AlaAlaSerLeuPheGluLysGlnLeuGluThrGluLysSerAsn----- 898
 Db 1954 CTTTAACT-----CAGATGAATCAGAAAAAGAAACTTCAGAGTAAATT 2001
 QY 899 -----TyrLysLysMet 902
 Db 2002 AATCACTTGAACCTTGTCTGAAGACACAGCAAAATAAAGTCATGATACACAGAGAA 2061
 QY 903 GluAlaAspLeuGlnLysGluLeuGlnSerAlaPheAsnGluIleAsnTyrLeuAsnGly 922
 Db 2062 GTAAGAACGCTGAGATGACAGAGAAAACTTAAGTGTGAGATCAGAAACCTTCACAAAC 2121
 QY 923 LeuLeuAlaGlyLys-----ValProArgAspLeuLeuSerArgValGluLeuGlu 939
 Db 2122 GTGTTAGACAGTAAAGTCAAGTGAAGTACAGACCCAGAAACTAGCTTATATGAGCTACAG 2181
 QY 940 LysLysValSerGluPheSerLysGlnLeuGluLysAlaLeuGluLysAsnAlaLeu 959
 Db 2182 CAGAAA---GCTGAGTCTCA-----GATCAGAAACATCAGAAAG 2217
 QY 960 GluAsnGluValThrCysLeuSerGluTyrLysPheLeuProAsnGluValGluCysLeu 979
 Db 2218 GAATATGAAATATATGTGTTTGAAGCTTCTCAG---CTTACGGCAGATTGAATATCTA 2274
 QY 980 LysAsnGlnIleSerLysAlaSerGluGluIleMet----- 991
 Db 2275 GAACACAGACTTCAAGTACTCTCAATGAATGAAGCAAAAGACCGGTGTACCAAGAC 2334
 QY 992 -----LeuLeuLysGlnGluLys----- 997
 Db 2335 TTGATGCCGAATATGAGAGCCTCAGGATCTGTAATCCAAAGATCTTCTGTGTG 2394
 QY 998 -----GluHis 999
 Db 2395 ACAATGAAGATCATCAGAGAAAGTCTTGGCTTTGATCAGACCTGCCATGATCAT 2454
 QY 1000 Ser---AlaSerIleIleSerLysGlnIleIle----- 1010
 Db 2455 TCCTTGCAATATATATTGAGAACAGAAAGACATGCTTCAGAGAGAGTGAATGTGCT 2514
 QY 1010 ----- 1010
 Db 2515 TTAGAGCAGACCAAGTCCGAAAAATTCTCCATCTTACAAATAGATGATTCACTT 2574
 QY 1011 -----MetGlnGluGlnSerGluGln 1017
 Db 2575 GAATTTTATTAGAGTCTCAAAAAACAGATGAATCAGACCTGCAAAACAGATGTGAAGAG 2634
 QY 1018 IleLeuGlnLeuThrAspGluValThrHisThrGlnSerLysValGlnGlnThrGluGlu 1037
 Db 2635 TTGGTGCAATCAAAAGAGAAATAGAGAAATATCATGAAAGACAGAACATGATCAAA 2694
 QY 1038 GlnTyrLeu-----GluMetLysLysMetHisAspAsp----- 1048
 Db 2695 AGTTTGTGCTGAACAAGTCAGCGCATTTAGTATACAGAAACATCTTCTGCTCAC 2754
 QY 1048 ----- 1048
 Db 2755 CAGAAATGTTGCTGAAACCTTAAGTCCCTTGAGAACAAAGAAAAAGCTGCACTT 2814
 QY 1049 LeuPheGluLysTyrIleArgAsnLysSerGlu----- 1059
 Db 2815 TTAATATGATTAAGTGAAGATCAGAGCAGAGATTAAGAATTAATAAAGACAAACAT 2874
 QY 1060 ---AlaGluAspLeuLeuArgGluMetGluAsnLeuLysGlyThrMetGluSerValGlu 1078
 Db 2875 CTACTTGAAGACTCTCTTAAGAGAGCTACAACTTTATCCGAAACCTTA---AGCTTGAG 2931
 QY 1079 ValLys-----IleAlaAspThrLysHisGluLeuGluGluThrLys 1093

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Db      2932 AAGAAAGAAATGAGTTCATCTCTAAATTAAGAAATGAGAGGTGACCCAA 2991
Qy      1094 Asp-----LysGlu-----GlnLeuLeuLeuLeuLysLysPhePhe 1106
Db      2992 GAGAAATGGAGCTCTTAAGAAATTAATGATCTTAAATCAAGAAATGAACTAATC 3051
Qy      1107 GlnAlaMetGlnThrIlePhe-----ProIleThrProLeu 1118
Db      3052 CAGAAAGTGAAGCTTTGCAAACTATATAGTGAAGGAGAAAGCATTTTCAGAGTTA 3111
Qy      1119 SerIlePheSerLeuProSerIleLysLeuVal-----GlnLysAsn 1131
Db      3112 TCTGATCGATCAACAGAAAGAAATCTTATTTTACTAACAAGATGTGAAGAAACCGGAAT 3171
Qy      1132 SerGlnAspProIle----- 1136
Db      3172 GCATATGAGATCTTATAGTCAAATAATCAAGACAGCAAGAAAGATTTCTAAATTAGA 3231
Qy      1136 ----- 1136
Db      3232 TGCTGTAATGAATGCACTAGTCTTTGTGAATAATAGGAAATAGATTGGAAACAGCTA 3291
Qy      1137 -----GlnLeuAsnAspTyrHisAsnLeuIleAlaLeuAlaThrGlu 1150
Db      3292 AAGGAGCATTTGCAAGAGAACACCAAGAAATTTCTTAACAAATTTAGCATTTGTGAGAA 3351
Qy      1151 ArgAsn-----AsnIleMetValCysLeuGluThr----- 1160
Db      3352 AGAAATTCGAATCTGATCTGTAAGTTGGAGACAGCAGCAAGCTCTGATCTGAGATG 3411
Qy      1160 ----- 1160
Db      3412 ACAGATAACCAAAATTTCTAAGACGCGAGCTGGTGTAAAGCAAGAAATCATGACT 3471
Qy      1161 -----GluArgAsnSerLeuLysGluGlnValIleAspLeu-----AsnThr 1174
Db      3472 TTAAGAGAAACAAACAAATGCAAAAGGAAATTAATGACTTTTTCACAGAGATGAA 3531
Qy      1175 GlnLeu-----GlnSerLeuGlnAlaGlnSerIle 1184
Db      3532 CAGCTGATGAAGATTAAGACTTAACATGAATGTCAAATCTGAATCTGAACAACTATT 3591
Qy      1185 GlnLysSerAspLeuGln-----LysProLysGln 1194
Db      3592 AGGAATCTGTGAAGAAAGAGAGAGTGAAGAAATCATGTAATTTTAAACCTCAGATG 3651
Qy      1195 AspLeuGlnGlnGlnValLysLeu-----LeuLeuGlnMetGlu 1208
Db      3652 GATCTTGAAGTTTAAAGAAATTTCTAGATAGTTATTAATGCGCAAGTGGTCAATTTAGA 3711
Qy      1209 LeuLeuLysGlnHisLeuThrAspSerGlnLeuSerIleGlnLysLeuGlnLeuLysn 1228
Db      3712 GCTATG-----CTAAGAAATAAGAAATTTAAACTTCAGAAAGTGAAGAGAAAG 3762
Qy      1229 LeuGlnValThrGlnLysLeuGlnThrLeuGlnGlnMetLysAsnIleThrIleGlu 1248
Db      3763 -----GAGTGCCTGCAGCATGAATTTACAGACAATT----- 3792
Qy      1249 ArgAsnGlnLeuGlnThr-----AsnPheGlnAspLeuLysAlaGlnHisAspSer-----Leu 1266
Db      3793 AGAGGAGATCTTGAAGAACAGCAATTTTGCMAAGCATGCACTCAAGAAATTTGTGCTT 3852
Qy      1267 Lys-----GlnAspLeuSerGln 1272
Db      3853 AAAGACTGTGAATAGATCGGAGAAAGATATTTTCAGGCGCTCATGAGTGTCTCAACA 3912
Qy      1273 AsnIleGlnGlnSerIleGlnThrGlnAspGlnLeuArgAlaIleGlnGlnLysArg 1292
Db      3913 AGTCAAAAGCAACATGACACCTTCAGTCTCTCTGCAAAACAACATGAACAAGCTGAAT 3972
Qy      1293 GlnGlnLysGlnLeuValAspSerPheAsnGlnGlnLeuLeuAspCysSerValGlyIle 1312

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Db      3973 GAGCTAGAGAAATATGTGAATTAATCTGACGCTGAAGAAAGATATGAACCTGTAACCTGAGCTG 4032
Qy      1313 SerSerProAsnHisAspAlaValAlaAsnGlnGlnLysValSer----- 1327
Db      4033 AATGATTCAGAGCTGAGATGATATCAGCAACTAGAGAAATATGCGAAGAGGTAGGAAA 4092
Qy      1328 -----LeuGlnGlnValAsnSerLeu-----GlnSerGlnMetLeuArgGlnLysArgAsp 1344
Db      4093 CTACTAAATGAAGTTTAAATTTAAATTAATGATGACAGTGTCTTCTCCATGTGAGTTAGTG 4152
Qy      1345 Gln----- 1345
Db      4153 GAAACATACAGAGAGGTGAATTTGTGAACAACCAATGAACAGACCCCTGTGTCTTG 4212
Qy      1345 ----- 1345
Db      4213 GCTCATTTGACGAGAGTAATCTTACAGACCTTGACATTTGTGACAAAGAGTTCAA 4272
Qy      1346 -----LeuGlnThrSerCysLysAlaLeu 1353
Db      4273 ATGACCTTTGCCGAATTTGCAAGAGAAATTTCTTATCTTCAAGGTGAACACAAATTTTA 4332
Qy      1354 -----ValSerGlnLeuGlnLeuLeuArgAlaHisValLysSer 1366
Db      4333 CATGATCAGCACTGTCAGATGAGCTTAATAATGTCAGAGCTGCAGACCTATGTTGACTCA 4392
Qy      1367 ValGlnGlnGlnAsnLeuGlnIleThrLysLysLeuAsnGlnLysGlnLysGlnIleLeu 1386
Db      4393 TTAAGCGCCGAAATTTGTGCTTGTCAACGAAATCTGAAACCTTCAAGGATGCTGTGTG 4452
Qy      1387 GlyLysSerGln-----GlnSerGlnValLeuLysSerMetLeuGlnAsnLeuLys 1403
Db      4453 AAGAGATGACCTGGCGCTTGAGAGAGGCTGCTTCATCTCTGTCACTCTTGTGTG 4512
Qy      1404 GluAspAsnAsnLysLeuLysGlnGlnAlaGln----- 1414
Db      4513 CCTGACAGCTGTAGCTTACAGAGTTTGGAGACCTCCTCTTACAGAGCTTTTGAAG 4572
Qy      1415 -----GluTyrSerSerLysGlnAsnGlnPhe 1423
Db      4573 CAGACAGAGATATGCTCTTTTGAATTAATTAAGAGGCGCTGTTGACGAAACACAGTGC 4632
Qy      1424 SerLeuGlnGlnValPhe----- 1429
Db      4633 AGTGTAGTGAAGATTTTTCAGACAGTCTGCAAGAGAGAAATCTGCACGAGAAAGAAC 4692
Qy      1430 -----SerGlnSerGlnLysLeuValAspGlnIle-----GluValLeuLysAla 1444
Db      4693 CTTTCGCGCCCGAGGAGAGGCTTGAAGAGCTTGAAGTCCCTCTGAGGCTTACCGGAG 4752
Qy      1445 GlnLeuLysAlaAlaGlnGlnArgLeuGln-----IleLysAspArgAspTyr 1460
Db      4753 TCCCTCGAGAGCTGAGAGAGAGAAATGCAAGGTCAGAGGATTAAGAAATAAGGAAATT 4812
Qy      1461 PheGlnLeuValGlnThrAlaAsnThrAsnLeuValGln-----GlyLysLeuGlnThrPro 1479
Db      4813 CAAGAGCTCGAGAGCTTAATTAAGTTCTGAAGAGCAAGAGCTTGACTGCTTAAGCAAGAG 4872
Qy      1480 LeuGlnAlaAspHisGln-----GluAspSerIleAspArgAspSerGlnGlnMetGln 1497
Db      4873 TATTTGTCAAGAAATGAACATGCGCAACAGAGCTGACACAGCGTGAAGTGTGAG 4932
Qy      1498 IleLysValLeuGlnGlnLysLeuGlnArgAsnGlnTyrLeuLeuGln----- 1513
Db      4933 TCCAAGTTGGCGCGCAAGAAAGAAACAGACGGAACAACATGTCATCTGAGCTGAGAAATGCA 4992
Qy      1514 ArgLeuGlnGlnGlnLysLeuGlnLeuSerAsnLysLeuGlnIleLeuGlnLysGlnMet 1533
Db      4993 CGACTCCAGCTCAAGAGCTGTGACTTAAGTTCTCGG----- 5028
Qy      1534 GluThrSerValLeuLeuLysAspAspLeuGlnGlnLysLeuGlnSerLeuLeuSerGln 1553
Db      5029 -----TCTTTCCTTGGCATGCAACAGAAAGTCTATTCAAGGC----- 5067

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QY 1554 AsnIleuLeuysgluaAnIleAspThrThreuleysHiseserAspThrGlnAla 1573
Db 5068 -----CGAATGAGAGCTGTGACATATCAAAAGAACCTACTTACAAAGCTACAGAA 5118
QY 1574 GlnLeuGlnLys-----ThrgInglInLeuGln 1583
Db 5119 AGAAGACCAAGCATGATGTTATCATGATTTGTATAAGATGCTCAGAGACCTCAAT 5178
QY 1584 Leu-----AlaLysAsnLeuAlaIleAlaIleAserAspAsnCyPProIle 1598
Db 5179 CTGACACATTGAGAAATTAAGTACGACTGTGCTGTAAGAACCAAGAGAGAGTCTGTGG 5238
QY 1599 ThrGlnGlnLysLeuThr-----SerAla 1606
Db 5239 GAAACAGTCCCCAGATACCAATTATGAGCTCCAGGGAGATAAACCCAGGGCTCTTCA 5298
QY 1607 AspCyValHisProLeu----- 1612
Db 5299 GAATGATTTCTGATTTGCTATTTCTGCTCAATGCTTGTGACTTATGATTCCTG 5358
QY 1613 -----GlnGlnLysIleLeuLeuThrGlnGlnLeuHisGlnLysThrAsnGln 1630
Db 5359 GGGAAATCAGAGAGATATCCATTAATCTTCACTGGGGTAAAGAGACATCAAAATGAGAAAT 5418
QY 1631 GlnLysLeuLeuHisGlnLysAsnGlnLeuGlnAlaGlnValGlnLeuLysCyPProIle 1650
Db 5419 TTGAGATTTACTTATGATGATGATGAGAGACCTGACAGA-----AAA 5457
QY 1651 ValGlnHisLeuMetLysSerMetIleGlnSerLysSerLeuGlnLeuHis 1670
Db 5458 GTTGAAGATTGCTTAATGAAGAAATGAAAGATTAGACTCAAAAGCT----- 5502
QY 1671 GlnLysHisAspThrGlnGlnLeuLeuAla-----LeuLys 1683
Db 5503 -----CATTTACAGAGGTACCAACTAATGACCAAAATGACATGATGATGAGAA 5556
QY 1684 GlnGlnMetGlnValValThrGlnGlnLysLeuGlnGlnInthrHisGlnLeu 1703
Db 5557 AAAATAGTTGGGAACTTAAGAAAGAAACTCAGATTTAAGTAAATTAAGTAAATTTT 5616
QY 1704 ThrAlaGlnValAspHisLeuLysgluaAnIleGlnLeu-----GlyLeuAsnProLys 1721
Db 5617 TCTTGATGATCACAGAGATTACTCCAGAGGTAGAAACTTCTGAAGCTCAATTTCTGAT 5676
QY 1722 AsnGlnValaGln-----GlnLysThrThrLysGlnGlnCysLeuLeuAsnGlnLys-- 1739
Db 5677 TTGAAATGATCATCAGATTAATCATCATCTGAAGATATTGAGATTAATGTGCCAAGGTG 5736
QY 1740 -----GlnLeuGlnGlnInserGlnHisAspGlnGlnCys 1750
Db 5737 AATGACAGCTGAGAGAGAGATTTCTTGATGTGAAATGAGCTGAGTACGATCAGATCG 5796
QY 1751 Gln-----IleGlnGlnLeuMetLysSerLeuLys 1760
Db 5797 GAGAAAGCTAGCATTTGAGCATGAAAGCTTACTGAGAGCTGACTTAAAGGTATTTCA 5856
QY 1761 AspLysGlnSerAlaLeuGlnThrLeuLysGlnSerGlnGlnValIle-----AsnLeu 1779
Db 5857 ACAGAGAGAGCTATTTAGAAAAAGCAATGAATTAAGCAGAAAGTTATGTCTGCTT 5916
QY 1780 AsnGlnGlnMetCysValMetLeuGlnMetGlnGlnLysLeuLysAsnSerGlnAlaGlnThr 1799
Db 5917 GAAAGAGAACTCTCAGCTGTGACAAAGTGAAGAAACCAAGCTGTGAGAAATTAAGTACT 5976
QY 1800 ValIleAlaGlnLys-----AspGlnLeuGlnAspAspLeuAspGlnSerValGln 1816
Db 5977 ATGTCAAAAAAACAAGCAGCTGATCAGTTGTCTGAAAAATGAAGGAAAAACAACA 6036
QY 1817 MetSerIleGlnThr-----GlnAspAsp 1824
Db 6037 ---GAGCTTAGTCTCATCAAGTGAAGTGTCTCATTTGATTCAGGTGACAGAGGAG 6093

QY 1825 LeuArgLysValaGlnGlnAlaLeuGlnGlnGlnLysAspLysValaGlnLeuThrSer 1844
Db 6094 GTGAGAGAAAGAGAGAACTCTTACAGACTTTGTCTCTGATGTAGTACGCTTTAA 6153
QY 1845 GlnHisSerValLeuGlnGlnLysIleSerLeuGlnAsnGlnMetLeuThrAsnVal 1864
Db 6154 GACAAATCATCTATCCAGAGAAAGCTGACAGAGTTTGGAAAAAGACTCACAGCAGCTGTCT 6213
QY 1865 AlaThrValLysGlnThrLeuSerGlnArgAspAspLeuAsnGlnInserLysGlnHisLeu 1884
Db 6214 TTGACAAATATGATGAGCTGAGAAAAACAATTGCACAACTGAATTAAGAGAAAGATTGCTT 6273
QY 1885 PheSerGlnIleGlnThrLeuSerLeuSerLeuGlnLysGlnPhe----- 1900
Db 6274 GTCAAGAAATCTAAAGAGCTGACAGCCAGACCTAGTGAATACAGATTATGAAGAGCTGAAT 6333
QY 1901 -----AlaLeuGlnGlnAlaGlnLysAspLysAlaAspAlaAlaArgLysThrIle 1917
Db 6334 GTCTCCAGAGCTTGGAGGCGGCAGCTGTGAGAGAAAGTGAAGTTCATTCATTCAGAGCTGAGC 6393
QY 1918 AspIleThrGlnLysIleSerAsnIle----- 1926
Db 6394 TCAACACAGAGAGAGATGATCATGAGAGAGAGATGAGAACTGAGAACTGAGATTCGCAAT 6453
QY 1927 -----GlnGlnGlnLeuLeuGlnGlnAlaThrAsnLeuLysGlnThrLeuThrGln 1943
Db 6454 GAGCCGATGAAAGAAAGAGAGCTGACATGCGAGAGAACTGAAGAAACCCGAGCGGAG 6513
QY 1944 ArgGlnSerLeuIleGlnCysLysGlnGlnAlaLeuAsnThrGlnHisLeuArgLys 1963
Db 6514 AATGATTTCACTT-----AAGATTAAGTGAAGAACTTGAAGCGAAATTCGAGATG 6564
QY 1964 ThrLeuLysSerLysAspLeuAlaLeuGlnLysMetGlnGlnLysArgAspGlnAlaIle 1983
Db 6565 TCAGAAAGAAACCAAGAGCTAGTGAAT-----CTTGATGCCAGAAATTCGAAAGCA-- 6615
QY 1984 AsnLysValIleAlaLeuThrGlnLysMetSerSerLeuGlnGlnGlnLeuAsnGln 2003
Db 6616 -----GAAATGAGACTTTAAACACAAATGAAGAGATG 6651
QY 2004 ValThrThrLeuLysGlnGlnLys-----GlyLysGlnThr 2016
Db 6652 GCCAGAGAGCTGAAAGCTTTTGAATTAAGACTTGTACAGTTAAGCTGAAAGAAAT 6711
QY 2017 PheThrLeuGlnArgProSerLysGlnGlnInserSerSerGlnMetGlnLeuLysArgLys 2036
Db 6712 CTGACAAACCAATTAACAGAAAGAAAGCTGAGTCTGAGAACTGACAAAGTAACTCTCT 6771
QY 2037 SerLeuLysThrLysAspLeuGlnGlnGlnAlaGlnLysGlnLysSerGlnAlaThr 2056
Db 6772 TCAATTAAGTCTGTGAGAGAAAGAGAGAGAGAGAGATTCAGATTCAAAGAGAAATCT 6831
QY 2057 -----AsnGlnIleLysAsnLeuThrAlaLysIleSerSer 2068
Db 6832 AAAAGTGAAGTGAAGATGCTTACGATTCAGATTAAAGAGCTTAATGAGAGATGAGAGC 6891
QY 2069 Leu-----GlnGlnGlnIleLeuGln-----AsnAlaSerIleLeuAsnGlnAlaValSer 2085
Db 6892 TTGTGTGTGATCCAGAAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6951
QY 2086 GlnArgGlnAlaAsnLeuArgHisSerLysGlnGlnLeuValSerGlnLeuGln----- 2102
Db 6952 GAAAGAGATGAGCTGAGAAATGAGATTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 7011
QY 2103 -----GlnLeuSerLeuThrLysLysSerArgAspHisAlaPheAlaGlnInserLysArg 2120
Db 7012 AAGAGACACTCTGTCTCTTACAAACAGAG-----GAAAGTGAAGAT 7056
QY 2121 GlnLysAspGlnAlaValAsnLysIleAlaSerLeuAlaGlnGlnLysIleLeuThr 2140
Db 7057 CATGCAAGATTACTTAAGGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 7116
QY 2141 LysGlnMetAsp-----GlnPheArgAspSerLys-----GlnSerLeu 2153

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Db      7117 ACAACCAAGAGATGACCTCTTGAGGAGAGAAATCCAAAGAGAGTAGAGACCTTA 7176
Qy      2154 GIngluGInserSerHisLeuSerGluGluLeuCyThrTyLeuThrGluLeuGlnMet 2173
Db      7177 AAGCAAAAATGAGAGGATGACCCAAAGTCTGAGAGGCTTGGAATTTGATGATTTACT 7236
Qy      2174 LeuGluGInGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 2193
Db      7237 ATAAGCTCAGAAAAAGAAATCTGCAAAATGAAATTAACAAAAAGACAGAGGAATATCT 7296
Qy      2194 GInLeuLeuGlnHisLeuSerSerLeuGluGluGluGluGluGluGluGluGluGlu 2213
Db      7297 GAATTA-----GAAATA 7308
Qy      2214 ArgAGnGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 2233
Db      7309 ATAAATTCATCATTTGAAAAAT----- 7329
Qy      2234 ILeuSerValLeuArgLeuMetGluGluGluGluGluGluGluGluGluGluGluGlu 2253
Db      7330 -----ATTTGCAAGAAAAAGACAGCAAGAAAGTACAGATGAAGAAATCAAGACT 7383
Qy      2254 ArgMetAspIleLeuGluSerArgAsnGluGluGluGluGluGluGluGluGluGlu 2273
Db      7384 GCCATGGAGATGCTTCAACA-----CAATTAAGAGCTCAATGAGAGGTGCA 7434
Qy      2274 AlaValTySerGluGluGlnHisThrLeuLeuSerSerLeuGluGluGluGlu 2293
Db      7435 GCCCTGCATATGACCA----- 7452
Qy      2294 ThrGluAlaHisIleGluHisCysMetLeuAsnIleGluGluSerSerThrLeuSer 2313
Db      7453 -----GAGGCTGTAG-----GCCAAAGACAGAAATCTTAGT 7485
Qy      2314 ArgSerPheGluSerLeuGlnThrGluHisValIleGluGluGlnThrGluGlnThrLeu 2333
Db      7486 AGTCAGATGAGTGTCTTGAACCTTGAGAGAGCTCAGTCTACAGAGCTTGATGAGGCC 7545
Qy      2334 LeuAsnIlePheGluValIleValTyArgThrAlaAlaValIleGluGluGluGlu 2353
Db      7546 AAAAATATATATATTTGTTTGAATCTTCAGT-----AATGCTCAT 7590
Qy      2354 LysAspTyGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 2370
Db      7591 CAGAAGTAAAGATGCGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 7650
Qy      2371 ArgLeuGlnLeuGlnCysLeuGluGlnHisGlyArgIleTyPheSerAspSerAlaSerGlu 2390
Db      7651 AAAAATCAAAATTCAGAGCCAGAGCTGTCTTAACTGTCCAGGTGGAAGAGAG 7710
Qy      2391 GlnLeuLeuPhe-----CysGluIleGluPheLeuAsnGluLeuPheLeu 2406
Db      7711 CACCAACTTTGGAAGAGCAAACTTAGAAGCTGAAATTCAGACAGTGAATTCAGAGCG 7770
Qy      2407 LysAlaAsnIleIleGlnSerValGlnAspAspPheSerGluValGlnValPheLeuAsn 2426
Db      7771 AAGATCCAGATGCTTACATCAAAATGCTCTTTCAGAGACACATTAAGAGTCTGCG 7830
Qy      2427 GlnValGlySerThrLeuGlnGluGluGluGluGluGluGluGluGluGluGluGlu 2445
Db      7831 AGTTCTTACAGAAATCTAGAGATGATGCTTGAATTCAGAAATGACAAATATGCTCTT 7890
Qy      2446 LeuGluGluPheGly-----AspLeuHisVal 2454
Db      7891 GTTGAAGAAAGTAAACAAATGACTGCAAGAAAGAACTGACAGAGAAATGATGATAG 7950
Qy      2455 AspAlaIleGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 2471
Db      7951 ATGAGCAGAGAAAGCAAGAGCTGCAAGAAAGCAAGCTGAGAGAGAAATAGCTTACT 8010
Qy      2472 SerThrIleGlnLeuThrIleArgLeuGluGluGluGluGluGluGluGluGluGlu 2491
Db      2491 -----

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Db      8011 GAGAGTTGAGTACTGTTGCAAGAAATTAAGAG-----AGCAAAATCA--- 8058
Qy      2492 GlnLeuThrValTyLeuAsnGlnPheGluAlaIleGluGlnGluGluGluGluGlu 2511
Db      8059 -----TTGAAGAGCTCACACATGAAAT 8082
Qy      2512 LysGluLeuMetArgArgMetGluHisIleGlyProSerAlaSerValMetGluGluGlu 2531
Db      8083 AGCGAATTGAAGAG-----AGCCTAGATTGATGACAAAGAG 8121
Qy      2532 AsnAlaArgLeuGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 2551
Db      8122 CAGGTGAAAAAGAGAG-----AAAGTCAGAGAGAAATAGCTGAATATACGTA 8172
Qy      2552 ArgIleLeuMetLeuGlnGluGluGluGluGluGluGluGluGluGluGluGluGlu 2571
Db      8173 CGG-----CTTCATGAGCT 8187
Qy      2572 GlnGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 2589
Db      8188 GAAAAAGAACACAGGCTTGTCTTTGAC-----ACAAACAAACAGATGATGATGTA 8241
Qy      2590 LeuAsnAlaMetGlnValIleGluGluGluGluGluGluGluGluGluGluGluGlu 2609
Db      8242 ATCCAGACATACCGAGAGAAATTCCTTAAGAAAGATGCTCAGTTCACAGAGCTG 8301
Qy      2610 GlnIleGluAsnLeuGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 2629
Db      8302 GAGATGAGCTTTTAAAGTCTAGT-----AAAGAAAGCTC 8337
Qy      2630 AspAsn-----LeuGluThrValValIleGluGluGluGluGluGluGluGluGlu 2642
Db      8338 AATTAATTCATGAAAGTACTACTCAGATTTTGAAGATTTGAAGAAATCAAGATGAC 8397
Qy      2643 LysIleLeuTy-----SerLysAlaThrAspGlnGlu 2654
Db      8398 AATCAAAATATGTAATCACTGGAAGAGAAATGAACTGCGCCAGGAGAAATGAG 8457
Qy      2655 AlaTyLeuGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 2672
Db      8458 TTGTTGATCAAAATCTCTGAACAGCTGGAAGAGAAAGAGATGCTGCAAGAAATCTC 8517
Qy      2673 GlnGluLeuArgGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 2692
Db      8518 TCTCACTTCAAGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 8553
Qy      2693 GlnLysAlaSerThrPheProValThrCysGluGluGluGluGluGluGluGluGluGlu 2712
Db      8554 -----GGTACTGTTATGATACC 8571
Qy      2713 AlaMetLeuValLeuGlnSerGlu-----LysAlaAlaLeuGlu----- 2725
Db      8572 AAGTTCAGATTAATTAACACTGAGATCAAGAACTGAAGAACTGTTGAAGAAAAACC 8631
Qy      2726 ArgGluLeuSerHisTyLeuGluGluGluGluGluGluGluGluGluGluGluGluGlu 2745
Db      8632 AAGAGGCAAGATGAATCTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 8682
Qy      2746 GlnAspArgLysTyLeuGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 2765
Db      8683 GAAAGTTAGAGAAAGCTAAAGAGATGTTAGAGACACAAAGTGGCCATCTGTTTACAG 8742
Qy      2766 His-----ArgGlySerProHisLeuThrGluThrTyArgHisGlyPro 2780
Db      8743 CAATCTAAACAGATTCCGAGAGTCTCT-----TTCGATAGGTCCA 8784
Qy      2781 ValThrProGluArgSerGluMetProSerLeu-----HisLeuGlySerProLys 2797
Db      8785 GTTCTTCAGAGACCATTCATCCCTCTGTTACTGAAAGAGGTTATCATCTGCGCAA 8844
Qy      2798 LysSerGluSerSerThrLysArgValIleSer----- 2808
Db      8845 AATTAAGCTTCAGAGCAAGAGCAAGATCCAGTGCATATGGAGAAATGCTGAGAGACA 8904

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Db 1187 -----GACACCCAGGAATGTGAGCCAGCTCCAAAGTGAAGAGCTCAAGAA 1240
 Qy 359 GlnLeuGluAsnLeuGluSerSerSerGluThrLysAlaGlnAlaMetAlaLysGluGlu 378
 Db 1241 CAACCTGGCGAGCTTCCTTCAGAGACAGACACCAAGAAAGCTTCCTGACCGAGACAA 1300
 Qy 379 HisThrGlnLeuLeuAlaGluLysGlnLeuHisLysGluLysGluLysArgLysIleThr 398
 Db 1301 AAGAACTACTAATATATGAGATATTTCCAG-----GAAACCAATGTTATTC 1345
 Qy 359 HisLeuThrAsnIleValValAlaSerSerGlnLysSerGlnLysAsnLysValLys 418
 Db 1346 TTT-----AGAAATCTGAACAGGAAAGAAAG----- 1372
 Qy 419 ArgLysArgArgValThrTyrLalProGluLysLleGlnAsnSerLeuHisAlaSerGly 438
 Db 1372 ----- 1372
 Qy 439 ValSerAspPheAspMetLeuSerArgLysProGluLysAsnPheSerLysLysAlaLysPhe 458
 Db 1373 --TCTCTGATAGAAAAGTTACCCCAATTAGAAGACCTCAACCTCAAGAAAGAAATTT 1429
 Qy 459 SerAspMetProSerPheProGluLysAspSerValCysThrGluPheSerAspPhe 478
 Db 1429 ----- 1429
 Qy 479 AspaAspAlaLeuSerMetCysAspSerAsnGlyLleAspAlaGluTyrAsnLeuAlaSer 498
 Db 1430 ----ATTCAATCTATAAATATGATGTAATAATCCGA---GAGCAT 1468
 Qy 499 LysValIleThrHisArgGluLysThrSerLeuHisGlnSerMetLysPheGluGlnIle 518
 Db 1469 CAATAATATACGCTTGGAAGAG---CTCCAC----- 1495
 Qy 519 SerAspSerValGlnPheHisAspSerSerLysGluAsnGlnLeuGlnTyrLeuProLys 538
 Db 1496 -----MAGAAATCCCGGAGAGTTTCTGCGCTGAG 1525
 Qy 539 AspSerGlyAspMetAlaGluCysArgLysAlaSerPheGluLysGluLysThrSerLeu 558
 Db 1526 GAGCAGCATCTTGTCTC-----TCAGAAATTAAGAAATGAGATTCMAACTCTG 1573
 Qy 559 GlnGlnGlnLeuGlnSerLysGluGluGluLysGluLeuValGlnSerPheGluLeu 578
 Db 1574 CGAGAACCAATAGAGACACCAACCCAGAGTTGCAAGATGATCTATGGAATAATATCCCTC 1633
 Qy 579 LysIleAlaGluLeuGluGlnLeuSerValLysAlaLysAsnLeuGluMetValThr 598
 Db 1634 AGG-----GAGGAGAAATAGAGACTGAGATT-----TTAAGCCTGTGAA 1675
 Qy 599 AsnSerArgGluHisSerLysAsnAlaGluValGlnThrAspValGluLysGluValVal 618
 Db 1676 AGAGCTCAAGAA----- 1687
 Qy 619 ArgLysGluMetSerValLeuGluLysAspSerGlyTyrAsnAlaSerAsnSerAspLeuGln 638
 Db 1687 ----- 1687
 Qy 639 AspSerSerValAspGlyLysArgLeuSerSerSerHisAspGluCysLleGlnHisArg 658
 Db 1687 ----- 1687
 Qy 659 LysMetLeuGluGlnLysLleValAspLeuGluGluPheLleGluAsnLeuAsnLysLys 678
 Db 1688 ---ATGAGATGCCCAACACCATTCGCAAAAGCTTTCTCTGCAATAAGTGCATG 1744
 Qy 679 SerGluAsnAspLysGluLysSerSerGluGlnAspPheMetGluSerLleGlnLeuLys 698
 Db 1745 GAGAAAGAGTCAAA-----AATCAGCAAGGATTTTCACTTAAGCTCAAGAAAGAG 1795
 Qy 699 GlnAlaIleMetAlaGluLysAlaAsnAlaLeuGluGluLeuAlaLeuMetArgAspAsn 718
 Db 1796 CCATGTTTCTTGCA----- 1810

Qy 719 PheAspAsnIleIleLeuGluAsnGluThrLeuLysArgGluLysLleAlaAspLeuGluArg 738
 Db 1811 -----AACCTAGAGAGTTAAAAAGCAACACTCTCGCAATTCAGACA 1852
 Qy 729 SerLeuLysGluAsn---GlnGluThrAsnGlnPheGluLleLeuGluLysGluThrGln 757
 Db 1853 GAGCTGAATATATCAACAGCAAGATATAGAGATTC-----AAAGACTTACT 1900
 Qy 758 LysGluHisGluAlaGlnLeuLleHisGluLysGlySerLeuLysLysLeuValGluAsn 777
 Db 1901 AGCAAAAGCAGCTGAATTTGGAATCAGAGCTTCAGTCTTTGCAAAAGCG----- 1951
 Qy 778 AlaGluMetTyrAsnGlnAsnLeuGluGluAspLeuGluThrLysThrLysLeuLys 797
 Db 1952 -----AACCTTAATCTTGAACCTTTTGGAGCA--ACAAAGCCTGCAAG 1996
 Qy 798 GlnGlnGluLleGlnLeuAlaGluLeuArgLys---ArgAlaAspAsnLeuGln----- 814
 Db 1997 CGGCAAGAGATT-----TCTCAGCTGAATTAATATCATGCTGAACACTTAAGATTATA 2050
 Qy 815 -----LysLysValArgAsnPhe-----AspLeuSerValSer 825
 Db 2051 ACTACACCAACCAAGGCTTACCACTCATTCGCCAGCACGATACCAAAATTAAGCCCTGAA 2110
 Qy 826 MetGlyAspSerGluLysLeuLysCysGluGluLlePheGlnLeuLysGlnSerLeuSerAsp 845
 Db 2111 ATGGGAACCTTGCTGCTCTA-----TACACTCAGAAATTCTAGCATATTAGATTAGT 2158
 Qy 846 AlaGluAlaValThrArgAspAlaGlnLysGluCysSerPheLeuArgSerGluAsnLeu 865
 Db 2159 AATGATATATTAATAGACCACTTCCTCTGAG----- 2191
 Qy 866 GluLeuLysGluLysMetGluAspThrSerAsnTyrTyrAsnGlnLysGluLysAlaAla 885
 Db 2192 -----ATGAATGAACCAACTTTT 2209
 Qy 886 SerLeuPheGluLysGlnLeuGluThrGluLysSerAsnTyrLysLysMetCylAlaAsp 905
 Db 2210 GAGGCCATTTCTGAAGACCTTAGAACAGTGAACAAATGAGTCTTTTAAGCCAAA 2269
 Qy 906 LeuGlnLysGlu-----LeuGlnSerAlaPheAsnGluLysAsnTyr 919
 Db 2270 CTGATGTAAGAAAGACATTAATAACTTAAGCTTACAGCAGCATGTTGACAAATGGAACAT 2329
 Qy 920 LeuAsnGlyLeuLeuAlaGlyLysValProArgAspLeuLeuSerArgValGluLeuGlu 939
 Db 2330 CATCTACCCCAATG-----CAGGAGCTTTTCTCATCGAAAGAAATT--- 2371
 Qy 940 LysLysValSerGluPheSerLysGlnLeuGluLysAlaLeuGluGluLysAsnAlaLeu 959
 Db 2372 -----GATTGACCAACAGACAGAGAGCTTCTCTCAAGTGAATGCTCTT 2419
 Qy 960 GluAsnGluVal---ThrCysLeuSerGluTyrLysPheLeuProAsnGluValGluCys 978
 Db 2420 GAAAGCAGCTTCAAGAGACTCAAACTTAATAATGCTTTTGAAGAAAGTACGATGAC 2479
 Qy 979 LeuLysAsnGlnLleSerLysAlaSerGluGluLleMetLeuLysGlnGlu----- 996
 Db 2480 CTGCGAGTAGTCTCATTTGCTGCAAGAGAGCTTCTTCAAGTGAATAATGATAGT 2539
 Qy 997 -----GlyGluHisSerAlaSerLleLleSerLysGlnLleLleMet 1011
 Db 2540 TCATTCAAAACGAATCAGAGAGAAAGAAATTCACAAACTTTCTGAAAGACATGATGTA 2599
 Qy 1012 GlnGluGlnSerGluGlnLleLeuGlnLeuThrArgGluValThrHisThrGlnSerLys 1031
 Db 2600 CAGCTTCAATTATGATATCTCAGGTTAAGAAAGAAAGCTCTTGAAGACAAAGCTCC 2659
 Qy 1032 ValGlnGlnThrGluGlnLysTyrLeuGluMetLysLysMetHisAspAspLeuPheGlu 1051
 Db 2660 CTACAGAGTATCTTATGACAACTTACAGAAATTAATGAATTAATGATGACCAACTTCA 2719

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QY 1052 LysTyrIleArgAsn---LysSerGluAlaGluAspLeuLeuArgGluMetGluAsnLeu 1070
DB 2720 AGAAACCTCCAAACTTCAAAAAAGAAATGAAACTCTGAATCTGATCTGAATATTTTG 2779
QY 1071 LysGlyThrMetGluSerValGluValLys-----IleAla 1082
DB 2780 ATGAGAGCTTCTGAGCGAAGAAAGAACCAATTAACAATTAATCATTACAGTTTGAAGA 2839
QY 1083 AATTATLysHisGluLeuGluGluThrIleArgAspLeuGluGluLeuHisGluLys 1102
DB 2840 GATTAAGAAACAGATTCTTAAGAAATCTTAAAGATTCTTGAGCGCTGCTACGAGGAA 2899
QY 1103 ---LysTyrPhePheGlnAlaMetGlnThrIlePheProIleThrProLeuSerAspSer 1121
DB 2900 CAGAAAGACCGGCGCAAGTGTGACGACGAGTGGCAAAAGTACAGAACTTAAGAGAGAC 2959
QY 1122 LeuProSerLysLeuValGluGluAsnSerGluAspProIleGluIleAsnAspTyr 1141
DB 2960 TTG----- 2962
QY 1142 HisAsnLeuIleAlaLeuAlaThrGluArgAsnAsnIleMetValCysLeuGluThrGlu 1161
DB 2963 ---CTTGGCTACTGAAAAA-----GTGATCAGTTCCCTGAGAAAGTCT 3001
QY 1162 ArgAsnSerLeuLysGluGluValIleAspLeuAsnThrGluLeuGlnSerLeuGlnAla 1181
DB 3002 AGAGATTCTGATTAAGAAATTTGAGCTGACCTTCAATGACCAAGATCCAGAGACTTAAGAA 3061
QY 1182 GlnSerIleGluLysSerAsp---LeuGlnLysProLysGlnAspLeuGluGluGlu 1200
DB 3082 TCGGCTGTGAGAAACAGAACTATAGACACCTCGAAACAGAACTGAAAGCATTAAT 3121
QY 1201 ValLys-----LeuLeuLeuGluMetGluLeuLeuLysGlyHisLeuThrAspSer 1217
DB 3122 TGCAAATCACTGCTTGGTTGGTTCAGAGAA-----GAGAGC 3160
QY 1218 GlnLeuSerIleGluLysLeuGlnLeuGluAsnLeuGluValThrGluLysLeuGlnThr 1237
DB 3161 AGAGTTGATCAAGAAAGCAGAAAGTGATTTCTGGATCTGAAAGAAACCTTAGG--- 3217
QY 1238 LeuGlnGluMetLysAsnIleThrIleGluArgAsnGluLeuGlnThrAsnPheGlu 1257
DB 3218 ---CTGAGATCTCTTCTGAG 3235
QY 1258 AspLeuLysAlaGluHisAspSerLeuLysGlnAspLeuSerGluAsnIleGluGln--- 1276
DB 3236 GACATA-----GAGAGGATATGCTCTGTGAGAGACTGCTCATGCCACTAGCAGCGCTG 3289
QY 1277 ---SerIleGluThrGlnAspGluLeuArgAlaIleGlnGlu 1290
DB 3290 AACATGCTCACAGAGGCTCAAAAAACACTCGGGGCTGCTGCAAGTCTGCCAGAGAGAA 3349
QY 1291 LeuArgGluGlnLysGlnLeuValAspSerPheArgGlnGlnLeuLeuAspCysSerVal 1310
DB 3350 CTGACCAAGAAAGAGACCTGATTCAGAACTTCAGCAACAAGTA----- 3394
QY 1311 GlyIleSerSerProAsnHisAspAlaValAlaAsnGlnLysValSerLeuGluGlu 1330
DB 3395 ---AACCAAAAGAAA----- 3406
QY 1331 ValAsnSerLeuGlnSerGluMetLeuArgGlyGluArgAspGluLeuGlnThrSerCys 1350
DB 3407 ---GAGGAAGTAGAAACAGAAAGAAATGATTAATTAATCTCAAAATG 3448
QY 1351 LysAlaLeuValSerGluLeuGluLeuLeuArgAlaHisValLysSerValGluGlu 1370
DB 3449 AGGCAACTA-----GAACATGATGATGATTTCTGCTGCTGAG 3484
QY 1371 Asn-----LeuGluIleThrLysLeuAsn 1379
DB 3485 GATCCCGCAGAGCTCTAAGACACACCTCACTTCAAAACATTTGGCAAAATCTCCGGA 3544
QY 1380 GlyLeuGluLysGluIleLeuGluLysSerGluGluSerGluValLeuLysSerMetLeu 1399

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DB 3545 ACACAAGAACAGAGATA-----GAAAGATGGAAGAGCCTCTAAGACTTCTTG 3592
QY 1400 GluAsnLeuLysGluLysAsnAsnLysLeuLysGlu-----GlnAlaGluLysSer 1417
DB 3593 GAACACCTTGTAAACAAAGCTTAATAGACACAGAAAGTCAAAATGCTAAATCTTCAGA 3652
QY 1418 SerLysGluAsnGlnPheSerLeuGluGluValPheSerGlySerGlnLysLeuValAsp 1437
DB 3653 ATGAAAGACAGTGGCTGTAATGAAATGAAACCTACCGCTGAAAGTCAAGCTTAATAGG 3712
QY 1438 GlnIleGluValLeuLysAlaGlnLeuLysAlaAlaGluGluArgGluIleLysAsp 1457
DB 3713 AAAAATGCTCTCTGCAAGCTCAGCTGAGTATTTAAAGACAAAGAAACACTGAT 3772
QY 1458 ArgAspTyrPheGluLeuValGlnThrAlaAsn----- 1468
DB 3773 CAGAAATCATCCAGATATATCAACAGCTGAAGAAATGAACAGAAAGATATCAAGAAAGA 3832
QY 1469 ---ThrAsnLeuValGluGlyLysLeuGluThrProLeuGlnAlaAspHisGlu 1485
DB 3833 CTTCAGAAAGTAAATAGTGAAGAAATGCTGA-----ATGAAGCAGACCTAGAA 3886
QY 1486 GluAspSerIleAspArgSerGluGluMetGluIleLysValLeuGluGluLysLeu 1505
DB 3887 GAAGTCCAAAGTCCCTTACAAACAAAGAGATGGAATGCTTAGAATGATCATGATGATC 3946
QY 1506 GluArgAsnGlnTyrLeuLeuGluLysGluGlnGluGluLysLeuLeuSerAsnLys 1525
DB 3947 GAACCAACCCAAATTTGGAGTCTTAAGCATTCGAGAAAGAAACAACTGATGATCAAG 4006
QY 1526 LeuGluIleLeuGlnLysGluMetGluThrSerValLeuLeuLysAspAspLeuGln 1545
DB 4007 CTGGAAGAAATGATGAAAGAAAGAGAGAAACATCCACAGAGATGAAATGTTAAGAAAG 4066
QY 1546 LysLeuGluSerLeuLeuSerGluAsn-----IleIleLeuGluGluAsnIleAspThr 1563
DB 4067 CAGCTGAGACTCTTCTGACGAGAAATGGAAGACTGTAAGTCAACCAAAATTTG----- 4120
QY 1564 ThrLeuLysHisSerAspThrGlnAlaGlnLeuGlnLysThrGlnGlnGluGln 1583
DB 4121 ---CATCAGAAAGATTCAGTACGTAGTACGCACTAAGAGAAATGTCAGG 4168
QY 1584 LeuAlaLysAsnLeuAlaIleAlaLysAspAsnProIleThrGlnGluLysGlu 1603
DB 4169 CTTCGTGAGAGACAGAAAGTTGGCTGCCGAAATGTAATTTTAAAGAAAGAAAGAA 4228
QY 1604 ThrSerAla 1606
DB 4229 AGTGAATCT 4237

RESULT 14
US-10-096-534-34
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; Publication No. US2003016687A1
; GENERAL INFORMATION:
; APPLICANT: The Brigham and Women's Hospital, Inc.
; APPLICANT: Yates, Karen
; APPLICANT: Mizuno, Shuichi
; APPLICANT: Glowacki, Julie
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF SKELETAL DEGENERATION CONDITIONS
; FILE REFERENCE: B0801/7244/KA/ERP
; CURRENT APPLICATION NUMBER: US/10/096,534
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; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 34
; LENGTH: 7694
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-096-534-34

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QY	982	nHleSerlysaIaSerGIuGIuIlleMeLeuLeuLyScInGluGIuGIuHISerAlaSe	1002
Db	1881	AGAACTTTGGCCCTTAGAAGATTGAGCTTCAGAAA-----	1917
QY	1002	rHleIleSerlySGInGIuIlleIleMeGIInGInSerGIuInIleLeuGIInLeuTh	1022
Db	1918	-----AAAGCAATCTCACAGAAAGTGAATAATAACTTCGGACCTTCA	1961
QY	1022	rASpGIuValThrHIStrGInSerLySeIyVaIGInGInThrGIuGIuGIuInTyrLeuGIuMe	1042
Db	1962	GCAGACACACAGACTTACAGACACTGAAATCTTGAAATTGGAAAGCTCT	2010
QY	1042	FLySLySeWchIaSaPaSaPeLeuPheGIuLySTyrIleArg--AenLySeSerGIuValaGI	1061
Db	2011	-----TTGCAAAAAAGCTTACAGAAAAACAAAAATCTCAAGTCAAA	2048
QY	1061	uASPeLeuLeuArgGIuMeTGIuASnLeuLySGIyThrMeGIuSeValGIuValySII	1081
Db	2049	AGATTGTG-----CCTGTTCACTCGGAAGC	2072
QY	1081	eAlaSPThrlySHISGIuLeuGIuGIuThrIleArgSaPySGInGIuLeuHISGI	1101
Db	2073	TGAAAAAATTAAGCCACATTAAGACATTACAGTC-----	2106
QY	1101	uLySeLyTyRPhPePheGInAlaMeTGIInThrIlePheProIleThrProLeuSerASpSe	1121
Db	2106	-----	2106
QY	1121	rLeuProProSerLySeLeuValGIuGIyASnSerGIuASpProIleGIuIleASnAPTy	1141
Db	2107	-----ATGCTTGAACAAACAC-----	2121
QY	1141	rHISaSnLeuIleAlaLeuAlaThnGILaRgASnASnIleMeTValCysLeuGIuThnGI	1161
Db	2122	-----AAGACAGA	2129
QY	1161	uARgASnSerLeuLySGInGIuInValIleASPeLeuASnThrGIn--LeuGInSerLeuGI	1180
Db	2130	ATTGGAAAGCCCTTAAGCATCAGCAGAGTCCCTTGGACTGTAAAACTCCAAAGCTTTAA	2189
QY	1180	nAlaGInSerIleGIuLySeSaPSeLeuGIuLySeProLySGInSaPeLeuGIuGIuGI	1200
Db	2190	GCACAAA-----TATCAGACTGAAATGCAAAAACTTAGGAAAAAGTGTCAACAAAAA	2243
QY	1200	uValLySeLeuLeuLeuGIuMeTGIuLeuLeu---LySeLyHISleuThrASp---SeGI	1218
Db	2244	AGAAACATTTGTGAAAGCAACAAAGAAATTATCTTCCAGGCCCACTAGACGAATGAATGA	2303
QY	1218	nLeuSerIleGIuLySeLeuGIuInLeuGIuASnLeuGIuValThrGIuLySeLeuGIInThrLe	1238
Db	2304	AAAGACTTGAAGAAAGCTTGATGTGACCAACACAGAA-----CTAGAAATCAATT	2351
QY	1238	uGInGIuGIuMeTlySaSnIleThrIleGIuARgASnGIuLeuGIuInThrASnPeGIuAS	1258
Db	2352	ATCTTCTGAACGTGCAGAAAGTATTAAGAACCCCGTCACAAACTAGAAAGAGAACTTTCTGT	2411
QY	1258	pLeuLySaIaGIuHISaPSeSerLeuLyGIuASPeLeuSerGIuSnIleGIuGIuInSerI	1278
Db	2412	TCTGAAAGATCAACAGATTAAATGACACAGAAATTAGAGCCCAAGATGAGAT-----	2463
QY	1278	eGIuThrGInASpGIuLeuARgAlaAlaGIuGIuGIuLeuARgGIuGIuInLySGInLeuVal	1298
Db	2464	-----GAACAGAAAAATCACTCACCCAGCCAGCAAGT	2492
QY	1298	IaSPSeRPhaRgGIuGIuInLeuLeuASpCySeSerValGIyIleSeSerProASnHISaS	1318
Db	2493	TGACAGCT-----ATCATTAAGAACACAGAGCT	2519
QY	1318	pAlaValAlaASnGIuGIuLySaIaSerLeuGIyGIuValASnSerLeuGIuInSerGIuMe	1338
Db	2520	ATCTATCCAGAGACTGGAAGGCAATTAAAGATCAAAATTATATCAACTT-----GAGCT	2573

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Db 3570 ATGGCTGAAGAA-----GAGGTGTTAAGCAGATACA-----ACATT 3608
 QY 1679 ULEUALALEUYSGLINMETGLNVALTHRGINLUYLSGLINLEUGLNTH 1699
 Db 3609 AATGAAATTACAGAACAGTTAAAGCAGAGTCTGCCATGTGAATCTCTTCCACAGCA 3668
 QY 1699 RHISGLNHLSEUThALAGLVALASPHISLEUYSGLUASNILEGLULEUGLYLEUAS 1719
 Db 3669 TGAACCTAACTGAAAAGCT-----CATCTT---GAAAAGCTGAGGTTACTTGAA 3716
 QY 1719 NPHEUYSASNGLUALAGLINLINYSRTHRLYSGULINCYSLLEUASNGLUASN- 1738
 Db 3717 T-----AAGTCTGGAAGGAAAATACTTTCTTCAAGACGAGCT 3755
 QY 1739 -LYSGULULEUGLINSEGINHISARGLEUINCYSGLUILEGLULEUMETYSSE 1758
 Db 3756 AGTTGAACCTGAAGCTGCGACAGAAAGATTAAGCCGAAAGTTTCTGAGTTGACTAGCAA 3815
 QY 1758 RLEUYSAPPLYSGUSERALALEUGLUTHRLYSGULUSERGLULINLYSVALILEAS 1778
 Db 3816 GTTGAATAACCAACGATGAGAAATTCAGAGTTGAAATCTTCACATGAATAA----- 3867
 QY 1778 NLEUASNGINLUETGLUMETVALMETLEUGLUMETGLULULEUYSASNSEGINAR 1798
 Db 3868 -AGTAACAAGCCTAGAGACAAAGAGCTTGAAATTTAAAAAAGCTG----- 3912
 QY 1798 GTHRVALLLEALAGLARGASPHINLEUGINASBPLEU--ARGLUSERVALIGLUME 1817
 Db 3913 -----TCTGAGAACTAGCCAGATCTGAGTATATTGCTGTAGAGAAACCAAGAC 3962
 QY 1817 TSERIEGLIUTHGLIASPASPLEUARGLYSALAGINLUALALEUGLINLINYSAS 1837
 Db 3963 CTATTAGAAAGCT-----AAACAATGACCTATCAACTTGTGTG 4007
 QY 1837 PHYSAVALINGULUEUThSERGINLESERVALLEUGINLUYSILSEUENLEUGI 1857
 Db 4008 TAAACTAATGACATCTTTCTTAGATTTCTCATTTGACACCGTCAACATAAATTAA 4067
 QY 1857 UASNGLMETLEUThYASNAVALATHRVALLYSGLUTHRLSEUGLURGHASBPLE 1877
 Db 4068 GAGGACACTGTATTAATAAACTTGACAGTTTCTGAA-----TT 4106
 QY 1877 UASNGLINSEUYSGLNHLSEUPHESERGLIUGLUTHRLSEUYSERLEUYSGL 1897
 Db 4107 AGAAGCACAACCTTAGACAGTTGACAGAGGCAAAATACATAAATTTCTTTCAACA 4166
 QY 1897 ULYSGIUPHEALALEUGLUGNALAGLUYSASP-----LYSNLASPAAAL 1913
 Db 4167 GGCTACTCATGAGTTAGAGAAAAGAAAATCAAAATTAAGACATGAGGCTGATTTGA 4226
 QY 1913 AARGLYSTHRLLEAPILLETHRGULYSILSEERASNILEGLUGLINLEUENLEUGI 1933
 Db 4227 AAGTCTT-----GTAAACGAAAA-----GAAGCCTTACAGAAAGA 4262
 QY 1933 NALATHRASNLEUYSGLUTHRLSEUYRGUARGLUSERLEUIE--GLICYSYSGI 1952
 Db 4263 AGGAGGCAATCAGACAGGCTGCTTCTGAAAAGAGCTTGTATTAACACAGTTGAAGA 4322
 QY 1952 UGLINLEUALALEUASNTHRGULHISLEUARGIUTHRLSEUYSERLYSASPLEUALAE 1972
 Db 4323 AGAGTTATCTGAAAACATCAAT-----GCTGT 4349
 QY 1972 UGLYLSMETGLUGLUGLARGASPHIUALAASNLYSVALILEALALEUThGLULY 1992
 Db 4350 CACATTTAGTAAGAAGAGCTTAAAGAAAAAGTTAGATTAGACAGCTTGTAGTAACA 4409
 QY 1992 SMETSERLEUENLEUGLINLINLEASNGLUASNVALTHRLTHLEUYSGLULYGLUGI 2012
 Db 4410 ACTTAAGTATTGAATGTTCAAGCTTCAAAATAGCATC----- 4446
 QY 2012 YGLUYSGLUTHRLPHETYLEUGLINARGPROSEUYSGLINSEUYSERGINMETGI 2032

Db 4447 -----AGCTATCCGAAAAAGA 4463
 QY 2032 UGLIUEAARGLUSERLEUThRLYSHASPLEUGINLEUGLUALAGLULYSGULI 2052
 Db 4464 AGCAGCCATTTATCATCACTAGA-----AAGCATATGATGAAGAAAA 4505
 QY 2052 ESEERGLUALATHRASNGLUILEYSASNLEUThRALYSILSEERSEUENLEUGLUGI 2072
 Db 4506 ATGTGAATTGCGGATCAGGTCCAGATTTATCTTTTAAAGTTGACACTGAGTAAAGA 4565
 QY 2072 U-----ILEUGLASNALASERILEUASNGLUALAVALSERGLUARGGLUAS 2089
 Db 4566 GAAAATTTCTGCTCTTGAGCAGAGTAGTACTGTGCATAAATTTCTCGAATGGAAGA 4625
 QY 2089 NLEUARGHISSEUYS-----GLINLEUVALSERGLULEUGLULENSE 2105
 Db 4626 GAAAGCACAGTAAAGATTTTACACAGCATTAACACTGTAAAGAAATG--CAGATCCA 4682
 QY 2105 RLEUThRLYSEUYSERARGASPHISALAPHEALAGINSEUYSARGGLULYSASPGLUAL 2125
 Db 4683 GCTTAGTTAAATCAAGAA-----GCTTATGAAGAAGATGAGCA 4724
 QY 2125 AVALASNLYSILEALASERLEUALIGLUGLUILEYSILEUThRLYSGLUMETASP-- 2144
 Db 4725 GATTAAT-----TTATGAGAGAGAGCTGATCAGCAAAATTAAGAATTGATTG 4775
 QY 2145 -----GLUPHEARGASPSERLYSGUSERLEUGINLUGINSEUYSERHISLEUSE 2161
 Db 4776 TTTAAAGGCTGAATGAGAAAGACAGACAGACAGATGAGAAAAGAGACTTTAATTGA 4835
 QY 2161 RGLUGLULEU-----CYSTHTRYLY 2168
 Db 4836 AACAGAGTTAAAGTCTCAACACAGCAAGAAATTATGGAATTAGAGACCATATTACCAGA 4895
 QY 2168 SFTH--GLUEUGLIMETLEUYSGLN-----GLINLYSGULASPII 2181
 Db 4896 AACTATTGAATAGAGTCTTAAATGAAGTCTTAAATTAACAATCAACAAAGAGATAT 4955
 QY 2181 EASNASNLYS-----LEUALAGLU----- 2187
 Db 4956 TGAAGCACAAGAAATGTTGTTACAGAACTTCACATTTCAAGAGTTAGGAGAAAGAAAGA 5015
 QY 2188 -----LYSVALIYSGLUALASPGLU-----LEUENGLNHLSEUYSERLE 2202
 Db 5016 CAACAGGTTAAAGAAAGCTGAGAAAGAAAATCTTAACACTTGAANAACAGTTATTCAT 5075
 QY 2202 ULYSGIUGINLEUASPGLINILEGLIMETGLULEU----- 2213
 Db 5076 GAAAGCTGAATCTGAAACTTAAGAAAGAAAGAAATTAACAATGTGAATTTAAGTGAAAAAG 5135
 QY 2214 -ARGASNGLUYSLLEUARGASNTYRGLU-----LE 2223
 Db 5136 CAAAGAGAGGAGTTAAAGGCACTGGAAGATAGGCTTGAGTCAGAAAGTGCTCAAAAT 5195
 QY 2223 UCYSGLUYSMETASPIILEMETGLULYSGLUILESERVALLEUARG-----LEUME 2240
 Db 5196 AGCAGAGTTGAAGAAAAAGCTGAACAAAAAATTCGTGCATTAAGACAGCTGTGTATC 5255
 QY 2240 TGLNASNGIUPROGINGLU-----GLUASBPVALALAGLUAR 2254
 Db 5256 TCAATGGAAGAGAAAGAAAGCACTATATAAAGTACAGAAACCATTTAGTGAGCT 5315
 QY 2254 GMETASPIILEUGLUSERARGASNGINLUILEGINLULEUMETGLULYSILSEERL 2274
 Db 5316 AAATCAAAATTTGAGGAAAGAAAGGAAAGGAAAGTTCAATCTTGAGAAAGAAAACTTAAGTC 5375
 QY 2274 AVALYRSEUGLUGIN--HISTHRLSEU-----SERSEUYSERSE 2288
 Db 5376 AGTGAAAGTACACAGTCAAGAACATTAATTTATCCACAGATAGCAAAAAAGCTGGCAC 5435
 QY 2288 RGLULEUGINLYSGIUTHRGUALAHISLYSHISCYSMETLEUASNILEYSGLUSERLE 2308
 Db 5436 ATATACGTAAACAAGAAAGAGATTTCCCAAGGCTGTGTGACAGACATATGAAGAAAA 5495

QY 2308 userSerThrLeuSerArgSerPheGlySerLeuGln----- 2320
 Db 5496 AATCAGTGTCTTACAAAGAACTTAAGTCAAAAAGAAAGCTTTGACAGGGTAGGGCA 5555
 QY 2321 -----ThrglnHisValIyLeuAenThrGlnLeuGlnThrLeu 2334
 Db 5556 CGAAAAAGAGAGAGAGTCTTCTCTCTCTTGAATTCGATGCCAATACAGAGAGCGCTT 5615
 QY 2334 uAenIyPheLeuValIyIyArgThrAlaIyValIyGlnAenPheSerLeuIyLeu 2354
 Db 5616 A-----ATAAAGCTAGACATGCTGAGCAAGCAACATGAAATGATGATGATAG 5669
 QY 2354 sAerPyrGlnIyLeuAenIyAlaIyGlnIyIyArgHisAerPyrLeuIyGlnLeu 2374
 Db 5670 TCATCTTCAAGAGAGCTTGAAGAAAAAACAAGAAATATTC-----TTGATAGTAC 5723
 QY 2374 uGlnCyLeuGlnGlnIyGlnIyArgIyTrpSerAerPheIyAserGlnIyLeuIyS-- 2393
 Db 5724 CCAAGCTGTGGAAGAAAGAGAGTAAATTAATACATACAGCAAGCAAAAGCTTGAAAA 5783
 QY 2394 ----PheCyGlnIyIyGlnPheLeuAenGlnLeuPheIyValIyAenIyIyGln 2412
 Db 5784 TGTGTTTGACGAGCTCCAG-----AAACCTTCAGAGAGAGAAAGAACTTAAGCTCA 5834
 QY 2412 nSerValGlnAerPheSerGlnIyValGlnIyPheLeu-----AsnGlnIyAlaG 2429
 Db 5835 GATTTTGAGCAAAAGATAAAGTAAAGCTGATCTCTGTTAGTAAAGCAAGAAAGATACA 5894
 QY 2429 ySerThrLeuGlnIyGlnIyLeuGlnIyIyValIyPheMetGlnIyTrpLeuGlnIyP 2449
 Db 5895 TAGAGTTGAAATGGAAGAGTGTGACCTCAAAATATGAAAAATTTACAGCTTTTACACAGAT 5954
 QY 2449 eGlnAerPheIyValIyAerPheIyLeuSerGlnIyMetGlnIyGlnIyAenIyArg 2469
 Db 5955 GGATGAGAAATTAACCCACAGAACTTTGGAAGAAAAACATGAGAAAAAGTCCAAA-- 6012
 QY 2469 glnIyAerThrIyGlnIyLeuThrIyValIyGlnIyValIyGlnIySerIyS 2489
 Db 6013 -----TCACATTTGGTCCAAACCCAAAT 6035
 QY 2489 eGlnAerGlnIyIyLeuThrValIyIyLeuAenGlnIyPheGlnIyAlaIyLeu-----G 2505
 Db 6036 GCTTAATACATGGAAGCCACAGCAATATCTGAGCTTAAATTTACCCGGGAGAGAGC 6095
 QY 2505 nGlnIyIyValIyGlnIyAenIyGlnIyLeuMetArgAerMetGlnIyHisIyGlnIyPheSerAl 2525
 Db 6096 GAGGAAACAGAACTGGGCAAGAGATTTGATTGACAGAA-----GACCT 6143
 QY 2525 aSerValMetGlnIyGlnIyAenIyAlaIyGlnLeuGlnIyIyLeuIyThrValIyGlnIyPhe 2545
 Db 6144 TCGAATTTGAGAAAGAGAGATCAGCAAGAAATTTGAAATCTTAAAGAAATATATGATCA 6203
 QY 2545 uSerIyIyValIyGlnIySerArgIyIyLeuMetLeuGlnIyAenGlnIyLeuAenIyValIyS 2565
 Db 6204 AGAAAG-----GAAGAGAAATCAACAGAGAGAGAAAGATCTTGAACCTGAAGCAAA 6257
 QY 2565 pAerAlaMetHisIyGlnIyGlnIyValIyAlaIyLeuGlnAerPheIyLeuIySerArg 2585
 Db 6258 TTCACATTA-----AAACAGCTGATGAGG-- 6282
 QY 2585 nAlaGlnIyAlaGlnIyLeuAenAlaMetGlnIyValIyLeuThrIyIyGlnIyAerPheIyLeu 2605
 Db 6283 -----GACTTTAAAT-----ACACAGCTGGGCAAAAGAGAAAGAAACAGAGCTGGA 6323
 QY 2605 nAlaIyAlaMetIyGlnIy-----IyGlnIyAenIyGlnIyMetValIyAlaIyGlnIyAlaIyP 2624
 Db 6324 AATGACCATTAAGAAAGAACTATCAATAAGCCGAGAGCTGAGAGCTGGAACCTTTAGAAAG 6383
 QY 2624 oTyIyIyGlnIyIyAerPheIyThrIyValIyValIyIyGlnIyMetGlnIyIyS 2644
 Db 6384 CCATCAAGAAAGACAAATCAGTTACTTAAAAAAATTCGAGAGAAAGAT--GATGATCT 6440

QY 2644 eTyIySerIyAlaIyThrAerGlnIyIyAlaIyTyIyLeuIySerCyLeuGlnIyAerPhe 2664
 Db 6441 AAAGCAAGACCCAAAGAAATATGAGAAATC-----CTTATGCTCG 6482
 QY 2664 sGlnIyGlnIyLeu-----ArgAerLeuIyGlnIyLeuAerArgAlaIyGlnIy 2680
 Db 6483 TGAAGAGAAATATGACTCAAAAGTAAGGAGCTGACAGACTCAACTGAGAGAGCTGAG-- 6540
 QY 2680 aAerPheAerThrIyValIyValIyPheIyAerPheIyIyValIyAerIyPheIyProva 2700
 Db 6541 -----AAGAAATCCAGCAAAACCTAGACAGAGAGCA 6572
 QY 2700 IyThrCyGlnIyGlnIySerGlnIyIyValIyGlnIySerThrAlaMetLeuValIyGlnIySer 2720
 Db 6573 GAACCTGGCAAT-----GATATGTAAACATTTATGAGCTTACAGACACA 6617
 QY 2720 uIyValIyAlaIyLeuGlnIyArgGlnIyLeuSerHisTyIyIyValIyTyIyHisIyLeuSerA 2740
 Db 6618 GTAGCAGACAGAAAGACAGCTTAACTCACTGATTCGAATTTGAAGACCAAGAGAGCTTACAGAG 6677
 QY 2740 gThrMetSerSerSerGlnAerArgIyIyIyValIySer----- 2755
 Db 6678 ACAGATTCAAAATTTAGAAAGACCGTTGAAAGAAATATGAAAGAAATGATATGCAACAC 6737
 QY 2756 -----AerAlaHisSerSerHisIyGlnIySerSerHisIyArgIyIyS 2769
 Db 6738 TGTGGGACACCTTAAAGAGTGGCAATTTGTACATACGATGCTCACTCTTTGGAGA 6797
 QY 2769 rProHisIyIyThrGlnIy-----ThyIyArgHisIyGlnIyProValIy 2782
 Db 6798 ACCTACCGAATTTAGATATTTGCGAAAGAGCTTTTGAATATATGATGGGTGCTGAGAG 6857
 QY 2782 rProGlnAerSerGlnIyMetProSerLeuHisIyLeuGlnIySerProIyIySerGlnIySer 2802
 Db 6858 TAAGACCATGCGCAAAAGTTATACACCGTACTGAAAGTTCCCT-----GATATCA 6908
 QY 2802 rThrIyIyValIyValIySerProHisIySerGlnIyIyTyIySerGlnIyValIyMetSerP 2822
 Db 6909 GACTCAGAAATTTTGTG-----GAAGAGAGAT-----GCTCGGCTGATGTTTCTTC 6956
 QY 2822 oGlnIyIyThrGlnIyMet-----HisIyValIyIyLeuSerProSerIyValIyG 2838
 Db 6957 ACCTCGACAGTATATCTTGTGAGTAAACATCAGTGTGCTTATGATACATGTCATG 7016
 QY 2838 yLeuHisIyIyValIyAerAlaIyLeuSerProHisIySerGlnIyMetProIyHisIyValIy 2858
 Db 7017 GCTC-----CGATCTTCACTTGAAGAGAA-----GT 7043
 QY 2858 eSerProGlnIyIyThrGlnIyLeuHisIyValIyAenIyThrGlnIySerThrLeuPheAerPhe 2877
 Db 7044 GACATTGGGTGACTGCTGCTG--GAAGAGCTGTCCACACTTGTCTCTTGTAGAGATGA 7100
 QY 2878 -----LeuSerSerProCyLeuIyGlnIyValIyGlnIyAenIy 2891
 Db 7101 AGTTGCAATTCACGGGCTCTCATGTAGCCAAAGACCAAGAAATCTG 7149
 RESULT 15
 ; US-09-814-353-21776
 ; Sequence 21776, Application US/09814353
 ; Publication No. US20030165831A1
 ; GENERAL INFORMATION:
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 ; APPLICANT: Thompson, Pamela
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 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
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 ; CURRENT APPLICATION NUMBER: US/09/814,353
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 PRIOR FILING DATE: 2000-12-21
 NUMBER OF SEQ ID NOS: 22037
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 21776
 LENGTH: 8063
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 1, 7851, 7842, 7843, 7844, 7845, 7846, 7847, 7848, 7849,
 LOCATION: 7850, 7851, 7852, 7853, 7902, 7903, 7904, 7905, 7906, 7907,
 LOCATION: 7908, 7909, 7910, 7911, 7912, 7913, 7914, 7915, 7916, 7917,
 LOCATION: 7918, 7919, 7920, 7921, 7922, 7923, 7924, 7925, 7926
 OTHER INFORMATION: n = A,T,C or G
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 7927, 8036, 8037, 8038, 8039, 8040, 8041, 8042, 8043, 8044,
 LOCATION: 8045, 8046, 8047, 8048, 8049, 8050, 8051, 8052, 8053, 8054,
 LOCATION: 8055, 8056, 8057, 8058, 8059, 8060, 8061, 8062, 8063
 OTHER INFORMATION: n = A,T,C or G
 US-09-814-353-21776

Alignment Scores:
 Pred. No.: 5,51e-56
 Score: 1032.50
 Percent Similarity: 40.62%
 Best Local Similarity: 22.25%
 Query Match: 6.99%
 DB: 12
 Gaps: 129

US-09-724-584-1 (1-2954) x US-09-814-353-21776 (1-8063)

QY 344 AAlaLeuLeuYsArGTYrArgLYeGLuIleuAspLeuYsGLInleuGLuAsn--- 362
 Db 331 GCCATGTTCAAGAAACGAAAGCAAAAGATCAGCGAGAGACAGCGAGCTCCAGCGCG 390
 QY 363 -----LeuGLuSerSerSerGluThrLYsAlaGlnAlaMetAlaLYsGLInGlu-HI 379
 Db 391 CTGGCTCTCTCTAGGCGGTCTCCATTCTTCAACCAACCAACAGAAATGAGAGACAGACA 450
 QY 379 sThrGlnLeuLeuAlaGluIleLYsGlnLeuHISLYsGluArgGluAspArgIleTrpHI 399
 Db 451 TCTTCATTTCACAGACCACTTGATGAAGGTACAC---CCAAATGAGAGTCAGGTGACACA 507
 QY 399 sLeuThrAsnIleValAlaLaserSerGlnSerGlnGlnAspGlnArgValLYsAr 419
 Db 508 C----- 508
 QY 419 gLYsArgArgValThrTrpAlaProGluLYsIleGlnAsnSerLeuHISAlaSerGlyVa 439
 Db 509 -----AGTCCTTTGCAAGAACTCCAG 531
 QY 439 lSerAsp-----PheAspMetLeuSerArg-----LeuProGlu 450
 Db 532 CTCGGGGTCCCTCCGTGAGAGTCTTTGTTTCAAGTCGATTAAGAAATCTCTATTCCGG 591
 QY 450 yAsnPheSerLYsLYsAlaLYsPheSerAspMetProSerPheProGluIleAspAspSe 470
 Db 592 TCTTCTTCAAGAGTCTTTGGTACCAACATCTTCCAGAGAAATCCCTGATGATTGA 650
 QY 470 rValCYsThrGluPheSerAspPheAspAlaLeuSerMetCtAspSerAsnGlyTI 490
 Db 651 CCTGAGCACTTCTACTGCGCAAGTTTGATCCACC---TCTGATATGATGATGAGAGGTGA 707
 QY 490 eAspAlaGluTrpAsnLeuAlaSerLYsValThrHISArgGluLYs----- 505

Db 708 AGACTGTGTAGGGAAT-----TCAGCACTCTCCAAAGAAACAGTTGATTCAGCGCTT 761
 QY 506 -ThSerLeuHISGlnSerMetIleAspPhe---GlyGlnIleSerAspSerValGlnPh 524
 Db 762 GCGAAGATGAAAGCAAGGCTTAAGTACAGAGGAAAAATATTCGAGCTGTCTTACAGC 821
 QY 524 eHISAsp-----SerSerLYsGlnAsnGlnLeuGlnHISLYsGluProLYsAspSerGlyAs 542
 Db 822 TTATCAGATCTCTCAGAGAGAGAAAGAAAGTACAAAGGTATTTAAGTCAGAGTCAGGA 881
 QY 542 pMetAlaGluCYsArgLYsAlaSerPheGluLYsGluIleTrpSerLeuGlnGlnIle 562
 Db 882 TAAATCA-----CTTCGAGAAATAGCAAGATTAAAGAGAGAGCT 920
 QY 562 uGlnSerLYsGluGluGluLYsGlnLeuValGlnSerPheGluLeuLYsIleAlaGlu 582
 Db 921 CCAAAATGACACACAGAGCAAGAAACATCTGCAAGAGAGGTTTGATGATCTTTAGAGGA 980
 QY 582 uLeuGlnGlnGlnLeuSerValLYsAlaLYsAsnLeuGlnMetValThrAsnSer---Ar 601
 Db 981 GAAAGATCAGTATATCAGTGTCTCCAAACTCAGGTTCTCTACTGAAACCAACGATTACG 1040
 QY 601 gGlnHISSerIleAsnAlaGluVal-----GlnThrAspValGluLYsGlu 616
 Db 1041 AAATGGCCCGAATGAATGTGATGATGTAACCACTTCTCTCAGTCGAAACACAGCTGA 1100
 QY 616 uValAlaArgLYsGlnMetSerValLeuGlyAspSerGlyTrpAsnAlaSerAsnSerAs 636
 Db 1101 AGCTTTCATTAAGAAAGCAAT-----CCAGAAAGTGA 1133
 QY 636 pLeuGlnAspSerSerValAspGlyLYsArgLeuSerSerSerHISAspGluCYsIleGlu 656
 Db 1134 TCGAAGCCAGATGATGTAAGATGCA-----ACTTCTGTAA 1169
 QY 656 uHISArgLYsMetLeuGlnGlnLYsIleValAspLeuGlnGluPheIleGlnAsnLeuAs 676
 Db 1170 AACACTGGAACACTCCACGAAAGAGTG-----AAGGCTCAAGGAACTTACT 1217
 QY 676 pLYsLYsSerGlnAsnAspLYsGlnLYsSerSerGluGlnAspPheMetGlnSerIleGlu 696
 Db 1218 TAAAGCTTTAAGAAACAAATTCACTCAGTCACATTAAGAAACAA----- 1257
 QY 696 nLeuCYsGlnAlaIleMetAlaGluLYsAlaAsnAlaLeuGlnGluLeuAlaLeuMetAr 716
 Db 1258 ---TGTACTATTATTACTAGTGAAGAAA---GAAGCTCTCAGAGA----- 1296
 QY 716 gAspAsnPheAspAsnIleIleLeuGluAsnGluThrLeuLYsArgGluIleAlaAspLe 736
 Db 1297 -----CAACT 1301
 QY 736 uGluArgSerLeuLYsGlnGlnGlnGluThrAsnGluPheGluIleLeuGluLYsGluThr 756
 Db 1302 GGATGAAAGAACTTCMAAACCTAGAAAGATAAGAAAGCACTTCATATGAGCCGAGAAAG- 1356
 QY 756 rGlnLYsGluHISGlnAlaGlnLeuIleHISGlnIleGlySerLeuLYsLeuValGlu 776
 Db 1357 -----ACTAACTTATCACTGATGCGTATGATGCAAGAACTTAATTGA 1400
 QY 776 uAsnAlaGluMetTrpAsnGlnAsnLeuGlnGluAsp-----LeuGlnThr 791
 Db 1401 A-----CAGCTTGAAACAAGATTAAGGGAATGTAATCCGACAGAGAC 1439
 QY 791 rLYsThrLYsLeu-----LeuLYsGlnGlnGlnIleGlnLeuAlaGluLe 806
 Db 1440 AAAAGCTCAATCATCAAGAAACCTGGAAGATGAAGAAAGAAATTA-----GCTCAACT 1493
 QY 806 uArgLYsArgAlaAspAsnLeuGlnLYsLYsValArgAsnPheAspLeuSerValSerMet 826
 Db 1494 CCCTAGCCGATCAAA-----CAGATGACTACCAAGAGAGGAATTTACGGGAACAGAA 1547
 QY 826 rGlyAspSerGluLYsLeuCYsGlnGluIlePheGlnLeuLYsGlnSerSerAspAl 846

1548 AGAAAGTCCGAAAGAGCTGTTTGTAG-----GAACCTGAAAAAGCTTTGAGTACAGC 1601
Qy
846 AGUAlaValIThrArgAspAlaGlnLysGluCysSerPheLeuArgSerGluAsnLeuG1 866
Db
1602 CCAAAAA--ACAGAGAGAGCAGAGAGAAAA--CTGAGGACAGAAATGATGATGA 1649
Qy
866 ULeuLysGluMetGluAspThrSerAsnTrpTyAsnGlnLysGluLysAlaIle 886
Db
1650 ACAAAATAAAACCTTCGAAAAACCAAGT-----GAGAGAGAGCCATCAGT-- 1695
Qy
886 rLeuPheGluLysGlnLeuGlnThrGluLysSerAsnTrpLysLysMetGluAlaAspLe 906
Db
1696 -----CTTCAACAGAGAAATTAGTCGGGTGAACAGAGGCTGTGATGCT 1739
Qy
906 uGlnLysGluLeuGlnSerAlaPheAsnGluIleAsnTrpLeuAsnGlyLeuLeuAlaG1 926
Db
1740 AATGAAA-----AAATCCTCAGAAAGAACAAATGTCTAGCTACAGAAAGCTCATGAAA 1793
Qy
926 YLysValProArgAspLeuLeuSerArgValGluLeuGluLysValSer----- 943
Db
1794 GAGAGCTGGCCAGA-----AAAGACAGAGAACTACCAAGAAAGCTTCAGACCCAGAG 1844
Qy
944 ----GluPheSerLysGlnLeuGlnLysAlaLeuGluGluLysAsnAlaLeuGluAsnG1 962
Db
1845 AAGGGAATTCAGAGAACAAATGAAGTAGCTCTTGAAGAAAGCTCAA----- 1890
Qy
962 uValIThrCysLeuSerGlnTrpLysPheLeuProAsnGluValGluCysLeuLysAsnG1 982
Db
1891 -----TCAGAAATATTGAAAGATCAGCCAGAAAGAAAGAA-----CAGCA 1928
Qy
982 nIleSerLysAlaSerGlnGluIleMetLeuLeuLysGlnGluGlnGluLysIleSerAlaSe 1002
Db
1929 AGAATCTTGGCCCTTGAAGAGATTAGAGTTGACAGAAA----- 1965
Qy
1002 rIleIleSerLysGlnGlnIleIleMetGlnGlnGlnSerGlnGlnIleLeuGlnLeuTh 1022
Db
1966 -----AAAGCAATCCTCAGAGAAAGGAAAGAAATTAACCTTGGGACCTTCA 2009
Qy
1022 rAspGluValIThrIleThrGlnSerLysValGlnGlnThrGlnGlnGlnTrpLeuGlnLume 1042
Db
2010 GCAAGAAAGCAGAGACTTACAGAACTAGAAATCTTGAATGAAAGTTCT----- 2058
Qy
1042 tLysLysMetHisAspAspLeuPheGlnLysLysLysIleArg--AsnLysSerGluAlaG1 1061
Db
2059 -----TTGAGAAAAAGCTTACAGAAAGAAACAAAAATCAGTCAAA 2096
Qy
1061 uAspLeuLeuArgGluMetGluAsnLeuLysGlyThrMetGlnSerValGluValLysI1 1081
Db
2097 AGATTG-----GCTGTTCACTCGGAAGC 2120
Qy
1081 eAlaAspThrLysHisGlnLeuGlnGlnTrpIleArgAspLysGlnLeuLeuHisG1 1101
Db
2121 TGAATAAAATATACACAAATAGAGATTAACGTC----- 2154
Qy
1101 uLysLysTrpPhePheGlnAlaMetGlnThrIlePheProIleThrProLeuSerAspSe 1121
Db
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Qy
1121 rLeuProProSerLysLeuValGluGluAsnSerGlnAspProIleGluIleAsnAspTy 1141
Db
2155 -----ATGTTGAAAAACAC- 2169
Qy
1141 rHisAsnLeuIleAlaLeuAlaThrGluArgAsnAsnIleMetValCysLeuGlnTrpG1 1161
Db
2170 -----AAGACAGA 2177
Qy
1161 uAspAsnSerLeuLysGlnGlnValIleAspLeuAsnThrGln--LeuGlnSerLeuG1 1180
Db
2178 ATTGAAAGGCTTAAAGCATAGCAGATGCCCTTTGACCTGAAAACTTCAAGCTTTAAA 2237
Qy
1180 nAlaGlnSerIleGluLysSerAspLeuGlnLysProLysGlnAspLeuGlnGlnG1 1200
Db
2238 GCAACAA-----TATCAGACTGAATGAAAACTTAGGAAAAAGTGTAAACAAGAAA 2291
Qy
1200 uValLysLeuLeuLeuGlnMetGluLeuLeu----LysGlyHisLeuThrAsp---SerG1 1218
Db
2292 AGAAACATGTTGTAACAAACAAAGAGATTATCTTCAGGCCCCACATAGAACAAATGAATGA 2351
Qy
1218 nLeuSerIleGluLysLeuGlnLeuGlnAsnLeuGluValIThrGluLysLeuGlnThrLe 1238
Db
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Qy
1238 uGlnGlnGlnMetLysAsnIleThrIleGluArgAsnGlnLeuGlnThrAsnPheGluAs 1258
Db
2400 ATCTTCTGAACCTGCAGAAATATTAAGACCCCGTCACAAACTGAAAGAGAACTTCTGT 2459
Qy
1258 pLeuLysAlaGlnHisAspSerLeuLysGlnAspLeuSerGluAsnIleGluGlnSerI1 1278
Db
2460 TCTGAAAGATCAACAGATTAATAAGAAAGAGAAATTAGAGCCCAAGATGAT----- 2511
Qy
1278 eGluThrGlnAspGluLeuArgAlaAlaGlnGlnGluLeuArgGluGlnLysGlnLeuVa 1298
Db
2512 -----GAAACAGAAAAATCATCAGCAGCAAGT 2540
Qy
1298 lAspSerPheArgGlnGlnLeuLeuAspCysSerValGlyIleSerSerProAsnHisAs 1318
Db
2541 TGACAGT-----ATCATTAAGAACACAGAGT 2567
Qy
1318 pAlaValAlaAsnGlnLysValSerLeuGlyGluValAsnSerLeuGlnSerGluLume 1338
Db
2568 ATCTATTCAGAGAGCTGAGAAAGCATTAATAAGATCAATTAATCACTT-----GAGCT 2621
Qy
1338 tLeuArgGlyGluArgAspGluLeuGlnThrSerCysLysAlaLeuValSerGluLeuG1 1358
Db
2622 TCTCTTGAAGAAAGGACACAGCATTTGAAAGACATCAGGCTCATGTAGAAAATTAGA 2681
Qy
1358 ULeuLeuArgAlaHisValLysSerValGlnGlyGluAsnLeuGlnIleThrLysLysLe 1378
Db
2682 G-----GCAAGATTAATAAGGCTGAGAGGGAAGCTCAGACAGCATCTGCTAGCT 2732
Qy
1378 uAsnGlyLeuGlnLysGlnLysGlnLysLysSerGlnGlnSerGluValLeuLysSerme 1398
Db
2733 GGAAGTTTTCAGCTTAC-----CAGAGTGCACACATGACGACGACAAAGCAT 2783
Qy
1398 tLeuGluAsnLeuLysGlnLeuAspAsnLeuLysLysGluGlnAlaGluGlnTrpYrseSe 1418
Db
2784 TGAGGAACAGTTGGCCCAATTGCGACGAGAGTTGTTGATTTGGAAAACAGAAACAATTCT 2843
Qy
1418 rLysGluAsnGlnPheSerLeuGlnGlnValIlePheSerGlySerGlnLysLeuValAspG1 1438
Db
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Qy
1438 uIleGluValLeuLysAlaGlnLeuLysAlaAlaGluGluArgLeuGlnIleLysAspAr 1458
Db
2898 GTTAGATGCTCACAAATATCCAGGTGCAGACTTAATGACCAACTTGAAAAACAAATTAG 2957
Qy
1458 gAspTrpPheGluLeuValGlnThrAlaAsnThrAsnLeuValGluGlyLysLeuGlnTh 1478
Db
2958 TGAATGACCAAAAGATTAATCTTTA--ACCAAGCTTAGAGTCCAAACTTGAGAG 3014
Qy
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Db
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 QY 1606 aspCysValHisProLeuGlu-----GluYsIleLeuLeuThrGlu-- 1621
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 QY 1622 -----GluLeuHis-----GlnYsThrAsnGluGlnI 1631
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QY      2858 eserProGlyLysThrGlnGLeuH1stLysAsnLeuThrGlusEThrLeuPheAspn-- 2877
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Job time : 2885 secs

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OM protein - protein search, using sw model

Run on: October 22, 2003, 21:06:57 : Search time 33 Seconds

(without alignments)
3787.463 Million cell updates/sec

Title: US-09-724-584-1

Perfect score: 14769
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3615	24.5	2662	4 US-09-595-684B-31	Sequence 31, Appl
2	1148.5	7.8	3248	1 US-08-353-700-1	Sequence 1, Appl
3	1148.5	7.8	3248	5 PCT-US95-16216-1	Sequence 1, Appl
4	1055.5	7.1	2482	1 US-08-328-254-6	Sequence 6, Appl
5	1051	7.1	1388	4 US-09-572-191-2	Sequence 2, Appl
6	1051	7.1	1388	4 US-09-723-262-2	Sequence 2, Appl
7	1051	7.1	1388	4 US-09-723-219-2	Sequence 2, Appl
8	1020	6.9	3878	4 US-09-914-259-11	Sequence 11, Appl
9	953	6.5	1234	4 US-09-592-054-8	Sequence 8, Appl
10	945.5	6.4	1232	4 US-09-592-054-2	Sequence 2, Appl
11	943	6.4	1231	4 US-09-595-684B-23	Sequence 23, Appl
12	906	6.1	1375	4 US-09-722-139-2	Sequence 2, Appl
13	906	6.1	1375	4 US-09-721-832-2	Sequence 2, Appl
14	906	6.1	1375	4 US-09-721-689-2	Sequence 2, Appl
15	890	6.0	963	4 US-09-914-259-20	Sequence 20, Appl
16	887	6.0	963	4 US-09-914-259-22	Sequence 22, Appl
17	877.5	5.9	1031	4 US-09-914-259-24	Sequence 24, Appl
18	874	5.9	967	4 US-09-914-259-21	Sequence 21, Appl
19	873.5	5.9	957	4 US-09-914-259-16	Sequence 16, Appl
20	868.5	5.9	975	4 US-09-914-259-19	Sequence 19, Appl
21	867	5.9	956	4 US-09-914-259-17	Sequence 17, Appl
22	866	5.9	10182	4 US-09-134-001C-3159	Sequence 3159, Ap
23	856	5.8	1032	4 US-09-914-259-26	Sequence 26, Appl
24	847	5.7	1027	4 US-09-914-259-27	Sequence 27, Appl
25	841.5	5.7	1279	4 US-09-724-517-2	Sequence 2, Appl
26	841.5	5.7	1279	4 US-09-641-807A-2	Sequence 2, Appl
27	841.5	5.7	1279	4 US-09-723-096-2	Sequence 2, Appl

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30	770.5	5.2	815	4 US-09-914-259-18	Sequence 18, Appl
31	769	5.2	3696	4 US-09-134-001C-5080	Sequence 5080, Ap
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36	758.5	5.1	1066	3 US-09-541-782-8	Sequence 8, Appl
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ALIGNMENTS

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RESULT 1
US-09-595-684B-31
; Sequence 31, Application US/09595684B
; Patent No. 6544766
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Ohashi, Cara
; APPLICANT: Sakowicz, Roman
; APPLICANT: Walsberg, Eugeni
; APPLICANT: Wood, Kenneth
; APPLICANT: Yu, Ming
; TITLE OF INVENTION: Human kinesins and methods of producing
; FILE REFERENCE: cytop036
; CURRENT APPLICATION NUMBER: US/09/595,684B
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 09/295,612
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 2662
; TYPE: PRT
; ORGANISM: Human
US-09-595-684B-31
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Best Local Similarity 32.0%;  Pred. No. 2.6e-169;
Matches 995;  Conservative 570;  Mismatches 935;  Indels 614;  Gaps 85;

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119 PPREFLRVSMEIYNEITVTDLLCGTQKKKPLIREDVARNVYVADLTVEVYTSMAWK 180
121 PPREFLRVSMEIYNEITVTDLLCGTQKKKPLIREDVARNVYVADLTVEVYTSMAWK 180
179 WIKGGEKRNHYGETYKNDHSSRSHITFRMIVSRDNDPTNSGENDGAVMVSHLNLDVDA 238
181 WITGGEKRNHYGETYKNDHSSRSHITFRMIVSRDNDPTNSGENDGAVMVSHLNLDVDA 237
239 GSERAAQTGAAGVRLKEGGINRSLFIIGQVIRKULSDQAGGFIVNRDLSKLTIRIIONSLG 298
240 GSERAAQTGAAGVRLKEGGINRSLFIIGQVIRKULSDQAGGFIVNRDLSKLTIRIIONSLG 297

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QY	229	SNAKVITICTIPVSEFDELSTLQOASPASTAKVHRMTPHNENVLDDALLKRRKETLIDK	358
Db	228	GNPKRIICTIPVSEFDELTLQOASPASTAKVHRMTPHNENVLDDALLKRRKETLIDK	357
QY	359	OLENSESSETAQOMAKEEHITQLAEITKOLHEKREDEIMHITINIVASQOES--QODORV	417
-Db	358	OLE--EVLSEITPAQOMEKQOLAQLLEBKDLQKQNEKINENITRLMYSSSLTLOQELKA	415
QY	418	KRRRVTWAPGKIONSLSHAGSVDFPMLSRJPGNFSKAKAGSDMSPFPEIDSVCTEFS	477
Db	416	KRRRVTWCTGKINKKSNVADQGN--IPTNITTYKHKLISNLTREIDSVCSGSEDV	471
QY	478	FDDALSMDSNIDENMLASGVNTHREKTSLSHQSIDGQSLSDSVQFDDSKENOLQYLR	537
Db	472	FSNLTLDTS---ELEMENTATKLINQE-----	494
QY	538	KDSGMAECRKASFEKEITSLQOQOQSKKEEKELVQSFELKIALEBQLSVAKNLEMV	597
Db	495	-----NISE	499
QY	598	TNSRHSINAEVQTDVEKEVVRKENSVLGDSGYNASNSLDQSSVDGKRLSSHDECIEH	657
Db	500	LNS-----	502
QY	658	RKMLEQKIVDLEEFLENKKSSENDKQSSBEDFMESIQLCEALMAEKANLLELMARD	717
Db	503	-----LRA	505
QY	718	NPDNITLENETLKREIADLERLSKQENOTNEPEILEKETOKENHEAQLTHEIGSLKTVEN	777
Db	506	DYDNLVLYEQLRTKEEMELKXKKNDDIDEFEALERKTKQDOEMQLTHEISNLEKNLVKH	565
QY	778	AEMYNONLEBDLETQTKLLEQEOLOLAELRKADMIQKRVNFDLSVSMGDSKLCBETIF	837
Db	566	REVYNQDLENELSSKVELLREKEDQIKKLQEVIDSQKLENIKMDLSYL-----ESIDPK	621
QY	838	QLKQSLSPAELVTRDAQOECSTFRLSENNELKKEKEDTSMWYNQOKEAKSLFEKOLETBS	897
Db	622	QMKQTLFPAETALDPAKRESAFRLRESENNELKKEKEMELATTYKQEMENDIQLQVQLEAK--	679
QY	898	NYKKMEADLOKELOSAFMEINYNGLGKVPRLDLSVELEKYSSEPSKOLEKALEBXN	957
Db	680	--KKMQVLEKELQSAFNEITKLTSLSDGKVPKDLCLNLELGAETLQOKELENEVEENE	737
QY	958	ALENEVOTLSEKFFPNEVECLKQNSIAXASEIMMLNOEGHSASISIKOEIIIMOQEQ	1017
Db	738	ALREVEIILSELKSLPSVEVERKAKTIQKSEBILHITTEKXKLPSVEVHNKSRQGLLE	797
QY	1018	ILQLTDEVTHQSKVQOOTEBOYLEMKKNHDDLFEKY-----IRKNSAEDLLREMENT	1070
Db	798	IGTKTQDLDATQOYNYSKTDOEFQNKFTLHMPFEQYKVVLEENERNQOELVNLSEAKQF	857
QY	1071	KGTMESVSVKADTGHLEETIRDEQOOLHEKKYFQAMQITFPTPLSDSLPSKLVG	1130
Db	858	DSSIGALTELSTYKTOELOEKTRFQOERLNEBQLEQLEN--RDSPLQYVEREKTLITE	915
QY	1131	NSODPIEINDVHNLTALATERNNIMVCLTEBRSNLSKEOV-----IDLNTQOSLOQAS	1183
Db	916	KLQOQTLF--EYKTLTQEKDLDKQLOESQIRBDQKSDIHNTVMNNIDTQOQLNALESL	973
QY	1184	IEKSDLOKPKODLEBGEVYKLLLEMLLKGLHTD---SOLSIEKIQLENIETVEKLOTLQ	1239
Db	974	KHOETINTLKSKISE--EVSRLNLMHEBNGETKDEFOQMGVIGDKQ--DLE--AKNTQTLT	1029
QY	1240	EEMKRITL-----ERNELQTNFEDLKAHBSLKDQLSNIEQISITQODELRAA	1287
Db	1030	ADVADKNEIIEQORKIFSLIOENKNEIQOMLESVIAKEKQDLKDKENIEMTLENBDELRL	1089
QY	*1288	QEBLEBOKOLVDSFQOQLLDCSVGISSPNHDAVANQOEVUSISGEVNSLOSEM-----LRGE	1342
Db	1090	GDELKQOQEIYAOEGNNAIK--KEGSLSTCRBLAVEKLEKESQOOLEKQOOLYNQOE	1148
QY	1343	RDELOTSCKALVSELELRAHVKS-----VEGENLEITRKLNGLEKEIIGKSEBSHV	1395

Db	1149	MSBQCK----	INELINUKKELKKELTLEMMETRELELAOKLENNBEVVSITKERVYL	1204
QY	1396	KSMLENNKEDNNKLKEQAEYSSKENOPSLBEVFSQKLVDEIVLKAOLKAABERLEI	1455	
Db	1205	KELQSPETERDHLRGY-----	INIEIATGLOETREBLKIAHIIHKENOETIDE	1252
QY	1456	KORDYFE-LVOTANTNLVEGLETPBLQD----	HEED-----SIDRSEEM-EIKVLG	1502
Db	1253	LRRSVSEKTAQIINTODLE-KSHTKLOEIRIVLHEEOELLPNVKVSSTQETNMELBELEI	1311	
QY	1503	EK-LERNQYLLERLOEBKLELSNKLEILOKMEMSVLLKDDLOQKLESLSENNIIKENI	1561	
Db	1312	EOSTTKOSTTARIEMERLYRINEKFOESOEIKSLTEREDWLKTTIKELYEVKHQOLKHEI	1371	
QY	1562	DTTLKHSDDTOAOKTOQOELQALAKNLAIAASDNCPIYOKE-----	TSADCVHPIEBKLI	1618
Db	1372	RETL-----AKIQESQSKOQSLNNKEXONNETTKIYSEWGEKRPKDSALLRIEIMLG	1424	
QY	1619	LTEBLHQKTNOEKLHEKNELEQAOVELKCEVHLKMSITSSLSLELOKHXDHTEOQ	1678	
Db	1425	LSKRLQESHDEMKSAKEXKDLORLOEVLQESDOL-----	KENIKEIYAKHLEETEE	1477
QY	1679	L-----LALQOMQVVOVTOEKKELQOQTHEITLAEVUHLKENIE-LGYNFQNEQOQTTHEOC	1733	
Db	1478	LKVAHCCLEKEEETINELRVLNLSKE-----	TEISTIQOLAIKDLQONKIQOELYEKBO	1533
QY	1734	LNNKKELEQSQHLLQCEIEBELMKSILKQESALFTLKESEQKVLN-----	NOQEMMV	1786
Db	1534	L-NIKQISEQVENVN-ELKQFKHRRKAKSALOSI---	ESKMELITLNRLOESQEBEQIM	1587
QY	1787	MLEMEELKNSQRTVIAERDQLODDLRSVSMSIEFTODDLRKAQOALQOQKVOELTSOI	1846	
Db	1588	IKEXEKMRVQOEAQIERDQKENTKEITVAKMSESQE--	KEYOPLKMTAVNETOEMKCEI	1645
QY	1847	SVLOEKISL-----LEN-----	QMLY-NVAIVKETLSBRDQNSQKHLFEBIEIETLS	1892
Db	1646	EHLKEQFETOKLNIENIETENIRLTQILHLENLEBMSVTKERDRLRSVEETLKVEROQK	1705	
QY	1893	LSLKEK-EFALQEAQKCK-----	ADARKTIDITEKISNIEBQLOQATNKETVL-YERE	1945
Db	1706	ENLBEETITRDLKEQBELKIYMHLMKHOETID---	KLRGIVSEKTNEI.SNNQKLEHNSD	1762
QY	1946	SL-----IOCKEQALANTHEURETLKSKDOLAKGMOERDEANVIALTEXMSSLEEQIN	2001	
Db	1763	ALKQODKIQEELRIAHMHLEKEQOETIDKLRGIVSEKTDKLSNNQKLENSNAKLOEXIQ	1822	
QY	2002	ENVTTLKEGESEKFTYIQRPSKOQSSQMBELRESLTKDQLOLEBAKEISEKATNEIKN	2061	
Db	1823	E-----LKANEHQLTTLKKDVNETQKVSSEMOQKQIKDOSLTLSKL-----	ELEN	1869
QY	2062	LTAKISLLEEBIILONASILNEAVSERENLRSKOOLVSELOLSLTL-----	KSRDHAFAO-	2117
Db	1870	L-----NLAQIHLNLEBMSVMKEROBLRVVEETLKLERDQLESLOETARBLEIQOE	1924	
QY	2118	-----SKREK-----	DEAVNKIASIAEBEIKILTKEMDFRDSKESLOEQSSHLEEBCTY	2167
Db	1925	LKTARMLSKHEKETVQDKLREKISIKTIQISDIQKDLCK-----	SKDELQKQIDELQ-----	1975
QY	2168	KTEILOMLKQOQEDINNNKLAEKVAVDEL-----	LQHLSSLEKQDQIQOM	2211
Db	1976	KKEEQIQLTR-VKEDVQMS-HKKINEMEQKQOFEPNYLCKCEMDNFOLTKKLHESLLEIRI	2033	
QY	2212	ELR-NEKLRNVELQCKMDIMEKELSVLRM-----	QNEPOOE--EDVAEKMIDLES	2260
Db	2034	VAKREDELRIKESLQKBE-RDQFIATIREMARTDRQNHQVQVPERKLLSDGOQHLMESIRE	2092	
QY	2261	RNOEIOELMEKISAVVSEOHNTLSLSSELOKETEAHKHGMILNKESLSSTLSRSPSLQ	2330	
Db	2093	KCSNIKELKRYKYSM--DDHYECUNRLBGDEKEIEFHR-----	2129	
QY	2321	TEHVAKNTQLOTLINKRVV--YFTAAVKEDSHSLIKUYEKDLAAEQKHDELRLQLOCLE	2378	

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Db 2130 -----IMKLYLVSVYTKIEQHECINKFEMDFIDEVOKELLIKIQHLQ 2177
Qy 2379 QHGKKSDBASBEKCEIEFLNELLPKANIIOQVDDPSEVQVNLVNGSTLOEELH 2438
Db 2178 QD-----CDVPSRELRLKLNQNMWL-----HIEILKPFSEBE--FPSIKTEFOVLN 2225
Qy 2439 KGFQWLEEFDPDLHDVAKKLESGMOQENRIASTLOLTKRLKAVQSKI---OREITV 2495
Db 2226 RKEMTQFLEEMINTRPDIKLGKGIQKENDRICQVNNFPNNRIAIAMNSTEREEESAT 2285
Qy 2496 YLNOPEAKLOEKEQONKELMRMRHHGSPASVMEENARLGLTKTVDE-----SKKL 2549
Db 2286 -SKWEQDPLSKLEKKEKELFKVYQTLKTSLASAQVN-----PTQONKPNHYVSRA 2337
Qy 2550 Q---SRIMKLENLVKKDDAHKGEKVALLODKL-LSRNAEELNAMOYKLTCKQDNQ 2605
Db 2338 QUTTEKIRELENSLHEAKESAMHKEKIIKQKELEVTNDIIAKL--QAKVHESNCKLE 2394
Qy 2606 AAMKEIENLOKMAKAVPYKEEIDNLKTRVYKIEKIKYSKATDOEIAVLKSCLEDEK 2665
Db 2395 KTKETIOVLQDQVVALGAKYKEIEIDLKYLKIDLEKKNAKAFKEKISATKATVEYOK 2454
Qy 2666 ECLRLKLEBRBAQDNITVCPKDYQKASTFPVTCGGSGIIVOSTAMVLQSEKALE 2725
Db 2455 EYIRLRLRELRSSQQAQDTSVISEHTDPQPSNKPFLTCGGSGIIVQNTKALLKSEHRL 2514
Qy 2726 RLSHYKKKKYHHLSTMSSEDEKKTAKASDAHSSTGSSHRSKPKETTYR--HGPT 2782
Db 2515 KEISIKLKQONQOL-----IKQKNELLSNNQHLSNEKTKERTKREAHKQYT 2562
Qy 2783 PRSEMPSLHSGPKSESSTKRVVSPNSEIYQSLVSPGKTCMHKHLSSKVLGHLK 2842
Db 2563 CE-----NSPK-----SPKVTGT-----ASKK 2579
Qy 2843 RALSPNREMPQHVYLSPGKGLHKLTESTLFDNLSPCKQKQVQENL--NSPKGLRD 2900
Db 2580 KQITP-----SCKERNLQDPPVKSPKSCFPD 2607
Qy 2901 VAKSMMPY-CBQCFDPSKGLDPSFELNLTESNDKSAENWYBAKETIPECKT 2953
Db 2608 SRSKSLPSHPVRYFQNSLSGLCPVQONAGAESVDSQPGPMHASSGKDVECKT 2661

RESULT 2
US-08-353-700-1
; Sequence 1, Application US/08353700
; Patent No. 5599919
; GENERAL INFORMATION:
; APPLICANT: YEN, TIMOTHY J.
; APPLICANT: RATTNER, JEROME B.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING A
; TITLE OF INVENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN,
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DANN, DOREMAN, HERRELL AND SKILLMAN
; STREET: 1601 MARKET STREET, SUITE 720
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,700
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: REED, JANET E.
; REGISTRATION NUMBER: 36,252

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3248 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HUMAN
; US-08-353-700-1

Query Match 7.8%; Score 1148.5; DB 1; Length 3248;
Best Local Similarity 20.5%; Pred. No. 3,3e+48;
Matches 716; Conservative 605; Mismatches 1159; Indels 1019; Gaps 139;

Qy 81 FAYGQTSSGKTYTMMGTSPSLGIITPOALQEVKTIQEIPIRREFLRVSYMEIYNETYKDL 140
Db 99 FOEGOLNSGK-----KQIEKLEQELRCKSELERSQQAASADVSUN 140
Qy 141 LCDDRK---KPLEIREDFENRVVYADLTPEELVMVPEHYIOWIKGGEKARHYGETKMDH 197
Db 141 PCNTPOKFTTLPITTSQYISGSKY-EDLKEKYNKEVE-----ERKRLAEVYALQA 190
Qy 198 SSRSHITFMIVESRD--RNDPTNSE-NCDCGVWVSHNLVLDLAGESRASQTAGCVRLK 254
Db 191 KKAQOTLPQATNMHNDIAHQASSVFSWQEKTSHTLS-----SNSQRT----- 235
Qy 255 EGCNINRSLFIIQYIKLSDQAGFIYRDSKLT-----RILNLSLGMNAKTVICTI 309
Db 236 -----PIRDPFSASYFSGELEVTPSRSTLQIGKDANSSFFGNSS----- 275
Qy 310 TPVSFPELTSLQFASHTAKVNRTPHVNEVLDDALLKRYKEIEDLKQLENLESSSET 369
Db 276 SPHLID-----QLKAQOELNN--KINEL--ELRQSHKE--MKQVVKFQ----- 316
Qy 370 KAQMAKEHTQLAEIKQLHKEREDRIWHLTNIVVASSQESQODQVRK-----KR 421
Db 317 ELQOLEKAKVELLEIEKEVLNKCDELVRTTAQYQASATKYVALQKLLKLTEDLSCQHQ 376
Qy 422 RVTMAPKTIQNSLHASGVSDPMLSRLPGNF-----SKAKKS-DMPSPPEIDDSVC 472
Db 377 NAEARSCLSEQKIKEXEKEFOBELSRQORSFOTLDOECIQMKARLTOELQCAKMMHNVQ 436
Qy 473 TEFSDFDALSMWDNGIDAEWNL-----ASVTHREKTSLSHQMIDFQJISDSVOFHS 527
Db 437 AELDKLTSVKQOLENNLEFFKQLCRAEOAFASQIKENELRSHBEMKKNLKSHE 496
Qy 528 SKENOLOYLPKDSGMABEGRKASFEKEITSLQOOLQSKKEEKELVQSFELKIALEBOL 587
Db 497 QKAREVCHLEALKNIKQCLNOS-----QNFABEKAKAKTSGETMLRDLQEKINQOENL 551
Qy 588 SYKAKLEKVTNSRSHSINAEOVTQVDEKVEVRKENSVLDSGYNANSNDLQSSVDGKRL 647
Db 552 TLEKLKLVAA-----DLEKQDSCODLLKKR-----EHHIEQLNDLSTKTESKAL 598
Qy 648 SSHHDECIENRKMLOKIVDLEEFLENLKK-----SENDK---QKSSBEDPFMS-----IQ 696
Db 599 USA-----LELKKEVEYELKEEKTLSFCMSSENEKLLTQMBSEKENLQSKINHLE 648
Qy 697 LC-----EAIMAKANALELALMBDNFNILLENETTLKREIADLERS-- 739
Db 649 TCLKTQOQIKSHENYRNVATLEMDRENLSVEINLNLVDSKSVLEVETQKLAYMELOQKAE 708
Qy 740 -----LKENQETNEFEIILEKETQKHEADLIHIEIGSLKKLVENAEWYNQVL 785
Db 709 FSDQKHQKEIENMCKLTQSLTQGVDDL-----EHKLQLLS-----NEIMDXDRCY-QDL 756
Qy 786 EEDLETCKRLKLEGEIQL-----AELKK 808

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Db 757 HAEYESLRDLKSDASLVTHNEHORSILAFDOOPAMHSPANIGGOSMPSEBSRCRL 816
 QY 809 RADN-----LOKVENFDLSVM-----GDSEKLCCEIFOLKOSLSDAVTRDQKE 856
 Db 817 EAOQSPKNSAILONRVDSLEFSLESQOMNSDLOKOCBELVOLKGELE--ENLMKAQOM 874
 QY 857 CSPLRSNLELKEKEMEDTSNWN-----QEKASLFEKOLETEKSNYKME-- 903
 Db 875 QSFVAETSORISLQOEDTSAHONVAETLSALENKEKELQDLNDKVTBQAEIOELKSN 934
 QY 904 ---ADLOKELO-----SAPFNINVLNGL-----AGKVPBDL 933
 Db 935 HLEEDSLKEJOLSETLSLEKENSIIISLNKREIEBELTQENGTLKAINASINOEKNLI 994
 QY 934 SRV-----ELEKKVSEFSKOLE-----KALEKNA-- 958
 Db 995 QKSESFANYIDEREKSISELSDQYKQKILLQRCSETGNAYEDLSQYKQAQEKISKLE 1054
 QY 959 -LENEVTCLSEYKFLPNEVECLKNQISKASEETWL-LKQEGHSASTISKQIIMO-- 1012
 Db 1055 CLINECTSLCENR--KNLELOLKEAFKHEQOEFITKLAFKAEERNQIMLELTVOQALRS 1112
 QY 1013 -----EOSE-----OILQDLDEVTHOSKV-----QOTEOYLEMKKMD--DLFEK 1052
 Db 1113 EMTDNQONSSEKAGLKOETIMTLKEBONKMOKEVNDLLOENBQIMKMKTKHCQNLSE 1172
 QY 1053 YIRNKSEADLLREMENTLKQTM-----SVEVKIADTKHELEETRDKE 1096
 Db 1173 PIRNSVAKERSEHNOQCFQMDLEVKEISLDSYNAQVQLEAMLNKELKLOESKEKE 1232
 QY 1097 QLLHEKFFQOMOTIFPTPLSDSLPPSKLVGNSODPLEINDY-----HNL 1144
 Db 1233 CLQHE-----LOTI-----RGDLTSLNOMQSOEISGLKDCIDEKYSISGPHLE 1279
 QY 1145 IALATERNNIMVCLETERNSLKEQVIDLNTQLOSLQASIE-----KSDQKQKODL 1196
 Db 1280 STSQONNAHOCLOTTANKLE-----LEKICEILOKELVTELEBDSRSECTITATRK 1335
 QY 1197 EBEVKLLLEMLLKG-----HLLD 1216
 Db 1336 ABEVGLKLENEVKILNDGSLHGELEVDPICGEGFGQPNQHPVSLAPLDESNSYHLN- 1394
 QY 1217 SQUSIEKLOLENLEVETKQTOLOBEMKNTIENNELOTPNEDLKAHDSLKODLSNINQ 1276
 Db 1395 --LSDREVQNHFAELOEKELSLQSEHKILHDQHCQMSKMSSELQTYVDSLK--ABNLVL 1449
 QY 1277 SIETODELRAAOBELREOKQVDSFRQOOLDCSVGISPNHDAVANOQKVSIGEVNLSQS 1336
 Db 1450 S-----TNLNFQODLVKQOL--GLEBGLVPSLSSQVDPSSLS-----SLGD--SSFYR 1497
 QY 1337 EMURGERDELQTSKALVSELE-----LIRAHVKSVEGENTETTKLNG 1380
 Db 1498 ALLE-----QTDGMDLNLNLEGAVGANOCVDEVEFCSSIQTYVDSLKAENLVLSTNLN 1551
 QY 1381 LEKEILKGE-----ESVFKSMLENLEKEDNNK--EQAESY-- 1417
 Db 1552 PGQDLVKEMQGLIEBGLVPSLSSQVDPSSLSLSDSSFYRALLEQTDMSLNLNLEGV 1611
 QY 1418 SKENQFSLEEVF-----SGSQKLVDEI--EVLKQOLKAAEERLE-- 1454
 Db 1612 VANQOSVDEVFCSLSQEBNLTRKETPSPAKGVESLESCLCVYRQSLKEBKESQOI 1671
 QY 1455 IKORDYFELVOTANTNLV--GKLETPLOQDHE--EDSIDRSEMEIKVYLGELERNQYL 1511
 Db 1672 MNKKEIOEIOELSSEROELDCIRKOYLSBENQOQKTSVTLMEESKLAQKQEQS 1731
 QY 1512 LE-----RIOEKLEISNKLIEIOKEMETSVLLKDXLOQLLESLSLNNITLKENIDTTLKH 1567
 Db 1732 LELVAKLOLOGIDUSSR-----SLGIDIEDAIOG-----RNSCDSIKSH 1773
 QY 1568 HSDTOAQOLK-----TOOELOL-----AKNIAIASDNCPTQEKET----- 1604

Db 1774 TSETTERPKHDVHOICDHOAQODLNLDEKITTETGAVKPTGECGSGQSPDNTYBPPGD 1833
 QY 1605 ----SADCVHPL-----DEKILLTEELHOKTNEOEKLLHEKNELEQAO 1644
 Db 1834 KYOGSSECSISELSPSPNALVPMDFIGNQEDHNLQKRVKETSNEMLRLHLYIEDR- 1891
 QY 1645 VELKCEVHLKMSMIESKSSLESLOHEKHDTEQOLLA-----LKQOMVVOEKKELQ 1697
 Db 1892 ----KVESILNEMKEDSKL-----HLOEVQWMTKIEACILEKIVIGELKENSIDS 1939
 QY 1698 QTHHEHTLAVDHLKENIEL--GLNFKNEAO--OKTKEOCLLNK-----ELEOS 1744
 Db 1940 EKLEYFSCDHOELQVETSEGLNSDLEMHADKSSREDIGDVAKNSWKRFLDVERE 1999
 QY 1745 QHRLQCE-----LELMKSLKDKESALETIKESPOKYI--NILQMEMVWLMEMEL 1793
 Db 2000 LBRISSEKASIHENALYLEADLEVQVTEKLCLEKNENQOKYIVCLBEBLSVYTERNDL 2059
 QY 1794 KNSQRTVIAER--DQLODDRESVEMSIET-----QDDLKQAQALQOQKDK 1838
 Db 2060 RGEIDTMSKKTALDQISEKMEKETO--ELESQSECLHCIOVAFAVEKTELLQTLSSD 2118
 QY 1839 VOELTSQISVLOEKISLENQMLYNVAITYKETLSERDLNOSKQHLFSEITFLSLKEX 1898
 Db 2119 VESLLKDKTHLOEKQSLKOSQALSITKCELENGIOALNKEKELLVXESLSQARLS 2178
 QY 1899 EF-----ALEQAEKDYADARKTIDITEKISN-----EQOLLOQATVL 1937
 Db 2179 DYKLNVSALBAALVGEFALRLSTQOEBVHOJRGIEKLRVNIADDEKQOLIAEVL 2238
 QY 1938 KETLYRESLQCKQOLANTHEHRETLKSKDIALGKNEQOERDEANRYALITKMSLIE 1997
 Db 2239 KERERENDSL--KQVENLERELOMSEBENELVI--LDAENSKA-----EVELTK 2284
 QY 1998 EOINENVTTLKEGE-----GEKETFYLOPSPKQSSQOMELRESUKTQOLOJEPKEX 2050
 Db 2285 TOIEMASSLKIFELDVTLSSEKENTLQIOEKQGOSELDKLSSTFSJLIEEKEOAI 2344
 QY 2051 EISEAT-----NEIKNLTAKISSL--EBEILLO--NASLINEAVSERENLRHSKOQVVS 2099
 Db 2345 QIKESKTAVENTLOQLKEINBAVALGQDEIMKATQSDLPRIEEOHQRNSTEKLRA 2404
 QY 2100 ELB-----QLSITLSRDBHAFQSKREKQDEAVNKIASLAEIKITLTKMD--EFRQSK 2150
 Db 2405 RLEADEKKOCLVLOOLK-----ESEHNDLKGVRVENLERELIARTQOENAALEAENS 2459
 QY 2151 ---ESLOESSHLSEBELCTYKTELQMLKOQKEDINNKLAEKVKEVDELLQHLSSLKQED 2207
 Db 2460 GEVETLXAKIGEMTOSLGLBIDVYTTISEKENLTNLELOKQOERSEL----- 2507
 QY 2208 QIOMELRNEKRLNVELCEKMDIMEKEISVLRIMONEPOQOEDDVAERMDILESNOEIOE 2267
 Db 2508 ----EINSSPEN-----ILOKEQEKVOMKEKSTAMEMLOT--QJKE 2545
 QY 2268 LMEKISAYVSQHTLS--SLSSLEQKETEBAHGMANTIESLSSTISRFGSIQTHV 2324
 Db 2546 LNERVAAHLNHOEAKQAEONLSSQVE-----CL-----ELEKAOLOGLDEAKNYI 2593
 QY 2325 KLNTQLOTLNKKFKVYRYTAVKEHDSILIKDYEKOLAAEQKRDHRLQLOCLFQHGKRW 2384
 Db 2594 VLOQSVKVLIO-----VEGOKKLEKKEDEIRIKNQIODOQOVLVSKL 2637
 QY 2385 SDSASEELKF--CELEFLELLFKKANITIQSVODSEVQVFLNOVQSTLQEBLE--HK 2439
 Db 2638 SQVBEHOLWMEKONLELNLTVLELOKIQOVLQSNKASLODTLVLOQSSYKNLENELETLK 2697
 QY 2440 KGFQOMLEEFQ-----DLHVDKAK--LSEGOQONRRIIASITOLITLTKRIVV 2485
 Db 2698 MDKQSFVAKVNMKTAKETELOREHNEVMAQKAEILOEBISGKNRLAGELQILLETIS-- 2755
 QY 2446 QSKIOREITVYINQFEALQEKKEQONKELMRMEHGHGSPASVMEENARLLGITLTVODE 2545
 Db 2756 -SKQO-----LKELTLENSBLK--SLDCMKKQDYKEXG--KYREE 2791

QY 857 CSEFLRENIEMKEMDTSNWY-----QKEREASLFKOLETEKSNYKME----- 903
 DB 875 QSFVAETSPRISKLQEDTSAHQNVAVETSALENKEKEJQLLNDKXVETQOAEIJOELKKN 934
 QY 904 ---ADJOKLQO-----SAPNEINYLGL-----AGVRPDL 933
 DB 935 HLEBDELKQLLSETLSLEKEMSSISLANKREIHELQENOTLKEINASLNQEKNNLI 994
 QY 934 SRV-----ELEKVSEFSKOLE-----KALEKKA--- 958
 DB 995 QKSESFANYIDEREKISELSDQYKQEKILLQRCETGNAVEDLSQKYAAQEKNSKLE 1054
 QY 959 -LENETJSEYKFLNEVECKLNQKSKASEIML-LKQEGHSAISIKQELIMQ----- 1012
 DB 1055 CLINECTSLCENR--KNLEBQLKEAPAKEHQBFLTKLAPABERNQMLLELTVQOALRS 1112
 QY 1013 -----EQSE-----QILOLTDVTHQSKV-----QOTEBOYLEMKMHMD--DLFEK 1052
 DB 1113 EMTDNQNNKSEAGGLKQEIIMTLKEQONKQKEVNDLLOENBOLMKVMKTKHECQULESE 1172
 QY 1053 YIRNKSADLLREMEMLKGTME-----SVEKYIADTYHELEETTRDXE 1096
 DB 1173 PIRNSYKERESERNQCNFKPQMDLEVKEISLDSYNQOLVOLBAMLNKLEKLOESEKEKE 1232
 QY 1097 QLLHEKVFQAMQTFPITPLSDSLPRSLVGNQODPFIENDY-----HNL 1144
 DB 1233 CLQHE-----LOTI-----RGDLTSLNLOMOQOESIGLQCEIADBEKXISGPHEL 1279
 QY 1145 IALATERNNIMVCLETERNSLKEQVIDLNTQLOSLQASIE-----KSDLQKRPDL 1196
 DB 1280 STSQNDNALQCSLOLTNNKLN-----LEKICEILOAKEVELTELNDSSBCTITRCK 1335
 QY 1197 EGEVLLLEMLLKG-----HLLD 1216
 DB 1336 AEEVGLNLEVKILINDSGLLHGLVEDIPGEGFQEPNQBHPVSLAPLDESNSYEHLLT- 1394
 QY 1217 SOLSTIKLOLENLEVEKLOTOLOEMKNITIERNELOTNPEDLKAHDSIKOLSNINQ 1276
 DB 1395 --LSDVEQMHPAELOEKFLSTLOSEHKILHDQHCSSKWSSELQTYVDSLK--AENLV 1449
 QY 1277 SIETODELRAAOELREKQOLVDSFRQOLDCSVGSSPNHDAVANQEKVSLGEVNSLOS 1336
 DB 1450 S-----TNLANFGQDLYKEMOL--GLEBGLVPSLSSSCVPDSSLS-----SLGD-SSFR 1497
 QY 1337 EMIRGERDELQTSKALVSELE-----LIRAHVKSVEGENEITRYKNG 1380
 DB 1498 ALLE-----QTDGMSLLSVLGAVGSANQCSVDEFCSSLOQTYVDSLKAENLVSTNLN 1551
 QY 1381 LEKEILIGKE--ESEVLKSMLENLKNEDNNKL-----FOABEYS----- 1417
 DB 1552 FGGDILKEMQOLGLEBGLVPSLSSSCVPDSSLSLGDSSFYRALLQOTGMSLLSVNLEGV 1611
 QY 1418 SKENQPSLEBEV-----SGSOKLVDEI--EVLKQOLKAAEBRL----- 1454
 DB 1612 VASANQCSVBEVFCSSIOEBNLTTRKETPSAPAKVEBELSLCEVYRPSLEKLEKMSOGI 1671
 QY 1455 IKRDYFELVOTANTNLVE--GKLETPLOADHE--EDSIDRSEMEITKVLGEKLEBNQYL 1511
 DB 1672 MNKKEIOTLEQLLSSBROELDCRQOYLSENEQMOQKLTSTVLEMSKLAAEKKQTEQLS 1731
 QY 1512 LE-----RIQBEKLELNKLEILOKEMETSVLLKDDILOKLESLSENIIKENIDITLLGH 1567
 DB 1732 LLEVARLOLOGLDLSR-----SLIGIDIEDALQO-----RNESCDISKEH 1773
 QY 1568 HSDTQOLQK-----TOEOLO-----AKNLAIASDNCPTIOKET----- 1604
 DB 1774 TSETTRTRTKRHYHOICDKDAQODLNDIEKITEGAVKPTGCSGQSDTYIYEPGED 1833
 QY 1605 ---SADCVHPL-----BEKILLTLEELHQKTNOBKULHEKNELEQAO 1644
 DB 1834 KTOGSSECTISELSFSGPNALVPMDFLQNGEDHNLOLRVAKETSNENMLRLHLHVEDR-- 1891

QY 1645 VELKCEVEHLMKSMIESKSSLESLOHEKHDTQOLLA-----LKQOMQVTOEKELQ 1697
 DB 1892 -----KVESLIANMEHEDLSKL-----HLOEVOLMTKIEACIELEKIVGELKKNSSDS 1939
 QY 1698 QTHEHLTAEBVDHLKENIEL--GLNFKNBAQ--OKTTEQOLLNENK-----ELEOS 1744
 DB 1940 EKLEYFSCDHQELLQVETSEGLNSDLMEHAKSSREDIGDVAKVNDMSKERFLDVENE 1999
 QY 1745 QHRLOCE-----IEELMSKLDKESALETLKESOKYI--NINQMEMVMMEMEL 1793
 DB 2000 LSRIRSEKASIEHEALYLEADLEVVOOTEKLCLEKONENQKVIICLEBELSVATSERNOL 2059
 QY 1794 KNSORTVIAER--DOLODLRESEVMSIET-----ODDLRAQOBALQOQKX 1838
 DB 2060 RQELDTMSKKTALLOLSKMEKEKQ--ELBSHQSECHQIOYABAWEKTELLQTLSSD 2118
 QY 1839 VOELTQSISVLQEKISLEENOMLYNVAIVKETLSERDDLNQSKHLSFSEITLSLKEK 1898
 DB 2119 VESLLKDKTHLOEKLOSLKESQALSTFKCELENQIAQLNKEKELLVKESSESLQARLSHS 2178
 QY 1899 EF-----ALQAEKQKADAKRTIIDITEKISNI-----EEOLOQOANTL 1937
 DB 2179 DYKLNVSXALBAALVEKEGFEALRLSSTQEBVHQURGIEKLRVRIEADKKQLHAETKL 2238
 QY 1938 KETLYERESLQCKEOLALNTEHLRETLKSKDLALGKMEQERDEANKVIALTEKMSLE 1997
 DB 2233 KERERENDSL--KDKVNLRELOMSENOGLVI--LDAENSKA-----EVETLK 2284
 QY 1998 EOINENVTTLKEGE-----GEKETFYLRPSQOSSQSSOMEBLEBSLTKDLOLEBAK 2050
 DB 2285 TQIEEWARSUKTIFELDLVTLRSEKENLTQIOEKQOQSELDTKLSSFKSLLEKQOAEI 2344
 QY 2051 EISEAT-----NEIKULTAKISL--EELILO--NASILNEAVSERNLHNSQOLVS 2099
 DB 2345 QIKESKTAWEMLQOLKEINBAVALCGDQIMKATEQSLDPPIEEHQLNRSLEKLA 2404
 QY 2100 ELE-----QSLTLKSRDHPAQSKREKDEAVNKIASLAEIKILTKEMD-----EPRDSK 2150
 DB 2405 RLEADEKQOLCVLOQK-----ESEHHDILKGRVENLERELIARTNOHEHALEENSK 2459
 QY 2151 ---ESLOEQSSHSEELCTYKTELQLOKQEKEDINNKLAEKVYDELLQHLSSLKEQLD 2207
 DB 2460 GEVETLIKAKIEGWTQSLRGLFEDVVTIRSEKENLTNLELOKEORISEL----- 2507
 QY 2208 QIQMBLREKLANVELCEMDIMEKEISVLRQMBQEPQOEBDVARMIDLESRQEOIE 2267
 DB 2508 ---EINSSPEN-----ILOKEQEKVQMKKSSSTAMEMLOT--QLKE 2545
 QY 2268 LMEKISAVYSPQHTLLS--SLSELOKETEAMHKCMINIKESLSSTLSRSFGSLQTEHAV 2324
 DB 2546 LNERVAALHNDQBACKAKQONISSQVE-----CL-----ELEKQOLLQIDEAKNNYI 2593
 QY 2325 KLNTOLOTLINKFKVYVTAAVKEDHSLIKDYEKDLAABOKRHDRLQLOCLQEGGRM 2384
 DB 2594 VLOQSVKGLQO-----VEDQKOLKEKDEEISRLKNGIQOQEOQLVSKL 2637
 QY 2385 SPSASBELKF--GEIFLNLPRKANNIIGSVODDPSEVQVFLNQVSTIOEBLE--HK 2439
 DB 2638 SQVEGHQOMKQONDELNLVLELOKIQVDSKNASLODTLEVLQSSYKNLENELETK 2697
 QY 2440 KGFQWOLBEFG-----DLHVDARK--LSEGMQOENRRIASTQLTLTKRLKAVV 2485
 DB 2698 MDMKSFVEKVNMTAKETELQREHMEHMQKTALELOELSSEGNRLLAGELQLLBEIKS-- 2755
 QY 2486 QSKIOREITVYLNQFEAKLOEKKEQONKELMRMEHHGPSASVMEENARLLGIKTVQDE 2545
 DB 2756 -SKDQ-----LKEITLSENLK-----SLDCMHKQOVEKEG--KVREB 2791
 QY 2546 SKKLOSRITMLENELNLVVDQDMHNGEK--VALLODKLLSRABAEALNMQVLTQKQON 2603
 DB 2792 IAEYOLR-----LHEAEKQOALLD--TNKOYEVEIQTAREKLTLSKEBC 2834
 QY 2604 LQAAKKEIENLOKVAKGAVPYKEEIDN-----LKTGVVATIMEKIKY-----SK 2648

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      2835 LSSQKLEIDLKSS-----KEELNNSLKATTOLEELKKTQMDNLKYVNOQKKENER 2886
Qy 2649 AFDQETAYKSC--LEDKEEGLRLKEELRRADNDTVVCYPKDYQKASTPVTGCGGS 2706
Db 2887 AOGKKKLLTKSCQKLEEEKEIILQKELSQLQAQEKOKT-----2924
Qy 2707 GIVQGTAMLVLOSE-----KALE---RELSHYKKKYVHLSRTMSSSEDRKKTAKSDAHS 2759
Db 2923 GIVMDTKVDELITTEIKELKTEBEKTEADEYLDKCSL--LISHKELEKAKEMLETGV 2981
Qy 2760 SHTGSSH-----RGSPHKTETRYHGPVTPERSEMPSL-----HLGSPKSSSS---2802
Db 2992 AHLCSQSQSKQDSRGP-----LLGPVYHGPSPIPSVTEKRLSSQGNKASGRQSSSGIM 3035
Qy 2803 -TKRVSPNRSIY--QVMS-----PDKTGM 2827
Db 3036 ENGRGPTPATPESFSSKSKKAVMSGIHPAEDTEGTEFEPEGLPEVYKKGADIPGKXISP 3095
Qy 2828 H-----KHILSPKVGHL-----KKRALSPNSEMTQHVISPCKTG 2864
Db 3096 YILRRTTARTSPRLAOKLALSPLSLGENLAESSKPTAGSGSRQKVKVAQRSFVDSG 3155
Qy 2865 --LHKNTLSTLFDNLSPCKQKQVQENINSPPGKLF-----DYKSR-----2904
Db 3156 TILREPTTKSVVNNLPERSPTDSPREGLRVKGRLVPAPKLDMSQLAVRTVRSSBALCV 3215
Qy 2905 SMPYCPSPFPDPSKLGDFS 2923
Db 3216 SDPMEVQSLIDRLCLQDFS 3234

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RESULT 4

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US-08-328-254-6
; Sequence 6, Application US/08328254
; Patent No. 5710022
; GENERAL INFORMATION:
; APPLICANT: Zhu, Xueliang
; APPLICANT: Lee, Wen-Hwa
; TITLE OF INVENTION: A No. 5710022e1 Nuclear Mitotic Phosphoprotein
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,254
; FILING DATE: 24-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/141,239
; FILING DATE: 22-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-CJ 1191
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-8949
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2482 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-08-328-254-6

Query Match 7.1%; Score 1055.5; DB 1; Length 2482;
 Best Local Similarity 21.8%; Pred. No. 8.7e-44;
 Matches 615; Conservative 482; Mismatches 937; Indels 781; Gaps 115;

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Qy 545 ECRKASFKEITSLQOOL---QSKEEKKELVQSFEIYAELEQOLSVAKNLEWNTSR 601
Db 2 ESEKENLQSKINHLETLCKLTQOIKSHENYNERRTLEMD---REMLSVIRLHNVLDQSK 57
Qy 602 EHSINAEVQTDVEKEVREKMSVLGDG--NANSNDLQDSSVDGKRSSSHDECIEHR- 658
Db 58 --SVETQKLAAMELOOK--AEFSDQKQKEIEEMCKLTSQLTQO-----VEDLEHKL 107
Qy 659 KMLEQKIYDLBEFINLKKSEN--DKQSSQDPMESIQLCEALMAEKANLEELALMR 716
Db 108 QLSNEINDKDCYDOLAEYVESLRLDKSKASLVTEHDQRSLL---AFDQAPAH 162
Qy 717 DNFNIIIE-----NETLKREIADLERSLKENQETNEPEILEKE 755
Db 163 HSFANIIIGQSGMPSEBSECRLEADQSPKNSAILQNRVDSLEFSLQSKQNM-----SD 216
Qy 756 TQKEHEAQLIHEIGSLKTLVENAEMYNQNLBEDELTQTKLKEQEIQLAEIKRADN--- 812
Db 217 LQKQCE-ELVQIKGEIIEMLAKAEQMOSFV--AETSORISIKLQEDTSAHQVVAETLSA 273
Qy 813 LQKVRNPDLSVMSDSEKLECEIFOLQKSLSDAVALTRDAQKESFLRENTLEKEME 872
Db 274 LENKEKEQLQNDKQETEO--AEIQELKRS---NHLEDSLEKELQL--SEFLSLEKEM 326
Qy 873 DTSNMYNOKERKASLFEKQLETEKSNYKMEADLOKE---LQSAFNEINYNGLLACKV 928
Db 327 SSTISLNKRE-----IEELQENGTLKEINASLQKEMNLQKESFPANYID----- 373
Qy 929 PDDLRSVLEKKEVSEFSKOLE-----KALEEKNA---LE 960
Db 374 -----EREKISISLSDQYKQEKILLQRCETGNAYEDLSQYKAAQENSKLECLL 425
Qy 961 NEVTLSEYKFLPNVECLKNOISKASEIML-LKQEGHSIISKQEIIMQ-----1012
Db 426 NECTSLCENR--KQLEQOLKEAFKQHEFPLKLAFAERNQNLMLLETYQOALRSEMT 483
Qy 1013 -----EQQE-----QIQLTDEVTHTOSKV---QOTEBOYLEKKKMHND--DLFEKYIR 1055
Db 484 DNQNNKSEBAGGLKQELMTLKEQNKQKQEVNDLQENBOLMKVKKTKHQCNNLSSEPR 543
Qy 1056 NKSEAEDDLREMEMNLKQTE-----SVEVKIADTKHELEETIRDKQQL 1099
Db 544 NSVKERESEBRNQCNKFPQMDLEVKETSLDSYNAQLVQLEAMLRNKLKQSEKEKECQ 603
Qy 1100 HEKKYFFQAMQTIPTPLSDSLPPSKLVEGNSQPIEINDY-----HNLIATL 1147
Db 604 HE-----LQTI-----RGDLSTSNLQDMQSQISGKCEIDAEEKYISGPHLETS 650
Qy 1148 ATERNNINWCLJETENSLKEQYIDLNTQLOSLQAQSI-----KSDLOKPKDLEEG 1199
Db 651 QNDNAHLQCSLQTTNKLNE---LEKICEILOAKETLVLTBLNDSRSECTATRKMAEE 706
Qy 1200 EVKLLLEMLLKG-----HULTDSQL 1219
Db 707 VGLKLINEVKILNDSGLHGLGELVEDIPGGEFGQGNQEQHPVSLAPLDSNSYEHILT--L 763
Qy 1220 STEKQLENLEYTEKLTQLQEBMKNTITERNELQTNFEDLKAENHSLKQDSENIEQSI 1279
Db 764 SDKEVQMFABELOEFELSLQSEHKLHQQHCMSQKMSKSELQTVYVSLK--AENLVLS-- 818
Qy 1280 TQDELRANQEBLREKQQLVDSFRQQLDQSVGISPNHDAVANGKSVSLGEVNSLOSEML 1339
Db 819 --TNLRNFQGDVVKMOL--GLEBGLVPSLSSSCVPDSSSLS-----SLGD--SFPYRAL 868
Qy 1340 RGERDELQTSKALVSELE-LLRANVKSVEGENLEITRKGLNGLEKELIGKSEES----- 1392
Db 869 E-----QTGDMSSLISNNEGAVSANQCSVD---EVF--CSSLQENLTKRKTPEAPAKG 916

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QY 1393 -EVLSMLENKEDNNKLEQAEVYSSKENQFSLSEVFGSQKLVDEIYVLAQOLKAAE 1451
DB 917 VEELSELCVYRQSLSEKKEKMEGIMGNK-----EIOELFOLSSERQ 961
QY 1451 REIENDROFVQVANTVAVGKLETPLOADHEEDSIDRSEEMEIKVLEKERNQYL 1511
DB 962 EIDCIRKQYLS-----ENEOOQKLTSVLWESKLAEEKQTEQLS 1003
QY 1512 LE---RLOEKELESNKLEILOKEMETSVLLKDLOQKLESLSENILKENIDTLYKH 1567
DB 1004 LELEVARLOQLDLSR-----SLIGITDEAIOG-----RNESCDISKEH 1045
QY 1568 HSDTQAOLOK-----TQOETLOL-----AKNLAIAASDNCPIQTEKET----- 1604
DB 1046 TSETTERTPKIDVHOICDKDAQODLINDIEKITERGALKPTGEGSGEQSPDTNVEPPGD 1105
QY 1605 ---SADCVHPL-----EKKILLTEHLHOKTVEQEKLEHKEKLEHOAQ 1644
DB 1106 KTOGSSSECISELSPGPNALVPMDFLGNQEDIHNLQVRKETSNNENRLLHVTEDRDR-- 1163
QY 1645 VELKEVEHLMKSMIESKSSLESLOHEKHDTQOOLLA-----LKOOMQVVTQEKKELO 1697
DB 1164 ---KVESILNEMKELDSKL-----HIOEVQMLTKIENCICILEKIVGELKKEGSDLS 1211
QY 1698 QTHEHLVAEVDHLKENIEL--GLNPKVBAQ--QKTTKEQCLINENK-----ELEOS 1744
DB 1212 EKLEFSCDHOELLQVRVETSEGLNSDLEMAHDKSSREDIGDNVAKVNDSWKERFLDVENE 1271
QY 1745 QHRLOCE-----IEELMKSLDKRESALETETKESEQKYI--NINOEWEMVLMEL 1793
DB 1272 LSRIRSEKASIEHBALYLEADLEVVOETKECLEKDNENKOKVYLCLEELSVTSEBNQ 1331
QY 1794 KNSGRVIAER--DOLODDRESVENSIF-----QDDLRKAQOALQOQKDX 1838
DB 1332 RGEIDTMSKKTALDQSEKKEKTO--ELSHOSECLHCIOVAEAEVKEKTELLQTLSSD 1390
QY 1839 VOELTQISVLOEKISLLENQMLYNVATVETLSEBDNOSQHLFSELETLSLKLK 1898
DB 1391 VSELLKOKTHLOKLOLEKDSQALSTKCELENOQAOLNKEKELLVKESESLQARLSHS 1450
QY 1899 EF-----ALBOEKOKADARKTIDITEKISNI-----EEOULLQOATUL 1937
DB 1451 DYKTLNYSKALEALVKEGFALRLSSTOBEVHQLRGIEKLRVIREADEKQOHLAEUL 1510
QY 1938 KETLYERESLIOCKEOLANTEHLRETLKSKDIALGMEQERDEANNTALTEKMSIE 1997
DB 1511 KEBERENDSL--KDKVENLERELQWSENOELVTL--LDAENSKA-----EVEETIK 1556
QY 1998 EOINENVTTLKEGE-----GEKETFYIQRPSKQOSSQMEELRESLTKDLOLEBAEK 2050
DB 1557 TOIEEMARSLKVELDLVTLRSEKENLTKQIOEKQOQSELDKLSSPFLSEBKEQOHEI 1616
QY 2051 EISEBAT-----NEIKULAKISL--EETILO--NASLINEAVSERENLHSHQOVLVS 2099
DB 1617 QIKESKIAVEMLOQOLKEINAVVALCGDOEIMKATEOSLPPIEBEHOJLNSIEKLA 1676
QY 2100 ELE---OLSTLSKRDAFAOSKREKDEAVNKIASLAEBIKILTKEMD---EPRSK 2150
DB 1677 RLEADEBKQOLCVLOQK-----ESEHHDLLKGRVENLERELIKARTOEHAAEAENSK 1731
QY 2151 ---ESLOBOSSHLSSELCTYKTELQMLQOKEDINNKLAEKVXEDVLLLOHLSLKEOLD 2207
DB 1732 GEVETLKAKIEGMOLOSRLGELDVVTIRSEKENLTNELQKEGRISL----- 1779
QY 2208 QIOMELRNEKLYNELCEKMDIMEKISVLRIMQNEPOQEBDVAERNDIIESRNOEIOE 2267
DB 1780 ---EINSSPEN-----ILOKEQEKVOMEKESSTAMEMQOT---OLKE 1817
QY 2268 LMEKISAVYSEQHTLLSSLESELOKETEBAKHCMINIKESISTLSRSFGSLQTEHYKLN 2327
DB 1818 LNERVALAHNDQ-----BACK-----AEQUNLSSQVECLEHEKXQOLL 1854

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QY 2328 TOLOTLINKKVVYRTPAAVEDHSLIKDYEKDLAAQKHDE---LRLOQCLSECHGRKN 2384
DB 1855 QGLDEKANNVYILOSSV-----NGLIOVEDGKOKLEKEDISRLKNGIDQOQOLVSL 1909
QY 2385 SDASASELKF-----CIEFLENLLPKKANIISOVDPEVQVFLNOSTLOEILE-HK 2439
DB 1910 SOVEGEHOLMKEONLELRNUTYELBEOKIOVLOSKRASLODTELEVLOSSYKNNLELTK 1969
QY 2440 KGFMOULEERG-----DLHVDACK---LSEGOENRRIASTIQLTKRILKAV 2485
DB 1970 MDKMSFEVKYNNKTAKETELQREHMEHMAQTALEQEBELSGEKRLAGELQILLEIKS-- 2027
QY 2486 OSKIOREIVYINQPEAKIOEKKQNKELMRMHHGSGASVMEENARLLGILTKVODE 2545
DB 2028 -SKDO-----LKEITLNSSELK-----SLDCMHKDOVEKEG---KVARE 2063
QY 2546 SKKLOSRIMLENEILNVKDDAMHGEK--VALLODKLLSRNAEALNAMOYKLTCKDN 2603
DB 2064 IAEYOLR-----LHEAEKKHQALLLD--TNQOYEVEIOTYERKLSKEC 2106
QY 2604 LOAMKEIENLOKMAKAVPYKEIDN-----LTKRVVKIEMEKIKY-----SK 2648
DB 2107 LSSOKLEIDLLKS-----KEELNNSLKTATQILBELKTKYMDNLKYVNLKENER 2158
QY 2649 ATDOEIAVLKSC--LEDKEEGLRLKELRARAQDNDTTCVCPDYQKASTFPVTCGGGS 2706
DB 2159 AQGRKMLIKSGKOLEKEKELLOKLSOLOQAOEKOT----- 2196
QY 2707 GIVOSTAMLVLOSE---KAALF--RELSHYKKKYHNLSTRWSSSEDRKTKAKSDAHS 2759
DB 2197 GTVMDTKVDELITTELKEITELKEKTEKADYLDKYGSL--LISHKLEAKKMLTQV 2253
QY 2760 SHTGSSH-----RQSPHKTETRYRHGPTPESENPSL---HLGSPKSSSTKRVG-- 2808
DB 2254 AHLCSQSKQDSKQSP-----LLGPVAPGSPPIPVTEKRLSSGOKKASGRORSSGIW 2307
QY 2809 -----PNRSEIYS---OLWMS-----PGKTGM 2827
DB 2308 ENGSGPTPATPESPSKSKKAVMSGIHPADBTGTEPEPEGLPBYVAKGFADIPGTGTS 2367
QY 2828 H-----KHILSPKVGILH-----KKRALSPNRSEMPTOHVIISPKGTG 2864
DB 2368 YILRRTMATRSPRLAOKLAUSPLSLGKENTABESSKPTAGSRSQKVAORSPVDSG 2427
QY 2865 -LHKNLTESTLFPNLSSPCKQOKVQENLNSPKGLF-----DYKSSMRYCSQ 2912
DB 2428 TIREPTTKGVPVNNLPERSPPTSPRGLAVKGRVLVPSFKAGLEBSKGSENCYQ 2482

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RESULT 5
 US-09-572-191-2
 ; Sequence 2, Application US/09572191
 ; Patent No. 6355466
 ; GENERAL INFORMATION:
 ; APPLICANT: Beraud, Christophe
 ; APPLICANT: Sakowicz, Roman
 ; APPLICANT: Wood, Kenneth
 ; TITLE OF INVENTION: No. 6355466e1 motor proteins and methods for
 ; FILE REFERENCE: 1017
 ; CURRENT APPLICATION NUMBER: US/09/572,191
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 1388
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-572-191-2

Query Match 7.1%; Score 1051; DB 4; Length 1388;
 Best Local Similarity 24.5%; Pred. No. 7.4e-44;
 Matches 417; Conservative 304; Mismatches 548; Indels 434; Gaps 60;

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QY 2 SEGDAVVCVVRPPIORE---QGOANLQWAGNNTTISQVDT---KSFNDRVFNSHS 55
DB 22 NEGDAIKVFRIRPAERSGSADGEO-NLCISLVSTSLRLSHNBPBKFTTDDHADVDT 80
QY 56 STSQIYOEIAPDIISALOGYNGTIFAYGQTSKGTYTMMG-----TPNSLGITPOAI 108
DB 81 TQSEVAFATVAKSIVESCMGNGYGTIFAYGQTSKGFTTMMGPESDNFSHNLRGVYPRSF 140
QY 109 QEVFKITQEI-----PNREFLRVSMETVNTVDLLCDDRRKPKLEIRDPNNVYA 163
DB 141 EYLFILIREKEKAGAGKSFLOKCSFIEIYNEQIYDVL--DSASGLYIRHRIKGVFV 198
QY 164 DLTEELVMPBEHVIOMIKKGEKNRHYGETKXNDHSRSHITPRMIYESRDR-NDPTNSBN 222
DB 199 GAVEOVVTSAAEAYOVLSGGMNRKRVASTSMNRBSRSRAVFTTITESKEKNEIYN--- 255
QY 223 CDGAVVWHLNLVDLAGSERASQTAGVRLKEGCNINSLFILQVITKLSDGQAG-G 280
DB 256 ----IRTSILNLVDLAGSERQKDTAEGWRLKEAGNINSLSCIGQVITALVDVGKQR 311
QY 261 FINYDSKLTIRLQNSLGNACTVITCTTPVS--FDELSTLQRPASTAKHVRNTPHNE 338
DB 312 HVCYDSKLTIFLRDLSLGNACTAIIVANYHPSRCFGETLSTLNFQRAKLIKNAVNE 371
QY 339 VLDDALLKRYKEITLDLKKOLENSESSETKAQMMAKEHTQLLAETIKHKEREDRW 398
DB 372 --DTGNVSQDAEYKRLKEQLAELASGOTPPESFTRDKKNTWEYFQ-----EAMLF 424
QY 399 HLTNIVASQORSQODORVYKRRVYTWAFGKIONSLSHAGSDPMLSLRPNFSKAKAF 458
DB 425 F-----KKSBEKK-----SLIEKVQLEJDLTKKEF 452
QY 459 SDMSFPEIDDSVCTEFSDFDALSMDNSNGIDAEMNLASKYTHREKTSLSHOSMIDFGOI 518
DB 453 ----ISNMKIYKFR--EDQITRLEK--LH----- 474
QY 519 SDSVQFHDSSKENOQOYLPKDSGDMAECKSAFEKEITSLQOOLQSKEREKELVQSPFL 578
DB 475 ----KESRGFLPEEBODRL--SELRNEDIQTLREQIIEHPVAKYAHENSHL 520
QY 579 KIALEEOLSVAKKYLEWYTNRSRHSINAQVDVEKVRKEMSVLGDGYNASNDLO 638
DB 521 R----EENRRRL--LEPVKRAQF----- 538
QY 639 DSSVDGKRSLSSHDECIEHRKMLEQKIYDLEEFLENLKKSSNDYKXSEQDPMESIQC 698
DB 539 ----MDAQITAKLEKAFSEISGMEKSDK---NQGFSPKAQKE 574
QY 699 EAIMAEKANALEELMRDNFNITLENETLKREIADLERSLKEN-QETNEFEILEKETQ 757
DB 575 PCLFA-----NTEKLAQOLQIOTELNNSQOEYEF-----KELT 609
QY 758 KEHEQOLHEIGSLKLVENAMENONLEDELETYKLLKEOEIOALERK-RADNLO-- 814
DB 610 KKRQLELSELOSLQKA-----NUNLENLEA-TKACKRQEV--SOJLNKHAETLKTI 659
QY 815 ---KVRNF--DLSVSMGDSERKCEBIFOLQKSLDAEAYTRDAQKESFLRSENL 865
DB 660 TTPTAYOUHSRPVKLSPMGSPSL---YTQNSSIIDNDIILNEPVPE----- 706
QY 866 ELKEKMEQTSNMVNOKEKASLFEKOLETEKSNYKMEADLOKE-----LOSARENIY 919
DB 707 ----MNEQAFEAISELRIVQDEOMGALQKDEEHRKOLKLOOHVDCLEH 752
QY 920 LINGLAGVPRDLRVELKEKVSEFSKOLEKALEKXNALENEV-TCSIEYKFLFNEVEEC 978
DB 753 HSTQW-----QELFSSERI-----DWTQOEELISQNLVLEKQLOETQRYKDNFLKSEVHD 802
QY 979 LKNQISKASEEITMLLKQF-----GEHSASIIISKQEIIMQOSEQOIIQLTDEVTHTQSK 1031
DB 803 LRVLHVSADKELSLSVKLEYSFKTQOEKFPNKLSEHMHVHVOQLDNLRLLENKLELSKAC 862

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QY 1032 VQOTEEOYLEMKNQKHDDLFEKYIRN-KSEABDLREMENTLKQTMESVEVK-----IA 1082
DB 863 LQDSVDNLQETWKFEIDQLSRLQNFKKENETLKSDLNMLLEBAKERNNKLSLOFEE 922
QY 1083 DTKHELEETIRPKEDOLHEK-KYFQAMQITFPIPLSDSLPSPKLVESNODPIEINDY 1141
DB 923 DKENSKEILKYLEAVROEKQETAKCEQAKVQKLEEST----- 963
QY 1142 HNLILATERNNIWMCFEYRSLKEQVIDINTQLOAQOAGIEKSD-LQPKODLEGE 1200
DB 964 ----LATEK--VISLEKSRDSKVVADLNNQIOELRSSVCETETITDILKQELKDN 1016
QY 1201 VK---LLEMEBLKGLTDSQSLIEKQLENELEVEKLTQLOEEMKNITIERNELOTFE 1257
DB 1017 CKYNSALVDRE-----ESRVLIKQGVLDLDEKTLR-----LRILSE 1054
QY 1258 DIKAEDSLKODLSNIEQ-----SIETODELPAEOBELREKQOLVDSFPOQLDGSV 1310
DB 1055 DI--ERDMICEDLAHATEQLNMLTBAASKHSGLSQAOBELTKKALIOELOHKL----- 1107
QY 1311 GISSPNHAAVANOEKVSLQEVNLSQSEMLRGRDELQTSKALVSELELRAHVKSVEGE 1370
DB 1108 ----NQK-----EVEQKKNYFMRQOL-----EHVDSAAE 1137
QY 1371 N-----LEITKKLNGLEKEILGKSESEVLKSMLEMLKEDNNKLKE--QAEYS 1417
DB 1138 DQOSKPTPRHPOTHLAKLLETOEBOI---EDGRASKTSLEBLVTKLMBDRVKNAEILR 1193
QY 1418 SKENQPSLEEVFSSQKLVDEIEVLKAOLKAAEFLKIDRDYFELVOTAN----- 1468
DB 1194 MKEQUREMENLRLESQOLIEKWMLOQOLDLDRQKENSQDNHPNOOLKNEQESIRER 1253
QY 1469 ---TNLVGKLETPIQADHEEDSIRRSEMEIKVLGSEKLENOVLRLRLOEKLELSNK 1525
DB 1254 LAKSKIIVEEMK--KRADEEVQSLYKMECRLMTEVERTQTLSESAFQEKQOLNSK 1311
QY 1526 LEILQKEMETSVILKDDLOQKLESLSSEN--IILKENIDTTLKHSSTQAOLOKTQOEIQ 1583
DB 1312 LEMWEERERBSQEMEMLRKQVECLAENGKLVGHQNL-----HOKIQYVRLKKEVNR 1365
QY 1584 LAKNLAIASDNCPIQOKEKETS 1606
DB 1366 LAEETEKLAENVFLKEKRSES 1388

RESULT 6
US-09-723-262-2
; Sequence 2, Application US/09723262
; Patent No. 6379912
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Sakowicz, Roman
; APPLICANT: Wood, Kenneth
; TITLE OF INVENTION: No. 6379912el motor proteins and methods for
; FILE OF INVENTION: their use
; CURRENT APPLICATION NUMBER: US/09/723,262
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: US 09/572,191
; PRIOR FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1388
; TYPE: prt
; ORGANISM: Human
US-09-723-262-2

Query Match 7.1%; Score 1051; DB 4; Length 1388;
Best Local Similarity 24.5%; Pred. No. 7.4e-44;
Matches 417; Conservative 304; Mismatches 548; Indels 434; Gaps 60;
QY 2 SEGDAVVCVVRPPIORE---QGOANLQWAGNNTTISQVDT---KSFNDRVFNSHS 55

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Dd	22	NEGDAIKFVAVIPRPAERSSGADDEQ-NLCCSVLSTSRHSNPEPRTFFFDVAVDY	80
Oy	56	STSOIQOIEAVPIIRLSALOGNGTIFAYGQTSSGKTYTMWG-----TNSLGIPOAI	108
Dd	81	TOESVFATVAKSIVESCWSGYNGTIFAYGQTSGKTFPMGPESDNESHRLRGVIRSF	140
Oy	109	QOEVKTIQEI-----PNREPLLRSYMTIMVETVKDILCDORRKKPLEIRDFPRNRYVA	163
Dd	141	EYLFSLIDREKEKAGAGKSFLLCKSFIEIYNEQIYDIL--DSASAGLYRHHIKKGAVV	198
Oy	164	DLTEELVWVPEHVLQWIKKGEKNRHYGTCKONNDSHRHTIFRMIYESGR--NDPTSEN	222
Dd	199	GAVEQVYTAABAVOVLSCGWRNRVASTSNRBSRSHAVFTITSEMEGNTIV---255	
Oy	223	CDGAVWVSHLNLVDLAGSERASQTGAEGVRLKEGGINRSLFIIQVYIKLSDQAG--G	280
Dd	256	-----IRTSJLNLVDLAGSERQKDTGAEGMRLKEAGNIRSLSCIGQVITALVDVGNGQR	311
Oy	281	FINYRDSKTYLTLONSJGNAKTYICITITPV--FDETSTLOFASTAKVNTPVHNE	338
Dd	312	HVCYRDSKTYLTELRLSDLSGNAKTAIIIAVHFGSRFCFGETSTLHPAQAKIIRKAAVNE	371
Oy	339	VLDDEALLKRYKXELLDLKKOLENLESSERKAQAMAEHTQJLAELIKOLHREGRIV	398
Dd	372	--DTQGNVSQLOAEVKRYKEQDLAEIASQOTPESEFTLTDKRTYVMEFQ-----EAMLF	424
Oy	399	HLTNIVVASOESQODCRVKKRRVYTMAPGKIONSLSHAGVSDPFTSRLPNGFSKTAFF	458
Dd	425	F-----KKSBEKK-----SLEKTYQLEDDLTKKEKF	452
Oy	459	SDMSPFEIDDSVCTEFSDFDDALSMDNSGIDAEWNIAKVTYHREKTSJLHQSMDIFGQI	518
Dd	453	-----KESRGFLPEODRLL-----SELNREIQTLEQIEHPRVAKYAMENHSL	520
Oy	519	SDSVQFHDSKENQOYLPKXSGDMAEKRKASFKEIETSLQOOLQSKBEKKELVQSPFL	578
Dd	475	-----KESRGFLPEODRLL-----SELNREIQTLEQIEHPRVAKYAMENHSL	520
Oy	579	KIALEEQLSYAKKULEMWTNSRHSIAEYQTDVEKEVARKENSVLGDSGYANSNDLQ	638
Dd	521	R-----EENRRRL--LEBYKRAQE-----	538
Oy	639	DSSVDGKRLLSSHDECIEHRKMLBOKIVLDEEFLENLKKSEDNQKSSBEDPMESIQOLC	698
Dd	539	-----MDAQITAKTERAFSEISGMEKSDK---NOOGFSPKQKE	574
Oy	699	EAIMAKRNALBEALMDNPNTILNEMTLKREIADLERBLKEN--QFTNEFELLEETO	757
Dd	575	PCLF-----NTEKKAQOLQOTELANSKOYEFE-----KELT	609
Oy	758	KEHEAQILHEIGSLKLVENAEWYQNLNEEDLETYTKLKEQETOLAEYLR--RADNIQ--	814
Dd	610	RKQOIELESELQSLQK-----NLNLENLLA--TKACQOEY--SOLNKIYHETLKII	659
Oy	815	---KVRNF-----DLSVSGDSEKICEEJIFOLKQSLSDAEVATRAQKESCFLRSENTL	865
Dd	660	TTPTKAYQJLHSPRVKLPBMSFCSL---YTQNSJILDNIDILMEVPBE-----	706
Oy	866	ELKEKMEJDTSNWYNOKEKQASLFEQULETKESNYKMMADIQKE-----LOSAPENIY	919
Dd	707	-----MNEQAFEAISEELTVQEQMSALQAKLIDEEHKNKLIKQOHVDKLEH	752
Oy	920	LNGLLAGVPRDLISRVELEKKVSPFSQOLEKALEEKALENEV--TCLSEKFLPNEVEEC	978
Dd	753	HSTQW---QELFESSERI---DWTQOQEBLLSQVLVLEKQOLEOTQKDFLAKSEVHD	802
Oy	979	LKNOJSKASEEIMLKQE-----GERSASIIISKOELIIMOQESHOILQITDEVTHTQSK	1031
Dd	803	LRYVLHSDAKKELSSYKLEYSSFKYNQKEKPNKLSRHHNVQLOLDNRLNEMEKLLSEKAC	862
Oy	1032	VOQTEEOYLEMKKMHDLFEKYIYN--KEBAEDLLEMMENLKGIMESVEVK-----IA	1082

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Db      863  LQSDYDNLQETIMKPEIDQLSHNLIQNFKKENETLKSJLNNIMLLEAKERNNKLSLQFEE  922
Qy      1083  DTKEHELEETTRDKQOLLHEK-KYFQAMQITFPPTPLSDSLPSKVLVGNSSODPIEINDY  1141
Db      923  DKENSSEKILLVLVAVQEQKETAKCEQOAKVQKLEESL-----  963
Qy      1142  HNLLALTERNINIVCJETERNLSLKEOVIPDLNTQLOSLQASLIEKSD-LQPKODLEEGE  1200
Db      964  -----LATEK-VISSLEKSHDSQKVVADLMNOIQELRSSVEKRTETIDTLQKOLNDIN  1016
Qy      1201  VK---LLELMELKGHITDSQLSLEKLOLENLEVEYTEKLTQLOEBMKNITIERNELQTNFE  1257
Db      1017  CKYMSALVDRE-----ESRVLIKQOEVDITLDKETLR-----LRILSE  1054
Qy      1258  DLKAEHSLKODLSLENIEQ-----SIFODELRAAQEELREQOLVDSFRQULLDSOV  1310
Db      1055  DI--ERDMLCEDLAHATEQOLNMLTEASKRHSGLQSAQOEBLTKKVALIOELQHL-----  1107
Qy      1311  GISSPNHDVANOKEKSVLGEVNSLQSEMLRGERDELQSCALVSELELRAHAKSVEGE  1370
Db      1108  -----NQKK-----BEVEQKNEVYFKRKQL-----EHVMSAAE  1157
Qy      1371  N-----LEITTKLNGLEKEILKSESESVLKSMLNLEEDNNKLE--QAEEYS  1417
Db      1138  DPQSPKTPRHQHTLAKLLETQEBEI---EDGASKTSLEHLVTKLNDEBEVNAELRL  1193
Qy      1418  SKENQFSLVEEVSSQKLVDEIVLVAQKKAEBRLIKDRYELVQOTAN-----  1468
Db      1194  MKEQLOREMENLRLESQOLIEKNWMLQLOGLDIKQKENSQDNHEDNOOLKNEQESIKER  1253
Qy      1469  ---INIVGKLETLOADHEDSDLRSESEMEIVLVEBKERNQYLLERLOEKELEISNK  1525
Db      1254  LAKSKIVAEYMK--MKADLVEVQSLAYNKEWECRLMDEBKRTOPLSKAQOKEQOLRSK  1311
Qy      1526  LEITQKEMETSVLLKDDLOQKLEBSLSEN--IILKENIDTTLKHSPTQAOLOKTOOELQ  1583
Db      1312  LEEVYEERERTSQEMEMLRKQVECLAENGLVGHQNL-----HQKIQYVRLKKEKVR  1365
Qy      1584  LAKNLALIASDNCPTQEKETS  1606
Db      1366  LAETEKRLAENVFLKEKKRS  1388

RESULT 7
US-09-723-219-2
/ Sequence 2, Application US/09723219
/ Patent No. 6391613
/ GENERAL INFORMATION:
/ APPLICANT: Beraud, Christophe
/ APPLICANT: Sakowicz, Roman
/ APPLICANT: Wood, Kenneth
/ TITLE OF INVENTION: No. 6391613el motor proteins and methods for
/ TITLE OF INVENTION: their use
/ FILE REFERENCE: 1017
/ CURRENT APPLICATION NUMBER: US/09/723,219
/ CURRENT FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: US/09/572,191
/ PRIOR FILING DATE: 2000-05-17
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 1388
/ TYPE: PRT
/ ORGANISM: Human
/ US-09-723-219-2

Query Match      7.1%; Score 1051; DB 4; Length 1388;
Best Local Similarity 24.5%; Pred. No. 7.4e-44;
Matches 417; Conservative 304; Mismatches 548; Indels 434; Gaps 60;

2 SEGAVKVCYCVRPLORE---OGDQANLQKAGNNTISQVDT---KSFNFDVFNQHE  55
22 NEGDIKIFVIRIRPAEAGSGADGEO-NLCLSVLSTSLRLHNSPDKPTTFITFDVAVDVT  80

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OY 56 STSOIYOEIAPPIISALOGYNGTIFAYGOTSSGKTYTMWG-----TPNSLGIIPQAI 108
Db 81 TOESFAIYAKSIVSCMSGINGTIFAYGOTSSGKFTTMGPSESDNPSHNLRGYIPRF 140
OY 109 OEVFKIOEI-----PNREFLRVSYMIEYNETVXDLLCDRRKKPLEIREDPNRNYYVA 163
Db 141 EYLFSLIDREKEKAGKSGFLCKSFIEIYNEQIYDLL--DSASAGLYLREHIKKGIVFV 198
OY 164 DLTELVMPVEHVIOVIKKGKRIHYGETKMDHSSRSTTIFRMIVESDR--NDPTNSGN 222
Db 199 GAVEGVVTSAAEAYVLSGGMNRVASTSMNRSSRSHAVPTITTESKEXNEIYV--- 255
OY 223 CDGAAMVHNLNVDLAGSEPARASOTGAEVYRLKEGCNINRSLFLLGOVIKLSDDQAG--G 280
Db 256 ----IRTSLLNLVDLAGSEROKOTHAEGMRLEAGNINRSLSCLOVITLALDVNGKOR 311
OY 281 FINYDSKULTRILQNSLGNNAKTVIICTTPVS--FDETLSTLOPASTAKHVRYNTPHNE 338
Db 312 HVCYRDSKULTRILRDSLGNNAKTIIIVNHPSRGGETLSTLNFQRAKLIKNKAVVNE 371
OY 339 VLDDBALKRYRKELTDLKQOLENBSSESTKQAMAKEHTQLLAEIKQHLKEREDRW 398
Db 372 --DTGANNVSOLQAEVYRLKEQLAEIASGOTPRESEFLTRDKKTYMEYFQ----EAMLF 424
OY 399 HLTNIVVASSOBSDODORVYKRVVTWAGKIQNSLHAGVSDPMLSLPGNFSKAKF 458
Db 425 F-----KKSBEKK-----SLIEKVTOLEBTLTKKEKF 452
OY 459 SDMPSPFIDSDVCTEFSDFDALSMDNSGIDAEMNLASKYTHREKTSLSHOSMIDFGOI 518
Db 453 -----IQSNKMIYKFR--EDQIRLEK--LH----- 474
OY 519 SDSVOFHDSSKENQOYIYRKOSGDMAECHKASFEKEITSLQOOLOSKEEKEKELVOSPEL 578
Db 475 -----KESRSGFLPREEDRLL--SELARNEIQTLREQIENHPRVAKYAMENHSL 520
OY 579 KIALEBEOISYAKRLMEWTNSREHSINAEVOTDVEKEVVRKEMSVLGGSGVNAANSIDQ 638
Db 521 R---EENRRLL--LEPVYKRAOE----- 538
OY 639 DSSVGDKRLSSHDECIEHRKMLEQIVDLEEFIEINLKNKSENDKOSSEODFMESIQLC 698
Db 539 -----MDAQTIAKLEKAFSEISGEMKSDK--NQOFSRPAKOE 574
OY 699 EAIMAEKANALBEALMRDNFDNIILENETLKRLEIADLERLSKEN--QETNEFEILEKETQ 757
Db 575 PCLFA-----NTEKLAQOLLOIOTELINNSKQEYEEF---KEIT 609
OY 758 KEHEQOLHEIGSLKLVENAMENYONLEEDLETYLLKQEOIQLAEIRK--RADNLO-- 814
Db 610 RKRQLELSELOSLQKA-----NUNLENLLAE--TKACKRQEV--SOJLNKHAETLTKI 659
OY 815 ---KVRNF-----DLSVMSGSEKLCBEIFOLKQSLSDAVALTRDAQKESCFRSENL 865
Db 660 TTPTAYOLHSRPVYKLSPEMGSFGL-----YTONSSIIDNIIINLEPVPE----- 706
OY 866 ELKEXMEDTSMWYNQEKKAASLFEKOLETEKSNYKMEADLOKE-----IQSAFNEIY 919
Db 707 -----MNEQAFEAISEBELRTVQOMGALQKLDREBHKMLKLOQHVDKLEH 752
OY 920 LNLGLAGVPRDILSRVELEKXVSFQOLEKALEBEKALNEV--TCLSEYVFLPNEVBC 978
Db 753 HSTQV-----OELFSSERI-----DWTQOQEBLLSQNLVLEKQLODETQKDFLSEVND 802
OY 979 LKNQISKASEIIMLKQOE-----GENSASIIKQOIIIMQOSQOILDTDEVHTOSK 1031
Db 803 LRVVHSHADKELSSYKLEVSFKTQOEKFNKLSERHNVQOQDNLRLKENKLLSEKAC 862
OY 1032 VQOOTEQVLEMKKMDHDLFEKYIRN--KSEADLLREMENTLKGTMESVEYK-----IA 1082
Db 863 LQDSYDNIQEIWKFEIDQLSRNLQNFKKENETLKSDLNLMLLELBAEKRRNKLSLQFEE 922

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OY 1083 DTKHELESTIRDKEOULLHEK--KYFPQAMOTIFPITPLSDSLPSPSKLVGNSODPIEINDY 1141
Db 923 DKENSKEILKYLEAVROEKOKETAKCEQOMAKVQKLESU----- 963
OY 1142 HNLIALATERNNIVCLETENSLKEOYUIDLTQLOSIQAOGSIKSD--LOKPKODLEGE 1200
Db 964 ----LATEK--VISLEKSRSDSKVADLMNQIOELRSSVCEETETIDTLKOEIKOIN 1016
OY 1201 VK---LLEBMLKHLNLSQOLSTEKOLENLEVETKQTOQEEMKNITIERNELOTNFE 1257
Db 1017 CKYNSALVDR-----ESRVLKQOEVDLIDLKETIR-----LRIISE 1054
OY 1258 DLKAEHDSLKODLSENIO-----SIETODELPAQOELEREOKOLVDSFRQOOLDGCV 1310
Db 1055 DI--ERDMLCEDLAAATQOLMLNLTGASKKHGSLQSAQEBLTKKALLQELQHKL----- 1107
OY 1311 GISSPNHDAVANOEVKVSIGEVNSLOSEMVLGRERDELQTSALVSELELRAHVKSVEGE 1370
Db 1108 -----NQKK-----BEVEQKQIEYNFRKQOL-----EHVMSAAE 1137
OY 1371 N-----LEITKRLNGLEKEILGKSESEVLSKMLLENLKEDNNKLKE--QAEYS 1417
Db 1138 DPOSPKTPPHQOTHLAKULETOEOTI---EDGRASKTSLSHLYTKLNEDEKVKNAEILR 1193
OY 1418 SKENQPSLEEVFSGSQKLVDEIEVLKQYLKAAERLEIKDRDPFELYOTAN----- 1468
Db 1194 MKEOUREMENLRLSEQOILKXMKVLQGLDDIQRQKENSDDQHPNQQOLKNOEBSIKER 1253
OY 1469 ---TNLVEGKETPLQADHEDSDIDRSEEMIKYLGKLEBNQYLLERLOEKELELSNK 1525
Db 1254 LAKSKIVEMLK--MKADLEEVQSAVYNKMECLMTEVEVERTQTLSEKAFQOEKOLRSK 1311
OY 1526 LEILOKEMETSVLKDOLQOKLESLSSEN--IILKENIDTLLKXHSDDTQAOLOKQOELO 1583
Db 1312 LEEMEYERERTSQEMEMLRKQOECLEENGKLVGHQNL-----HOKIQVYVRLKENVR 1365
OY 1584 LAKNLAIASDNCPIQOKETSA 1606
Db 1366 LAETEKLAERAEVFLAKEKRSES 1388

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RESULT 8
US-09-914-259-11
; Sequence 11, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 3878
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-914-259-11

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Query Match          5.9%  Score 1020; DB 4; Length 3878;
Best Local Similarity 19.0%  Pred. No. 8,1e-42;
Matches 691; Conservative 639; Mismatches 1148; Indels 1152; Gaps 143;

OY 143 DDRKKPLEIREDFNRNVYVADLTLELVMPVEHVIOV-----IKKGKRNRYHGETKMDH 197
Db 3 DEERQKLEAGAKIEELSLAFIVRQLAQFQRKQNSQGGSPSKQKKR---KTSSSKH 59
OY 198 SRSHTTFRMIVESDRNDPTNSENCDAVNVSHNLNVDLAGSEPARASOTGAEVYRLK--- 254
Db 60 DVSAHHDNLINQSQCNEMVYINSQGVSESTVIPESTIMKTLHSGEITSHQOGFSVLESEI 119

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QY 255 --- EGCN---INRSLEIIOQVIAKKLSGAGGFINYRDSKLTIRILONSJGAKTVIICT 308
 Db 120 STTADDCSEVNGCSFVM-----RTGKPTNULREEBFG----- 152
 QY 309 ITPVSEDELSTLQIPASTAKVANTPHVNEVLDDALLKRYKEIILDKOLENLESSE 368
 Db 153 ---VDDSYS-----BQAGDSPTLHEMMESELGAKOH--ELIELRELEEMKVTG 198
 QY 369 TKA-----QAMAKEH---TOLLAEIKOLHKEEDRIWHLNINIVASSQESQODQRYK 418
 Db 199 TGLGLOOLQEPFAAIKORDGIITOLTANLOQARREKETWREFEL-----TEGQOKQ 251
 QY 419 RRRRYTAPGKIONSILHAGVSD-----FMLSRLPQNFSK----- 454
 Db 252 IQFOOLQASETLRNSTHSTADLLQAKQIILTHQOQLEOBDHLLDYOKKKEDEFTMQJS 311
 QY 455 ---KAKESDMPSPFPIIDSVCTEFSDFPDALSMTMSNGIDAE--WNILASKVTHEREK- 506
 Db 312 FLOEKIKVYEMODKKVENSKEEIOEKETIIEELWTKIIEBEKTLLEKDKLTADKLL 371
 QY 507 -SLHOSMIDFGO-----ISDSVOFHDSKKNOLQVLPKDSGDMAEGRK-----ASPE 552
 Db 372 GELIOEIOVKNQOEIFKMKLELTNSKOKEROSSEITQLM---GIYBEIOKRNHKSQPE 427
 QY 553 KEITS-LOOQLOSK--BEEKKEIVQSPFKIAELBEOL--SVAKULEWVTNSR--EHSI 605
 Db 428 TUIVOMEQETQRLKEQLAELEDMYGOQIVQKQELLROHMAQMEKTRHKGEMENAL 487
 QY 606 NAEVQTDVKEVYVRKMSVUGDSGYASNSDLODSSVDGKRILSSHDECIEHRKMLEQKI 665
 Db 488 RSYSNITTVEDQIK--LMNVAINELNKIQDTISOKEKLEBELGLILLEKCALQROL 542
 QY 666 VLLEPFIENLNKSENDKSSRODFM-----ESIOCEAIMAKANALE--ELAL-- 714
 Db 543 EDLVEBELSREIOIQAROTIAEQSKLNAEAKSISTVEDIKAEIYASASESKELELKAE 602
 QY 715 ---MRDNFNILLENETLKEIADLER-----SLKE-- 742
 Db 603 AEVTNYKIKLEMLEKKNVLDPMASQOE-ALERLARTOLLPSEBELSKLEDELEIHR 661
 QY 743 ---NQTNEPEIL--EKETOKEHQAOLIHETGISAKKULEVNA 778
 Db 662 INIEKLDNIGIHYKQOIDLQENMSQKLETMOPEKDNLITKQONLILISIKDKLOQS- 720
 QY 779 EYWNQULEE---DLETRTKLKE-----OEIOI--AELERKADNQ 814
 Db 721 -LVNSSEEMTLOINLOKEIILROBEKEKGLBEVQELQKTLLEKQKMEKENDIQ 779
 QY 815 KIVRNFDLSVS-MGDESKLCEEIQLQKSLSDAEAV-----TRDA--OKESGFLRS 862
 Db 780 EKFAQLEANSITLKDEKTLDEMLKIHTPVQOEERLIFLDSIKSKSDSWEXEIEILIE 839
 QY 863 EN-----LELKEKNEEDTSNMYNOKEKASLFEKOLETEKSYKKNEMADLO--KEL 910
 Db 840 ENEDLKQOIOINEIEKORNTFSAKNEFVANYOELQOEYACLLKVKDLBESKXKQEL 899
 QY 911 O-----SAFNEINVLN-----GLAGKVPRLD-- 933
 Db 900 EYKSKIKALNEBELHORINPTTYKMSVFPDEKTVAAETLMEGAVEVEKOTTELMKLEV 959
 QY 934 ---SRVELEKVSSEFKOLEKALEKKNALENEVTCLSEYK---FLPNEVECHKN-- 981
 Db 960 TKREKLELSQRLSDSEQLKQKHGEISPLNEBEVKSJKOEKEQVSLACRELEIILINNRAE 1019
 QY 982 ---QISKASEEIMLKQBS-EHSASTISK-----OEIIMQOSQO 1017
 Db 1020 NVQSCDPTQVSLIDGVVITVSRGABGSVSKVNSFBEESKIVEDKVSFENMNVGBESQ 1079
 QY 1018 ---IIOQTDQVHTOS--KVQOTEEOYLE-----MKKMDLPEKVIIRKXSEAE-- 1061
 Db 1080 EOLILHLSVTKESSLRATQSEENDKLOKELNVLASBOQDL--RLQMEQORICLSL 1134
 QY 1062 ---DLIRE-MENLKGT-----MESVEVKIADTKHELE-ETIR--DKQO 1097
 Db 1135 VYSTHVDQVREYMEKKAOLCSLKEBELIFPAEKEIKELQKIHQLELOTMKQOETGDEGK 1194
 QY 1098 ILH-----EKKYFQAMQTIPIPTPLSDLPSPKLVESNODPIEINDY----- 1141
 Db 1195 PHLHLIGLQKAVSECSYFILOTLCV-----LGEYTPALKCEYNAEDKENSQYISEN 1249
 QY 1142 ---HNLIALATERNNIMVCLTERNSLKEQVIDLNTQLOLQAO 1182
 Db 1250 EDPQLQDYRYEVQDFQENMHTLANKVTEYNNKLVLQIRLSKIMQOQTD-----GM 1300
 QY 1183 STEKSDLOKPKQDLEEGEVKLLMEELLKGHITBQLSIEKQLENLVT--EKQOTLOE 1240
 Db 1301 KLEFGEENLPKX-----ETEFPLSIH--SQMT--NLEDIVNNHKSLSLQD 1342
 QY 1241 EKMNTIRBRELQTNFEDLKAHSDLSKODLSB----- 1272
 Db 1343 ---LEKTKLEBOVQELBESLISLQOQKETEBOYAEIHCLOKRIQAVSESTVPBL 1396
 QY 1273 ---NIEQSIETODELRAQOE-----ELREQOLVDSF 1301
 Db 1397 PVDVAVITESDAQRTMYPGSCVYKKNIDGTIERSGEFGVKEETNIVKLEKYOQOLEBEV 1456
 QY 1302 ROQLIDCSVGI-----SSPNHDAVANOEKVSLGEVANSLOSEMRLGERD 1344
 Db 1457 AKVIVMSIAFAQOTELSRISGKENTASSKQAHAVCOQEOHYFNMKLSODQIGFOTFE 1516
 QY 1345 ELQTSCKALVSEL--ELRAHVAVSVEGEN-----LEITKULNGLEKE--ILGKS 1389
 Db 1517 TVDVKFKBEFKPLSKELGHEKKEILLNSDHPDIDESKDCVLTIEEMFSKTKTIVQOS 1576
 QY 1390 ESEVILKSMI-----ENLKEDNNKLEQAEVSSKENQFSLB--VFGSQOKLV 1436
 Db 1577 IHDEISVSMASRQOLMNEBQLEDMQOELVQYQEHQOATQSSIDNENILVSEBRVLL 1636
 QY 1437 DEIEVLKQOLKAAERL--ETQDRPYFELVQTNANVLVBGKLETLQADHEDSDIDRSE 1494
 Db 1637 BELLEALKQSLAGREKLCCELENS--TOTONENQOGEVE--EOTFKERKIDRKE 1689
 QY 1495 EMEIKVLEKLERNOYLLERLOEKEKLELNKLEIIOKEMETVLLKDD-----LOOK 1546
 Db 1690 DVPPEILSNE--RYALOKAN-----NRLKILLEVAKTTAAVEITIGRHVGLDRS 1739
 QY 1547 LESLSENIILKENIDTTLK--HNSDTQAOLOK-----TOQELQ 1583
 Db 1740 SKSGQSASLIWRSABASVSCVHEHTRVTDSPISYSGSDMPRNDINMMSKVEEGTE 1799
 QY 1584 LAKNL--ALASDNCPIITOE-----KETADCVHPLBEKILLT 1620
 Db 1800 ISQRLVRSQFAGTEIDPENEBELMNISSRLQAAVEKLELALISSTISQLEHAKVOTELMR 1859
 QY 1621 BELHQKTNQOEKL-----LHEKNEL--EQAOVELCEVENHKNMSIESKSSLESIOH 1670
 Db 1860 ESFROKQOATBSLKOEBELREHLESARABEVLAVLS-KAGGVADYADEKTLTEROQ 1918
 QY 1671 EKHND--TEQOLLAQOQVYVTOEKELOQOTHEHLTAEVNDLKENIELGINFNEAQ 1726
 Db 1919 EKTIDILDRLEQELCASNRLQELBAEQOIOERBELLSROKRAMK--AEAG----- 1967
 QY 1727 KTTKQOCLINKEKLEBQSOHRLQCEIIEBELMSLKRESLLETLSKSEQVNLNLOEMEMV 1786
 Db 1968 --PVEQOULOETEKLMKELEVOCAQKVRDLOQVAYLE-----IDIVEQVSR- 2015
 QY 1787 MLEMEELKNSQRTVIAERQDLODDRESVEMSIETODPLRKAQOALQOQKDYQOELTQOI 1846
 Db 2016 FIELEQOKNTLMM-----DLRQONQALEKOLEKMKRFLDQO 2051
 QY 1847 S-----VLOEKIISLENQMLYNAATVKETLSERDDLNOSKQHLFSEITLSLSEK 1898
 Db 2055 AIDREHERVFPQOEIOKLEQOQ--KVVPFQCISE-----HQTREVEQLAHLKEX 2100
 QY 1899 E-----FALQAEKQADARKTIIDITEKISNIEBOLLOQATNMLKETLYRE--SLQO 1950


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Db 2101 TDKCSLLSKSQLOJDIORNEIEKLEFRVLEQOALLVSADTFQVDRKHFQAVEA 2160
Qy 1951 KQOLANT--EHRLETKSDALGKMEQ-----RBEANKVIALTEKSSLEQINENV 2004
Db 2161 KELSLEVOLOQERDAIDRKEKITNLEQLEQFRELENKNEEVOQLHMOLEIQKEAT 2220
Qy 2005 TTLKEGEKETFYLOQPSKQOSSQOMEELRESLTKDLOLEAE-----KEISEAT 2056
Db 2221 TLOLEQENKLF-----KDMELGLAIKESDAMSTODQVULFGKRAQIOIQE 2270
Qy 2057 NEIKULTAKISLEEEIIONASLINEAVSERENLRHSKOOLVSELOSLTKSRDHARA 2116
Db 2271 VEIDQNEQVTKLOOL--KITDNKVEE-----KNELIRDETQTECLMSDQECVK 2321
Qy 2117 QSKREDEAVNKIA-----SLAEELKILTKENDERDSKESIQEOS 2157
Db 2322 NRREIEIQNLNVEIKLOELANIGOKTSMNASHISEADSLKHQDVLVIAEKLALEQOV 2381
Qy 2158 SHLSSELCTYKT-----ELQMLKOOKEDINNKLAEKVVEDE-----LLOH 2198
Db 2382 ETANEBMTMKVULKETNFKMQLTOELFSLKRESV-----EKIQSIPENSVAVAIDH 2436
Qy 2199 ISSLEQLOLOIME-----LRNEK-LRNYELCEKMDIMEKISVLR 2239
Db 2437 LSKDPELEVLITPDALKSLENGQYFKSPEENGKSIINLETRILQLESTVSAKDELTO 2496
Qy 2240 -----NONEPOQEEEDVAERMDIESKNOEIQEIM-EKISAVSEQHTLSSLSSEQ 2291
Db 2497 CKQIKDMOEOGCFE-----TEMLQKKIVMLQKIVEKVA-----ALVSOIO 2539
Qy 2232 KET--EAHGMN-----IKE-----SLSTLSFSGSLQTEHYKANT 2328
Db 2540 LEAVEVAFCCDNQOTISEPERTNIQNLQREBELSGDIALTRISELSQVEEMT 2599
Qy 2329 QLOTLNFKKVYRTAAYVEDSLIKDYEKDLAEGRHDELRLOQLOCHGRKWSDA 2388
Db 2600 SL--ILEKQVEIAEKNVLEKKEKULELOKLEGNKQKREKE-----KKRSPD 2647
Qy 2389 SEELK-----FCIEPL-----NELLFKANTIQ 2412
Db 2648 VEVLKTTTELPHSNESGFFNELALRAESVATKALASYKEKAEKLOELLVKETN-MT 2706
Qy 2413 SVQDDFSEQVFLNGSTLQ-----ELEHKKG----- 2441
Db 2707 SLQKDLQVHRDLAEKELSLKEDETEVESKACAFPEPLPIKLSIASQDTGTLK 2766
Qy 2442 -----FMQLEBFGDLHYDAKKLESGMQO 2465
Db 2767 ISSNQTOQLVKNAGIOINLOSECSEVEETIEISQFTKIKMOELH-----AEILDM 2821
Qy 2466 ENRRIAST-----IOLLTKR--LKAVVOSKIQREITVYLNQ----- 2499
Db 2822 ESRHISETEITLKRHYVAQOLKEBCGTLKAVIQCLRSKEVGFYMMCFSTLSDSGDWG 2881
Qy 2500 -----FAKLOEKKEQN-----KELMRMEHNGPSA----- 2525
Db 2882 QGITVTHSQGFIAEGRESEESATDSFPKKIKGLRAVHNGQVLSLSTESPYSDGD 2941
Qy 2526 -SVME-----BENARLLGILKTVODESKLQSRIMLENEINLVYDDMH-----KGE 2572
Db 2942 HSIOQVSEPMLEBRKAVINTISSLKDITKMO-----LOREAVDSDSGSHSFSQDWGE 2996
Qy 2573 KVALLODKLL-----SRNAEALINAVQVLTKKODNLQAMK----- 2609
Db 2997 LLLAQOVFLERSVILAAFRTELTAAGTTAVGLNCLQRIQOEGVAYQAMCLOKA 3056
Qy 2610 -----ELENQXVAKAVPYKEID-----NLKTK-----VAKIEMEKY 2646
Db 3057 DRRSLSETQALHAQNGRKITLKRQESKPSQELLEVENIQOKOSQMLEMVELSSMK- 3115
Qy 2647 SKATDOEIAVYKSCLEDKEGRLKLEELRAQADNDTVCVPKYOXKASTFPVTCGGS 2706
Db 3116 DBATE-----LOBQLSSEKVVVAELKSLAQTKLELTTLLKQOHGHLK----- 3158

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Qy 2707 GIVQSTAMLVLOSEKALERELSHYKKKYVHLHLSRTMSSEDR-----KTKKASDAH 2758
Db 3159 -----ELBAFLEVKDXTDEVHLNDLNTLASQKKSRELQMALEKAK----- 3201
Qy 2759 SSGTSSHRGSPAKTETYRNG-PVTPERSEMPSLHGSFKSSESTKRVVSPNRSEIYSQ 2817
Db 3202 ---LGRSEERDKKELEJDLKFLSESQKQNRNLQNTLLLEQOKULNSQOKIESQRMLYDQ 3258
Qy 2818 LVMSPGKGMKHHTIISPSKVJLHKRPAISPNSMPTQHVISPQTLGHKMLTSTLPDN 2877
Db 3259 LSEEGRMLELOVLLSESEKVRIREMSSTLDRERELHAQLOSSDGTGOSRPLPSBLLKE 3318
Qy 2878 USSPC--KOQVQENTN--SPKGLFDVKSX 2904
Db 3319 LQKQLEBKSGRIVELNLETETKYKLSLOTR 3348

RESULT 9
US-09-592-054-8
; Sequence 8, Application US/09592054
; Patent No. 6440684
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Finet, Jeffrey
; APPLICANT: Sakowicz, Roman
; APPLICANT: Wood, Kenneth
; TITLE OF INVENTION: No. 6440684e1 motor proteins and methods for
; FILE REFERENCE: 1016
; TITLE OF INVENTION: their use
; CURRENT APPLICATION NUMBER: US/09/592,054
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1234
; TYPE: PRT
; ORGANISM: Human
; US-09-592-054-8

Query Match
Best Local Similarity 25.3%; Score 953; DB 4; Length 1234;
Matches 358; Conservative 245; Mismatches 444; Indels 370; Gaps 55;

Qy 3 BGDVAVCVVRPLQIRE--QGDQANLQWKAGNNTISOVDGT-KSFNFDVFNHSESTSQ 59
Db 6 KIPVRAVALRCPKPLPKPKEISEGQWCLSFVPGETGV--VVGDTKSFYDFVDPCTEOBE 63
Qy 60 IYQELAVPLISALQVNGTIFAYGQTSKGTYTMG-----TPNSLGITIPALQIOBF 112
Db 64 VNKAVAPLIKIFFGYNAVTALVAGQTSKGTYSGAVYTAEOENEPTVGIIPVIOQLF 123
Qy 113 KIIQEIIPREFFLRYSVMEIYNETVKKDLLCDRRKPKLEIREDFNRVNYVADLTIELVMV 172
Db 124 KEIDQKSPFETLKYSYIEINBEILDLDCSREKQAQININEDPREGKIYQGLTEKTVLV 183
Qy 173 PEHVIOWKKEKKNHGETKXNDHSSSHITFRNIVESRDRNDPTNSENCDAVMVSHL 232
Db 184 ALDVTSCLEQGNNSRTVASTMNSQSSRSHAIFTLSLEQKKSDKNSS-----FRSKL 236
Qy 223 NLVYDLAGSEPRASQTAEGVRLKEGNTNRSLEFILGOVYKXISDQAGGFVNYRDSKTRI 292
Db 237 HLVDLAGSEBRKKTAEGBDRLEGINIRGLCLGNVTSALGDDKGSFVPRDSKLTRL 296
Qy 293 LQNSLGGAKTVIITIPV--SPDETSLTOFASTAGVNTPHVNSVLDLDEALLKRYR 350
Db 297 LQDSLGGNSHTLMTACVSPADSNLEETISTLRVADRAKIKNKPVYV-----IDPHT 348
Qy 351 KEIIDLKQLENLESSSETKAQAMAKEEHTLLAEIKQLHKEREDRIWHLNIVASSQE 410
Db 349 AELNHLKQOVQOL-----QVLL----- 365
Qy 411 SQQDQVRVKKRKYVWAPKIQNSLHAGVSDPFMDLSRLPGNFKSKAKKSPDMSPEIDDS 470

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Db      366  -----LQAHG-----GTLPSIAAE-----PS-----362
QY      471  VCTEFSDDALSMMDNSGIDAEWNILASKVTHREKTSIHSMTIDFGIDSVGFHDSKE 530
Db      383  -----ENLQSLMEKN-----OSLVE-----ENE 400
QY      531  NOLQVLPKDSGDMAEGRKASFEKEITSLQOOLOSKEEKE-----LVQSFELKI 580
Db      401  KLSRCLSKAAGQTAQMLERIILTE--QVNEKLNALKEELHQAACKLIDQKLVETLEDQ- 457
QY      581  AELEEQSLVAKKLEMTNSRHSI--NAEVQTDVEKVEYVRKEMSVLGDSCGNASNDL 637
Db      458  -ELKEVEVEIICNLQOILTQSLDETVACTAAIDTAVEE-----AQVETS 501
QY      638  ODSSVQCKRLSSHDECIEHRKMLEOKIVDLEEFI-----ENLKKSNDPKQKSEDDPME 693
Db      502  PETSRSDDAFTTQH--ALHQAOMSKEVELNNAALKEALVKRMQNDNQ-----IQ 551
QY      694  SIQCEALMAKANAELALMRDNDNIILENETLKREIADLERST--KENQETNEPE 750
Db      552  PIQF-----QYQDNIKNLELEVINLQKEKEELVRELOQAKKANQAKLS 595
QY      751  ILEKETQKEHEAOL-----IHEIGSLKLVENAEVMTNLEEDLETKTKLKEQETQLA 804
Db      596  EHRKRLLOLEGOIADLKKKLINQOSKLLKKESTERTVSKLNOEI--RMKNQREVOL- 650
QY      805  ELERKADNLQKVRNFDLSVMDSEKICEIFOLKQSLSDADAVRDAQKESFPRSEN 864
Db      651  -MRQMEDAE-KRQW-----KQKRDKEVIQKE-----RDRKQO-----YEL 686
QY      865  LELKEKMDTSNNYNQKEKASLFEKQLETEKSNYKMEADLOKELQSAFNEINYINGL- 923
Db      687  LKIERNFQOSNVLRKTEBAANAKRKDALQKQEV-ADKRKEQOS-----RQME 737
QY      924  -LAGKPRDLISVLELKKVSEFSKOLEKALEKNALENEVTLSSEKFLPNEVECLKNO 982
Db      738  GTPAARVRLMGNIEVWVSTEEKRLHNDLEDRKLIADVVQKE-----783
QY      983  ISKASEIMLLKQEGHSASIIKQELIMOQSEQIOLLDVEVTHQSVKQOETEGYLM 1042
Db      784  -----KKSRENPPPKLKTFTFSLEVHGQVLESDDCIT--KOIESLETMEEL 829
QY      1043  KQMH-DLPEKYIRNKSSEADLRE-MENLKGTMESEVVKIADTKHELEBITRKEQLIH 1100
Db      830  RSAQIADLOQKLL--DAESEDRPKQCMENIATILEA--KCA-LXVLIGELVSSK--IH 880
QY      1101  EKKYFFQAMQTFPIPTPLSDSLPSPKLVESGNSODPIEINDYHNLIALATERNNIVCL 1160
Db      881  -----VTKLENSLRQSKASCADMQKML-FEBOHNFSEIETELQAEIVRMEQ 925
QY      1161  ERNSLKEOVIDLNTQOSLO--AQSIKES-----DLQPKQDLEEGV 1201
Db      926  QH--QEKVLYLVQLOESQMAEKOLEKASKEPEQVSTLQOQDELEKMEVCEQNO- 981
QY      1202  KULLEWELLKGHILTDQSLSEKLQLEN--LEVTEKLQTLQOEMKNTITERN--ELQTFP 1256
Db      982  QLLQEBEITIKQKLILOVASRQKHLNDTLSPDSFEVYIPRPKRSRYKEXKLEJBSMDI 1041
QY      1257  EDLK--AEHDSLKQDISENIEQSTETODE-----LRQAQEBELR-----EQQLV 1299
Db      1042  EBLKCYSEHSVNEHEDGDGDSDEADDEWKPTKLVKYSRKNIQCSCKGKGNKQC-- 1099
QY      1300  SFRQOOLDCSVGIS--SPNHDAVANQEKVSLGEVNSLO 1335
Db      1100  GCRKQKSDCGVDCSDPTKCRNRQQKSDSLGIVEQO 1136

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RESULT 10
 US-09-592-054-2
 ; Sequence 2, Application US/09592054
 ; Patent No. 6440684
 ; GENERAL INFORMATION:

```

; APPLICANT: Beraud, Christophe
; APPLICANT: Finer, Jeffrey
; APPLICANT: Sakowicz, Roman
; APPLICANT: Wood, Kenneth
; TITLE OF INVENTION: No. 6440684el motor proteins and methods for
; FILE REFERENCE: 1016
; CURRENT APPLICATION NUMBER: US/09/592,054
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1232
; TYPE: PR
; ORGANISM: Human
; US-09-592-054-2

Query Match      6.4%; Score 945.5; DB 4; Length 1232;
Best Local Similarity 24.6%; Pred. No. 9,6e-39;
Matches 372; Conservative 275; Mismatches 499; Indels 369; Gaps 61;

QY      3  EGDAYKVCVRVPLIORE--QGDQANLQWKAGNNTISQVDT-KSPNPDVFNHSHSTQ 59
Db      6  KQIPVRLRCPVLPKELSEGCQCLSFVCEPQV--VGTDKSFTYDVFVDPSTBOBE 63
QY      60  IYQELAVPLIRSRALQYNGTTFAYGQTSQKTYTMG-----TPNSLGIIPAIOEVF 112
Db      64  VENTAVAPLIKVFPGVNAVTALVAGQTSQKTYSGAVTAQENEPVGVPRVITQLLF 123
QY      113  KIQELPNREFLLRYSMEIYETVKDILCDRRKPLEIRDPFNKNRYVADLTIELVMY 172
Db      124  KEIDKSPFEFLTKYSLEIYNEIIDLCPREQAQINIRDPREGIKIVLTKETVLV 183
QY      173  PEHVQWIKKQKGNHYGSETKNDHSRSHTFRMIVSRDNDNTSENCGAVVSHL 232
Db      184  ALDTVSCIEQGNSTVSTASTANSSSRSHALITTSLEQKKSDKNS-----FRSKL 236
QY      233  NLVDLAGSERASQTAEGVRLKEGGINRSJLILQOVIKLSDQAGGFINYRDSKLTRI 292
Db      237  HLVDLAGSERQKTAEGGRLEKGINRGLICGNVISALGDDKKGAPVPRDSKLTRL 296
QY      293  LQNSLGNNAKYIYICTTPV--SPDETSLTQFASHTAGVNTPHVNEVLDLALKRYR 350
Db      297  LQDSLGGNSHTLMICVSPADSNLEETINTLRVADARKIKKPTVN--IDPQT----- 348
QY      351  KEIILKKOLELJESSSETKQAMAKEHTOLLAETKQLHKEREDRIHMLTNIIVASSQE 410
Db      349  AELNHLKQVOOL-----QVLL-----365
QY      411  SQODQVRKRRKRVTPAPKIQNSLHAGSVSDPDMLSRLPGNFSKAKFSPDPSPEIDDS 470
Db      366  -----LQAHG-----GTLPGSITVE-----PS-----382
QY      471  VCTEFSDDALSMMDNSGIDAEWNILASKVTHREKTS--LHOSMTDFQIDSVGFHDS 528
Db      383  -----ENLQSLMEKN-----OSLVENEKLSGLSEAAQTAQOMERIITWQOA 426
QY      529  KENQOLVLPKDSGDMAEGRK-ASFEKEITSLQOOLQOSKE-SEKKELVOSFELKIALEBO 586
Db      427  NE-----KNNAKLEELRQHAACKLIDQKLVETLEDKLENVEITICNLQOILTQSLDE 479
QY      581  ISVKAKNLEMTVNSRHSINAENVQTDVEKVEYVRKEMSVLGDSCGNASNDLQDSSVDGR 646
Db      480  -----TACMAAALDTAVQEAQVETSPB-----TSRSSDAFTTQHLYR 518
QY      647  LSSSHDECIEHRKMLEQKIVDLEEFIENLNK-SENDQO-KSSDDPFMESITQCEALIAE 704
Db      519  QAQSKRELVEINAKALAK-----EALARKMTQNDQLOPQIOYQYQDNI----- 561
QY      705  KANALEELALMRDNDNIILENETLKREIADLERLKNOETNEPELEKETQKEHEAOL 764
Db      562  KEPELEVINLOKEK-EEVLVELOQAKKANQAKLSERRRKLQLEGOIADLKKK----- 615

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Qy 765 IHEISLKLKLVENAMYNONLEEDJETTKLKEGEIOCLAEIRKXADLOKKVNRFDLSV 824
Db 616 LNEGSKLKLKKESTRITVSKLNOEL-----RMMKNORVU--MRQKEDAE--KFRW----- 664
Qy 825 SMOGSEKLCEEIIFOLKOSLSDAEAVTRDAOKECSFLRSEINELKEKMETSDTNWYNQKEKA 884
Db 665 ----KQKDKVEILOKE-----RDRKQ-----YELKLBNFQKSNVLRKTEE 706
Qy 885 ASLEPKOLETEKSNYKKMEADLOKELOSAFNEINYNLQ--LAGVPRDDLIRVLEKKV 942
Db 707 AAAANKRLKADLOKOREV-ADKRKETOS-----RQMEGTAAVRKMWLGNIEIVWYST 757
Qy 943 SEFSKOJEKALEEKNALENETVCTSEYKFLPNVEBCLKNQSKSAEELMLKQGEHNAS 10020
Db 758 EBAKHLNLDLEDRKITLQADVAQLE-----KKEGSENNP 793
Qy 1003 IISKOELIMQOSEOILQLTDEVTHTQSKVOOTEBOYLEMKMHDLPEKTYIRNKSEAD 10622
Db 794 KLRRRTFELTEVRQVSESDSIT-KQESLDETEHFFSAQIA-DLOQKLL--DAEED 848
Qy 1063 LLRE-----MENIKGTWSEVEXIADTKHELE--TIRDKOQLHEKKYF 11055
Db 849 RPKORWENIATILEKAKLKYLIGELVASKIQVSKLESLSKQTSKSCADMOKMLFEERNH 908
Qy 1106 FOAMQTFPIPTPLSDSPSKLVBESNQDPIEINDYNHLILATERNNIMVCLTERNSL 11655
Db 909 FAELIETEL-----QAEIWRNEQOHPERKV-----LYLLSQLOOSQMA-----EKOL 948
Qy 1166 KEQYIDINTQLOS-LQAOSIEKSDLOPKRQKQBLEGEVCLLEJEMELKHLTDSQUSIEKL 12244
Db 949 EESVSEKQOQLOSTLKQD---BELKKRREVCBOQO-QLLENEI IKOKTLLILOVASRQK 10004
Qy 1225 QLEN--LEVTEKLQTOQEMKNITIERN--ELQTFEDLK-----AEHDSLKODLSE 12722
Db 1005 HLPRDTLLSPDSSEFYVQPRKPKRKYVEKFLQESMDIEDLKYCSBHSVNEHEDGDGDDDE 10644
Qy 1273 NIEOSIELQDELRAPAOEFLR-----EQQQLVDSFQOQLDSCVQ--ISSPNHDAVANO 13233
Db 1065 GDDEEMWPTKLVNYSRKNIQOCSCGKMGNNQOC--GCKRQKSDGVDCCDPTKCRNRQO 11222
Qy 1324 EKVLGEVNSLOSEMLRGERDELQTSKALVSELELRAHVKSGENLEITTKLNGLEK 13633
Db 1123 GKDSLGVVERTQ-----DSSESRK-----LE-----DTEVTGSLFFNP 11577
Qy 1384 ELICKSESEVILKSM--LENLKE-----DNMKLEQAEEX-----SSKENOFSL- 14255
Db 1158 --VCATNRSKILKEMCDVEQVLSKTPRAPSFPDLPELKHVATREYGENKSGKKKKRALA 12155
Qy 1426 --EEVFSQSQKLVD 1438
Db 1216 SNTSFSGSCSPIEEE 1230

RESULT 11
US-09-595-684B-23
; Sequence 23, Application US/09595684B
; Patent No. 6544766
; GENERAL INFORMATION:
; APPLICANT: Berand, Christophe
; APPLICANT: Onashl, Cara
; APPLICANT: Sakowicz, Roman
; APPLICANT: Valsberg, Eugene
; APPLICANT: Wood, Kenneth
; APPLICANT: Yu, Ming
; TITLE OF INVENTION: Human kinesins and methods of producing
; TITLE OF INVENTION: and purifying human kinesins
; FILE REFERENCE: cytopo36
; CURRENT APPLICATION NUMBER: US/09/595,684B
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 09/295,612
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 23
; LENGTH: 1231
; TYPE: PRT
; ORGANISM: Human
US-09-595-684B-23

Query Match      6.4% Score 943; DB 4; Length 1231;
Beet Local Similarity 24.5%; Pred. No. 1,36-38;
Matches 376; Conservative 258; Mismatches 491; Indels 410; Gaps 60

OY 3 EGDAAKVCVVRPLQIRE--OGDQANLQMAKGNNTISQVDGT--KSFNFDVRVNSHSTSQ 59
DB 6 KGIPRVALRCPRLVPKKEISGCGMCCLFVPEPQV--VGTGDKFTFYDFVDPSTEQE 63
OY 60 TYQEIAPDIIRSAAGVNGTTPANGQTSGGKTYTMG-----TPNSIGIIPQAIQEVF 112
DB 64 VFNTAVAPLILKGVFQGNATVLAYQGTSGSKTYSMGCAVTAQENEPETGVIPRYQLLF 123
OY 113 KIIOEIPRREFLRSMVEIYNETYKDLLCDRRKKPLPIEPDFRNRYVALTELVNV 172
DB 124 KEIDKSDPFEFTLKVSYLEIYNEELIDLLCPGREAAQINIREDPKEGIKIVGLTEKTVLV 183
OY 173 PEHVLIWIKKEKKNRYHGETKMNDSHRSHTIFRMIVSRDNDPTNSNCGAVVSHL 232
DB 184 ALDPTVSCLEQGNNSKTVA STMSSSHALFTLSLQGGKSDKNS-----FRSLV 236
OY 223 NLVLDASGERASQTGAEGVRLKEGGINRSLFILQVITKSLDQAGGFINYRDSKLTRI 292
DB 227 HLVDLAGSERQKTKAEGDRLEKGININRGLLCLGNVIALGDGDKKGAPYRDSKLTRL 296
OY 293 LQNSLGGNAKTVIITCTPV--SPETSLTLOFASTAGHVRTPHVNEVLDDEALLKRYR 350
DB 297 LQDSLGGNSHTLMAICVSPADSNLEETLNTLRADRAKIKKPIYV--IDPQT----- 348
OY 351 KEIIDLKQOLNLESSSETKAQMAKKEHTLOLAETIKQLHKREDRIIMHLTIVVAASQE 410
DB 349 AELNHLKQVOQL-----QVLL----- 365
OY 411 SQODQVRVKRRVTPWAPGKIONSLHAGSVSPDMLSLPGNFSKAKKSPDMPSPPEIDS 470
DB 366 -----LQAHG-----GTLPGSLTVE-----PS 382
OY 471 VCTEBSDFDALSMDNSGIDAEMNWLASKVTHREKTS--LHOSMIDFQIISDVQPHDS 528
DB 383 -----ENLQSIIMEKN-----QSLVENEKLSGLSEAAQOTQMLERIIMTEQA 426
OY 529 KENLOQVLPKSGDMAECR-----KASEKEITSLQOOLQSKKEEKKVLVSFELKINEL 583
DB 427 NE-----KNNAKLEELRQHAACLDLOKIVETIDQEL---KENVEITICVLQOLITVL 475
OY 584 EEOLSVAKNLEMTNSREHSINAEVQDVEKEVEVRKEMSVLGDGVAANSNDLODSSVD 643
DB 476 SDE-----TYACMAAALDTVAEGEAVQVETSP-----TSRSSDAPFTQH 514
OY 644 GKRLSSHDECIEHRKMLQKIVLDEEPIENLANK--SENDKO--KSSQEDFMESIQLCEAI 701
DB 515 ALRQAKMSKELVELINKALATK-----BALARKMTQNDQOLOIQYOQONI----- 560
OY 702 MAEQAKNALEALMRDNFNIILENETIKREIADLERLKENQETNEFEILEKETQXHE 761
DB 561 ---KEPELEVINLOKEK--EELVLELOTAKKAKANOAKSEERRKRLQOLEGOIADIKKK-- 614
OY 762 AOLTHEIGSLKVLVENAMVQNLEEDLETKLLKEOEIOUAEILRRKADNLOKKVRND 821
DB 615 ---LNEGSKLLKLESTERTYVSKLNQEL---RMMKQORVLD--MRQMKEDAE--KFRQW-- 663
OY 822 LSVMSGSEKLCSEIFOLKOSLDAEAVTRDAQECSFLRSENLELKEKEMEDTSSWYNQK 881
DB 664 ---KQKRDKEVILQKE--RDRKRO-----YELKLLENFQOSVILRRK 702
OY 882 EKASLSFEKQLETSKNYKKMEADLOKELQSAFNEINVLNL--LAGKVPDDLSRVLE 939
DB 703 TEELAAANKRLKDALQKOREV--ADKRRKETOS-----RQMEGTAAARVVKWMLNGEILVM 753

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QY 940 KVVSEFSKQLEKALEKNALENEVTCLSEYKFLPNEVECLKNQISKASEITMLKQEGH 999
D 754 VSTEEKRHLNDLLEDRKILAQDVAQLKE-----KKESEEN 789
QY 1000 SASIISKOEIIWOESEOILQLTDEVTHTQSKVQOOTEBOYLEMKMHDDLEFKYIRNKE 1059
D 790 PPPKLRRTFFSLTEVRGOV-----SE 810
QY 1060 AED-LIREMENIKGTMESVEVAKIADTKHEL---EETIRDKEO-----LHLEK---KYFF 1106
D 811 SEDSITKQIESLETMEFRSAQIADLOQKLDABEDBPPKORWENIATILEAKCALKLYI 870
QY 1107 -QAMOTIPIITPLSLSPPSKLVESNODPIEINDYHNLALATERNNIWCLETERTNSL 1165
D 871 GELVSSKIQVSKLTESLSKOSTKSCADMOKML-FEERNHFAIETELQAEIVRMEOQH--- 926
QY 1166 KEQVIDLNTLOSLQAOASIEK-----SLOKPKODLEGEVYKL 1204
D 927 QEKVYLLSQLO--QSQMAEKQLEBSVSEKQOILSTLKCODELEKREVECEQNO--QLL 983
QY 1205 LEMELKGLHTDSQSLSEKLOLEN---LEVTEKLQTLQEMKNITTIERN--ELQTNFEDL 1259
D 984 RENETIKQKLTLLQVASHQKLPKOTLLSPDSFEVYQPKRPSRVAKELQESOMDIEDL 1043
QY 1260 K-----AEHDSLKQDLESENI EOSIETQDELRPAQBELR-----EOKVLDSFRQO 1304
D 1044 KYCEHSHVNEHEDGDDDEGDEEMKPTKLVNYSRKNIOGSCGKMGCKNQO--GCRKQ 1101
QY 1305 LLDGCVG-ISSPNHDAVANOEKYSLGENVNSLOSEMLEGERDELQTSKALVSELELRAH 1363
D 1102 KSDGCVDOCCDPPTCRNRQOGKOSLGTVERTQ-----DSBSFK---LE--- 1142
QY 1364 VKSEGENLEITTKLNLGEKEIIGKSESEVYLSKM--LENLKE-----DNKLKE 1411
D 1143 -----DPTVTPGLSPFN--VCATPNSKILKEMCVGEVLSKTPPAPSPDLPELWH 1194
QY 1412 QAEY-----SSKENQFSLEVPFSGQKLVD 1438
D 1195 VATEYOENKAPGKKKKRALKALASNTSFRSGCSPIEE 1229

RESULT 12
US-09-722-139-2
; Sequence 2, Application US/09722139
; Patent No. 6355471
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6355471el motor proteins and methods for
; FILE REFERENCE: 1055
; CURRENT APPLICATION NUMBER: US/09/722,139
; NUMBER FILING DATE: 2000-11-24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1375
; TYPE: PRF
; ORGANISM: Human
US-09-722-139-2

Query Match 6.1%; Score 906; DB 4; Length 1375;
Best Local Similarity 25.5%; Pred. No. 9, 5e-37;
Matches 413; Conservative 247; Mismatches 531; Indels 430; Gaps 71;

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QY 105 POAIQEVFKIOEI---PNREFLLRVSYMEIYNETVKDLCDDRKKP-----LEIREDEN 157
D 123 PRICEGLFSRINETTRWDASFRTEVSYLEIYNERVRLD---RRKSXTFLRVAREHAK 179
QY 158 RNYVADLFEELMVVEEHYIOWMKKEGKRNHGETMTDNHSSRSHTIF--RMIVSRDRN 215
D 180 EGPYVEDLSKHLVONGVDEBELMDAGNINRTTAAGMDVSSRSASHAIFTIKFTQAKPFSE 239
QY 216 DPTNSNCDGAVVWSHNLVDLAGERASQTAGEVRLKEGCNINRSLFTLGQVKKLSD 275
D 240 MP-----CE---TVSKHVLVDLAGERADATGATVRLKEGNINXSLVTLGAKKQV-- 289
QY 276 GQAGFINRDSKLRILONSIGNAKYIITCTIP--VSFDEITSLTQFASSTAGHVNT 333
D 290 -----FVPRDSVLTWLKDLSIGNSKTI MATISPAOVNGETSLTRVYANRANIN 344
QY 334 PHNVEYLDDEALIKRYKEILDLK-----KQLENTLESSSETKAQAMAKKEHTOL-LAEI 386
D 345 PTINEDANVK-LIRELRABEIALKTLTLLAQNOIALDPSPT-----ALSMERKLOQNEARV 398
QY 387 KQHLKEREDRIWHLNIVVASSQESQDQRYKRRRTWABGKIQNSIHASGVDPMLLS 446
D 399 QELTKEWTKN-WNET-----QNLKEQTL-----ALRKEGIG----- 429
QY 447 RLPGNFSKAKRSPDWPSPPEIDDSVCT-----ERSDPDDALSMND--SNGIDA 492
D 430 -----VLDSELPHLIGIDDLISGIIILYHKEGQTYVGRDASTEDQIVLHGIDL 481
QY 493 E-----WNLASKYTHREKTSLSHOSMIDFQGISDVQFHDSS-----KENOLQY-LRPDS 540
D 482 ESEHCIFENIGIYAT-LPLSGSQSVNGQVIVETHALNGQAVILLRTNMFRRNHKEA 540
QY 541 GDMACRCK-----ASPEKEITSLQOOLSKSEBEKELVQ-----SPELKLALEEQLSVK 590
D 541 AKLREKRSGLSSFSYSMTDL-----SKSRENLSAWMLNPGLEFRRORELEKLESK 595
QY 591 AKNLEMYTNSREHSHINAEOV--TDVEKEVVRKEMSVLGDGYNASNSDLODSSVDGKRSS 649
D 596 RKLIEEM-EBKQSDKALEMRQOEVEFQKKEITV-----QLO-----IR 635
QY 650 SHDECIEHRKM-LEQKIVDLBEFTENLNKSSENDKQKSSQDFMESIQICEAIAEKANA 708
D 636 KOESLSLRKRSFHIENKKDL-----LAEKEKEEERLEHQ----- 670
QY 709 LEEELALNRDNEFNILNETIKREIADLER--SIKENQOETNEFEILEK--ETQKEHEAOL 764
D 671 -QEIELOKRR-----QEEFTFLAVQEBLQRLKELNNKAEKQIFQEBLDQLOKEXDEOY 724
QY 765 IHEIGSLAKULVENAE---MYONLEEDLETK--TKLKEOEIOLEALRKRADNLOKV 817
D 725 A-KLELEKKRLEBOEKEQVWLVAHLEQULREKQEMIQLLRGEVQWVEEKR----- 775
QY 818 RNFPLSVSGDSEKLEIFQLKOSLS-----DAEATYRDAQKCSFLRSENELEKEMED 873
D 776 -----DLGIRBSLRLVAKARAGDEDEELEKQALRFFEFKRLQVLVLEKD 825
QY 874 TSNWYNQEKERAASLFEKQLETENSNYKMEADLOKELQSAFNEINYLNLGKAVPRDL 933
D 826 LVOQKDLKKEVQEOBIELECLCKEHDKESRLLEKXIDESVTD-----VTEVQDDE 876
QY 934 SRVLEKKYSEFSKQLEKALEKNALENEVTCLSE-----YFPLPNEVECLKN--QISK 985
D 877 KIRPVEYRLQYKERQLOQ-----YLLQNLPTLLEKORAFILDRGPLSLNNTLYOYER 930
QY 986 ASEEIMLKQEGHSAIISKOEIIWOESEO-----QILOLTQEVV---HTOSKYQOQPEE 1037
D 931 EMBE-----KEBOLAQYQANANOQLOKQATPEFTANLARQEKYRKKEK 974
QY 1038 QYLEMKMHDDLEFKYIRNKSSEADLLREMEVNLKGTMESVEVAKIADTKHE--LEETIRKE 1096
D 975 EILS-----REKQOREALERALARLERRSHALQ-----RHSTIGTEIEBOR 1016

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Db      1095 PLMDARINAYIE-----EVQRRLQDHLRVISEGCSADTMKDNKEXLHNGTIOBKLY 1148
Qy      1254 TNFEDLK-----AEHDSLKODLSENIEOSIETODEL-----RAAOBELRQK 1295
Db      1149 ELCRDLCLVLMPEPDAAACANHPLLQODL---VQJSLDMKTEIPDLVLPNGVQVSSKQOT 1205
Qy      1296 QLVDSFRQOLLDCSVGISPNHDAVANOEKVSLGEVNSLOSEMLRGERDELQTSCKALVS 1355
Db      1206 TLVDNI--YFLHGNMENVVP-----SLAEVQULLTYTVKMGDSGHDQCSQILV- 1251
Qy      1356 ELELIRAHVKSVE-----GENLEITKKNLGLK-----ELIGSESESV 1394
Db      1252 ---LNTHTIALVKECCVFPRIKRNIPRPAQDPVL-KCHALSEPRCVVPEKKNVSTV 1307
Qy      1395 LKSMLENIKEDNNKLIKQEAEEYSKEN--QFSLEEVPSGQKLVDEIVLKAOLKAABER 1452
Db      1308 ELVFLQKLKPSVSGSRNSPPEHLQEPANVQLFTTPLYLQGSQNVAP--EVMKLTJNSQDEA 1365
Qy      1453 L 1453
Db      1366 L 1366

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RESULT 14
US-09-721-689-2
; Sequence 2, Application US/09721689
; Patent No. 6440685
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6440685el motor proteins and methods for
; FILE REFERENCE: 1055
; CURRENT APPLICATION NUMBER: US/09/721.689
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1375
; TYPE: PR1
; ORGANISM: Human
US-09-721-689-2

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Query Match      6.1%; Score 906; DB 4; Length 1375;
Best Local Similarity 25.5%; Pred. No. 9.5e-37;
Matches 413; Conservative 247; Mismatches 531; Indels 430; Gaps 71;

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Qy      6 AVKVCVRVPLIQRGGDQAN--LQWKAGNNTISQV-----DGTKSPNFDVRF 51
Db      3 SVKVAVRVRPMNRKEDLEAKFLIQMEKSTITTNLIKIEGGTGDSGRERTXTFTYDSF 62
Qy      52 NSHSTS-----QIYQELAVPIIRSALOGVNGTIFAYGOTSSGGTTYMTGTPNSLGI 104
Db      63 YSADTSPRYVQSEMWFKLTGTDVVSAAFEYNACFAYGQTSYGSGSYTMGNSGDSGLI 122
Qy      105 POAIQGVFKIOET---PNREFLRVSYMEIYNETVKDLCDRRKKP---LEIRDEPN 157
Db      123 PRICEGLFSRINETTWDSEAFSTREYSYLEIYNERDILL---RKSSKTFPLARKREHPK 179
Qy      158 RNVYVADLLEELVMPENHYIOWIKKGEKRAHGETRKMDHSRSHTFI--RMIVESDRN 215
Db      180 EEPYVEDUSKHLVQNGVDVEELMDAGNIRRTAATGMNDVSSRSHAFITIKFTQAKPDS 239
Qy      216 DPTNSCNGAVMVSHLNLVDLAGSEBASQTAGEVRLKEGCNINRSIFLIGOVYIKKSD 275
Db      240 MP-----CE---TVGKIHVLDLAGSEBRADATGATGRLKEGGINVKSLLVTLGAKKKQV-- 289
Qy      276 GGAGGFINRBSKLRILIONSLGNAKTVITCTIP--VSPDELSTLQFASSTAKHAYNT 333
Db      290 ---FVPRDSVLNMLKDSLGNSKTIMIATISPADVNYGETLSTLRVYANRKAHNIIN 344
Qy      334 PHNVEVLDEALLKRYREIIDLK-----KQLENLBSSETKQAOMAKEHHTOL-LAET 386

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Db      345 PTINEDANVK-LIRELRARLAKTLLAQNQIALDSTP-----ALSMEEKLQONEAV 398
Qy      387 KQJHKEREDRIYHLNIVVASSQESQODQVRKRRRTVAPGKIONSLHASSVSPFMDLS 446
Db      399 QELTKEMTNK-WNET-----QNLKEQTL-----ALRKEGIG----- 429
Qy      447 RLPGNFSKAKSPDMSPEIDDSVCT-----EFSDFDALSMDP--SNGIDA 492
Db      430 ---VVDSELPHLIGIDDDLSTGILLYHLKEGQTVYGRDASTODIYVHJGLD 481
Qy      493 E-----WNLASKVTHREKTSLHQSMDPGQISDSVOFHDSS-----XENOLQY-LPKDS 540
Db      482 ESEHCIFENIGTIVT-LIPLSGSQCSVNGVOIVETHLNGQAVILLGTTNMRFPNHPXA 540
Qy      541 GMAEGRK---ASPEKETSLOOQLOSKBEKKELVQ-----SFLKIALFELQSLVK 590
Db      541 AKIREKRSGLISSLSLSTDL-----SKSRNLSAVALYNPGLEFFERQOREELEKLEBSK 595
Qy      591 ANNLEWNTSREHSINAEVO-TDVEKEVVRKEMSVLGDGYNASNDLQDSSVQGRUSS 649
Db      596 RKLIEEM-BEKQSKDAELERMQOEVETQKETEIV-----QLQ-----IR 635
Qy      650 SHDECIEHRKM-LEQKIVDLBEFFIENLNKKSSENDQKSSQDFMESIQLCBAINAERANA 708
Db      636 KOEESLKRSRPHIENKLDL-----LAEKKEFEERLRQO----- 670
Qy      709 LEELAMRDNFNNILLENETLKREIADLER--SLKENQETNEFELER--ETQKENEQOL 764
Db      671 -QEILQOKR-----QEBETFLRVQOELOKRLKELNNKAKRFQIFQELDLOKKEQOY 724
Qy      765 IHEIGSLKLVENAE---MYNONLEEDLETK---TKLKEQETQLAEIRKRNLDQKV 817
Db      725 A-KLELEKRLBEQKEQVWLVAHLEBQLRKQMIQILRRGEVQWMBEER----- 775
Qy      818 RNFDSVMSGSEKLCIEIFQLOKOSL---DAVAVTRDAQKESFTLRSENLEIKERMED 873
Db      776 ---DLEGREBLRKEARAGGDEGELEKAQRFPEFRQRQLVTKLVNLEKD 825
Qy      874 TSNWYNOKERKAASLFEKOLETEKSNYKMEADLOKEQASAFNEINYLNGLAGVPRDL 933
Db      826 LVQOKDLIKKEVQEGEILEBCLKCEHDKESRLKHEBSYTD-----VTEVPDPE 876
Qy      934 SRVLEKKVSEFSQLEKALBEKNALENEVTCSE---YKLPNEVECLKN---QISK 985
Db      877 KIKPEYERLOYKEROLO-----YLLQNHLPILLEKQAFELIDRPLSLDNTLVQVEK 930
Qy      986 ASEIMLKQGEHSASIIKQELIMQOSE---QILOLJDEVY---HTQSKVQOTEE 1037
Db      931 EMEB-----KEBOLAQYQANANOLQLOQTFFFTANIRAOEERKVRKKEK 974
Qy      1038 QYLEMKAMHDLFEKYIRNKSSEADLLREMENTKGTMESVEVKAIDTKHE-LBEITRDKE 1096
Db      975 EILLES-----REKQOREALERALARLERRHSAQO-----RHSJGTLELEBOR 1016
Qy      1097 QLHKKYFFQANQTIPIPIPLSDSLPSPKLVGSGNQDPIEINDYANLIALATERNNIN 1156
Db      1017 Q-----KLASLNGS-----SREDSGLQA 1034
Qy      1157 CLTERNSLKEQVYIDNTQLOSLQASIEKSDLOKRODLEBEV-KLLLEMLLGHJLT 1215
Db      1035 STEABQERALEKQDERLEVEIQOKKIKIYVDVQKHGHGTLBEKVASSSLPVSAAKSHLV 1094
Qy      1216 ---DSQLS--TEKQLENLEVEKLOTL-----QEEKNKTIITERNELO 1253
Db      1095 PLMDARINAYIE-----EVQRRLQDHLRVISEGCSADTMKDNKEXLHNGTIOBKLY 1148
Qy      1254 TNFEDLK-----AEHDSLKODLSENIEOSIETODEL-----RAAOBELRQK 1295
Db      1149 ELCRDLCLVLMPEPDAAACANHPLLQODL---VQJSLDMKTEIPDLVLPNGVQVSSKQOT 1205
Qy      1296 QLVDSFRQOLLDCSVGISPNHDAVANOEKVSLGEVNSLOSEMLRGERDELQTSCKALVS 1355

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Db      1206 TLVDM1--YFLHGNNEVNP-----SLAEVOLLTYTVKVMGDSGHDOCSLV- 1251
Qy      1356 ELELRAHVKSVE-----GENLEITTKLNGLEK-----EILGKSESEV 1394
Db      1252 ---LINTHATLVKEDCVFPRIIRSRNIPPPGAOFDTI-KCHALISERCVAVBEKKNVSTV 1307
Qy      1395 LKSMLENLKEDNNKLEKEAEYSKSEN--QFSLEEVSGSKLVDEIEVLKAQLKAEBR 1452
Db      1308 ELVFLQKLPKPSVGSNRNSPPEHIOEAPNVOLFTTPPLYLGSSQNVAP--EVLWKLTFNSQDA 1365
Qy      1453 L 1453
Db      1366 L 1366

RESULT 15
US-09-914-259-20
; Sequence 20, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 963
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-914-259-20

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Query Match 6.0%; Score 890; DB 4; Length 963;

Best Local Similarity 27.5%; Pred. No. 3.8e-36;

Matches 298; Conservative 196; Mismatches 343; Indels 246; Gaps 41;

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Qy      7 VKVCVRVPLQRE--OGDOANLQWKAGNNTISOVDGTSFNFDRVFNSESTQIYOEI 64
Db      9 IKVMCRFRPLNSEVNRGDKYIAKFO-GEDTV--VIASKPYAFDRVFOGSTSQEQVYND 65
Qy      65 AVPIIRSAOGVNGITFAIGQTSSTGKTYTMMG---TPNLSGIIIPQAIQVFKIQEI-PN 120
Db      66 AKKIYKDVLEGYNGTIFAYGQTSSTGKTHMEGLHDPEEMGIIPRIVODIFNYISMDEN 125
Qy      121 REFLLRVSMELVNETVYKDLLCDRRKRPLEIREDFNRNVYADLTLEELVMVBEHYIOWI 180
Db      126 LEFHIKVSYFELYLDKIRDL--DVSKTNLSVHEDKNRPVYVKGCTERFVCSPEDEYMDTI 183
Qy      181 KKGKRNRYHGETKANDHSSRSHTFPMIVESRDRNDPTNSENCDAVMVSHNLVDLAS 240
Db      184 DEGKRNRYAVATNMHESSRSHSIF--LINVQENQTEQK-----LSGLYLVDLAS 235
Qy      241 ERASQTAGAVRLKGCNINRSLFIIGUYIKLSDGAGCFINRDSKLTIRLQNSLGN 300
Db      236 EKVSITGAAGVALDEAKNINKSLISALAGST--YVPYRDSKMTIRILODSLGN 293
Qy      301 AKTVICTITPVSPD--ETLSLQFAPSTAKHVRNTPHNEVLDDEALLKRYRKEIIDLK 358
Db      294 CTTTIVICSPSSYNESETKSTLLFGQRAKTTIKNTVCUNVELLAQWKKRYEKE----- 347
Qy      359 QLENSESSETKAQAKEHTQLAEIKQLHKEREDRIWHLTNIYVASSQESQODORVK 418
Db      348 -----KEKNILKNTIOWL--ENELNMRNGETYPIDEQFDKEKANLE 388
Qy      419 R---KRRVTWAPGKIQNSLHASGVSDPDLSPGNFSKAKAFSDMPSFPEIDSVCTEF 475
Db      389 AFTVDKDIT-----LTNDKPATAIG-----VIGNFTDAER-----RKCEBEIAKLY 429
Qy      476 SFPDALSMDNSGIDAEWNLASKYTHREKTSLSHOSMIDFGQISDSVQFHDSSKENQLO 535

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Db      430 KQLDK-----DEEINQSOQLVERKLT-----QMLD-----QEBLLAS 462
Qy      536 LFKDSGDMAEGRKASFKEKITSLQOOLQSKKEPKKELVOSFE---LKTALKEEOLSVKAK 592
Db      463 TRRDQNM-----QAEINRLQAEENDASKKEVKEVLQALEELAVNYDQSKQOEVEDTK 514
Qy      593 NLEMYTNSREH-----SINAEVQ-----TDVER-----EVRKENSVLDSGYNANSNDL 637
Db      515 EVELLSDELQNSATLASIDALQKLEKNTNQQKRAEMMASLKLDALEIATAGNNDV 574
Qy      638 QDSVVDG-----KRLSS-----SHDECTEHRKML----- 661
Db      575 KQEGCTGMIDEEFTVARYLYISPKKSEVKTMYRCKQLESTQTESNKKMEENEKEILAACOL 634
Qy      662 -----EQKIVDLEEFTEFNKKSSENDKQSSQODMESIQCEALMAEKANLLEELALMR 716
Db      635 RISQHBAKIKSLTEYLQNEQK---KQLESVDALSEELVQLRAQEKVHEME-----K 685
Qy      717 DNFNIILENETLKEIADLERSLKENOETNEFEILEKETQKHEBAQLIHEIGSLKIVE 776
Db      686 EHLNKVQTADEVKQ---VEQIQSHRETHQOI-----SSLRDEVAKAKLIT 731
Qy      777 NAEWYNQMLEEDLETKLKLKEQEIQLAELRRADNLQKVRNFDLSVSMGSEKLCDEI 836
Db      732 DLQDQNM-----MLQERLVEHEKLTQDOEKSRKLTHELTVWQDRREQARODL 782
Qy      837 POLKQSLDAEAVTDAQKESFLRSENLEKXNE---DTSNMYNQKKAASLFEKOL 892
Db      783 KGLEETVAKELQTLNLRK--LFVODLATRVKKSADISDDTGSGSAQOKK-ISFLENNL 839
Qy      893 ETEKSNYKKM---BADLOKLOSAPNEINLYUGLAGKVPRLDLSRVELEKTV---SEPS 946
Db      840 EQLTVYHQVLVDNDLRCLEP-----KLEKRLRATAEV 874
Qy      947 KQLEKALEKXALENEVTCLESEYKFLPNEVECLKQISKA-----SEEIMLLQKQEGH 999
Db      875 KALESALKE--AKENASRDRKRYQ---QEVDRIKAVVSKMMARGHSAQIAKPIRPGH 929
Qy      1000 SAS 1002
Db      930 PAA 932

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Search completed: October 22, 2003, 21:12:54

Job time : 66 secs

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Db      964 -----LATERK--VTSLEKSRDSPKVVADIMNOIGELAFVSCBETIDTLKQELKDIN 1016
Qy      1201 VK---LLLENEBLKGHLTDGQSLSEIKQLENLEVENTKQTLQI0EBMKNTIERNLQTNFE 1257
Db      1017 CKYNSALVDRE-----ESRVLTKQEVILDLKETLR-----LRIlse 1054
Qy      1258 DLKAHSDLSKQDLSSENTEQ-----SIETODELRAAOEELREBQKOLVDSRQOLDCSV 1310
Db      1055 DI--ERDMCEDLHAATEQMLMLTEASKKSGISGLQSQOEBELTKREALIOELQKTL----- 1107
Qy      1311 GISSPNHDVANAQDEKVALGEVNSLSQESMLRGERDELQTSKALVSELELLRAHYKVSVEGE 1370
Db      1108 -----NQKK-----EVEBQKREYVFKRKQL-----EHVMSAAE 1137
Qy      1371 N-----LEITKLNGLEKEELIKGSESESVLKSMLENKEDNNKKE--QAEYS 1417
Db      1138 DPOKPTPPHPQTHLAKLELETOEOEI----EDGRASSTSEHLVTKLNEDEEVKNAEILR 1193
Qy      1418 SKENQFSLSEVFFSGSQKLVDEIVTLKQALKAABERLTKRDYDELQOTAN----- 1468
Db      1194 MKBOLREMEINRLRESQOLIEKNMILLQOQLDDIKQOKNSDQNHQDNOQLKNEQSESTIKER 1253
Qy      1469 ---TNLVEGKLETPLOQADHEEDSIDRSESEMEIKVLSEKLERNGYLLERLOEEXLELSNK 1525
Db      1254 LAKSKIYEEMK--MKADLEEVQSAVLNKKMECECRMIDDEVERTQTLSSKAFQEBEQJRSK 1311
Qy      1526 LEIIOKEMETSVLLKDDLOQKLESLSEN--IITKENIDTTLKHSSTQAOAQKTOELO 1583
Db      1312 LEEVYERERERTSQEMEMLRKQVECLAENKGLVGHQNL-----HOKIYVVRKKEENVR 1365
Qy      1584 LAKNLAIASDNCPIIOEKETSA 1606
Db      1366 LAETEKLRANVFLKEKRSES 1388

RESULT 2
US-10-171-311-4
; Sequence 4, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatc, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoersch, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; FILE REFERENCE: OF CERVICAL CANCER
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 3899
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-171-311-4

Query Match 6.9%; Score 1015; DB 15; Length 3899;
Best Local Similarity 19.6%; Pred. No. 1,5e-43;
Matches 700; Conservative 630; Mismatches 1164; Indels 1072; Gaps 148;

181 KKGKNEHYGCTKKNHSSSHITFRMIVBSRDRNDPTSNBDCGAVMVSHLNLVLDLGS 240

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Db 34 KQOKKR---KTSSEKHDSAHNDLIDSOQCNEMWYNSSQVSESTVPESTIMTLTSG 90
Qy 241 ERASQTGBGVRLK-----EGCN--INRSLFIIQVYIKLSDOAGGFIVRPSKLT 291
Db 91 EITSHOQFSVLBESEISTTADCSSEVNGCSFVM-----RQKPTN 132
Qy 222 ILONLGNNAKTVIICITTPVSFDETLSTLOFASTAKHVRNTPHNVENLDEALLKRYK 351
Db 133 LREBEFG-----VDDSYS-----EQAGDPSFTHLMMESLAGKH-- 169
Qy 352 EILDKCOLNLESSSETKA-----QAMAKEH---TOLLAETIKOLHEKEDRIWHLT 401
Db 170 EIEELNRELEBMRVYGTGLOQLOEFELAIKORNGIITQLTANIQAARREDEMTREPL 229
Qy 402 NIVASSQESQODQVKRRVTPAPGKIQNSLHAGVSD-----FDMLSR 447
Db 230 EL-----TEOSQKLOIOFOOLOQASETLRNSTHSTADLLQAKQOILTHOQOLEODH 282
Qy 448 LRGNSK-----KAFSDMPSPFEIDSVCTEFSDDDLMSMDSNGIDAE 493
Db 283 LLEDYQKKEDFTWQISFLQEKIKVYEWQDKKVENSKKEIOEKETIIEELNTKIEBE 342
Qy 494 ---NLASKVTHREKT--SLHOSMIDFGQ-----ISDSVQFHDSSKENLOYLPRXS 540
Db 343 KKTLELKXLTADKULGELQEQIYQKQOIKNMKLELTNSQKXROSSEILKOLM---- 398
Qy 541 GDMACRK---ASFKEKITS--LOQOLOSK--EBEKKEIVOSFELKIAELEBOL--SYKA 591
Db 399 GTVELQKRNHNDQSOFETDIYQRMEOQTORKLEQRAELDEMYGQOIYQMKELIRQMA 458
Qy 552 KNLBNVTR---EHSINAEVOTDYEKVENKEMSVLQDSGYNANSNDLODSVNGKLS 648
Db 459 QMEKTKHKKEMENALRSYSNITVNEQIK---LNMVAINELNIKQDTNSQKELK 513
Qy 649 SSHDCIHRKMLJEOKIVDLEEFENLNKKSSENDKQKSEODFM-----ESTIQLEATA 703
Db 514 EELGILBEKCALQOLEDVLELFSRQIOIRAQOTIAEDSKLNEAKHKSISTYEDKA 573
Qy 704 EKANALE---ELAL-----MRDNFNDIILENTLKEIADLER----- 738
Db 574 EIVSASESRKELELGHBAEVNTYKIKLEWLEKKAVALDRMAESQE--ALELRLTQLLFS 632
Qy 739 ---SLKE-----NOTNEPELL--EKETOKEHE 761
Db 633 HEEELSKLKEDELEHRIINIEKLDKNLGIHYKQOIQDQONEMSQIKETMQFEKMLITQ 692
Qy 762 AOLIHEISLKLVLNAEMYNQNLBE-----DLETKTLYKE-----OEIOL 803
Db 693 NOLILEISKLDLOOS--LVNSKSEMTLQINELQKEIFILQOEKEKKTLEQOVBOL 750
Qy 804 ---AELRKADNLOKKVRNFDLSV--MGDSEKLCEBIFOLKOSLDAEAV----- 849
Db 751 KTELLEKQMKKENDLOEKFAQLAEANSLIKDEKTLDEMLKIHHPVSGEBLLIFLDSIK 810
Qy 860 ---TRDA--QKESCFRSEN-----LEIKEMERTSNWYNQKQKQASLFEQOLETSKN 898
Db 811 SKSKOSVWEKEIIEENEDLKQOQIOLNEIEIKQRYNFSFAEKNFVYEOLEBYAC 870
Qy 899 YKKMADLO---KELQ---SAFEINYLN----- 921
Db 871 LLKXVDLEDSKNOLEKYSKLYALNEBHLQRIINPTTVKXKSVFDEDKTFVATLTM 930
Qy 922 GLLAGKVERDYL-----SRVELEKVSFESKOLEKALEKNALENEVTLSSEYK-- 970
Db 921 GEVVEKOTTELMEXKLEVTKREKLEISQRLSDSEQDKQNGEISFLNEBVKSLKQEKQV 990
Qy 971 -FLRNEVECLK-----QISKASEIMLLKQEG--EHSASITISK----- 1006
Db 991 SLRCELEIITINHNRAENVQSCDTQVSSLLDGVVMTSGAGSVSKVXKSGEBSKIMV 1050
Qy 1007 ---OEIINOGESEO---ILQLTDEVTHNQS--KVQOTEQOYLE-----MKXNHDPLF 1050

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Db 1051 EDKVSFENMTVGEESKQEQILDLHLPSVTKESSLRATQPSENDKLOKELNVLKSEOND- 1109
Qy 1051 EKYIRNKSEAE-----DLRE--MENIKT-----MESVEKTAIDTKH 1086
Db 1110 ---RLQNEAORICLSLVSTHVQVREYMEKQKALCSLKEELIFAQOEKIKLOKIH 1165
Qy 1087 ELE-ETIR-----DKEOULL-----EKKYFQAOQTIPIPIPLSDSLPPSKLV 1128
Db 1166 QLELOMTQOETGBGKRLHLILGKLOKQAVSEBGSFYQTLQSV-----LGEYTPALKC 1220
Qy 1129 EGNSDQPIEINDY-----HNLLALATERNNIMVCLET----- 1160
Db 1221 EVNAEDKENSQDYISENDEPELODYREVOPQOEMWHTLLNKVTEBYKKLVLOTRLSKI 1280
Qy 1161 ---ENSLKEQV-----IDLNTOLOSLQOISTEKSLOKPK 1193
Db 1281 WGOQTDGKMLEFGEENLRKEETEPFLSIHSQMTNEDIDVNHKSKLSLQDEKTYLEQV 1340
Qy 1194 ODLE-----EGEVKLLLEMLKGHU-----TDQSLSI 1221
Db 1341 QLEBLSLSLOOQLKETQNTQNAEHLICLOKRLQAVSESTVPSLPVDSVVTESDAQRTM 1400
Qy 1222 ---EKLQLENLEVTEKLOTLQOEMKNITL-----ERNE 1251
Db 1401 YPGSCVKKNIQDITIEFSGEFGVKEETINIVKLEKQOQLEBEVAKVIVMSIARAQOTE 1460
Qy 1252 L-----QTNFEDLKAENDSLKODLSENI EOSIETPODLBRAQ 1288
Db 1461 LSRISGKENTASSKQAHAVCOOEQHYFNEKLSQDQOGFOTFETVD--VVRKEFKPLS 1518
Qy 1289 EELREQ--KQVDSFRQ-----QLDSCVGIS---SPNHDVANO--EKVSLGEVNS-- 1333
Db 1519 KELGHEGKEIILSNSDPHDIDESKDCVLTIEBMSKSKTPIVROSHIDEISVSSMDSR 1578
Qy 1334 ---LOSEMLRGEDELQTSKALVSELELR--AHVKSVEGENLEITTKLNGLEKEILKS 1389
Db 1579 QLMNEBQLEBMRQELVAYQOEHQATELLROAHMRQNE-----RQ 1619
Qy 1390 ESEVYLKMLNENKDNKKLEQOAEYSSKENQPSLEVPFGSQKLVETIYKALQKLA 1449
Db 1620 REDQ-----BOLQEIIRLROLAORSSINENIYVSE---REVLRLBELALKQSLAG 1670
Qy 1450 EERL--EIKDRDYELVOTANTNLVEGKLETRPLADHEDSDIRRESEMEIKVJGEXLER 1507
Db 1671 REKLCCETLNNSS---TOTQNGENQGEVE--BOTFEKELDKREVPPEILSNF--- 1720
Qy 1508 NOYLLERLOEBKLELNKLEILOKEMETSVLLKD-----LQOKLESLSENIILKE 1559
Db 1721 -RYALQKAN-----NRLKITLLEVVKTTAAVEETIGRHVGLIDRSSKQSSASLIVRS 1773
Qy 1560 NIDTTLK--HNSDTQALQK-----TOBELQAKVL--ALIAS 1593
Db 1774 EAELASVKSCHVEHTRVDESIPSYSGSDMPRNDIMMSKTEBETELSORLVNSGFAGT 1833
Qy 1594 DNCPIQOE-----KETSADCVHREKILLTTELXOKTNEOKL 1633
Db 1834 EIDPENELMNISSRLQAAVEKLELAISETSQLEHNAKVTTQTELMRSFPOKQOATSL 1893
Qy 1634 ---LHEKNEL--EQAOVELKCEVENLKMMSITESKSLSELSOHEKHD---TEOOL 1679
Db 1894 KQOEBLRLRLBESARQOVLAVELS--KAEVIGDQADBKTLFEPHQIOKTDIIDLREBEL 1952
Qy 1660 LALKQOMQVTOEKKELQOTNEHLTAEVDHLKENIELGLNFKNEAQOKTTQECSLLENK 1739
Db 1953 LCASNRLOELBAQOQIOEBRELLSROKEMAK--AEAG-----PVEOQLODTE 1999
Qy 1740 ELESQNRHLOCEIEELKMSLKDKSALETLKESEQKVNILNOEMEMWMLMEBELKNSQRT 1799
Db 2000 KLMKEKLEVOQOAEVVRDLOQVAYALE-----IDVEQVSR--FIELBOEKNTBLM 2049
Qy 1800 VIAERDQLODRLRESVENSJETODLRKAOELAQOKXQVOLTQSULV----- 1849
Db 2050 DLROQNALERKOLEMKRKFLEQOALDRNEHNDVFOQ--EIQKLEQOLKVVRFRPQISHO 2107

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QY 1850 OEKISLLENQMLYNVATVETLSERDDLNQSKHLPSEIETLSLSEKEFAL----- 1902
DB 2108 TREVGEOLANHLKEKTKSCSELBSLSEQLOBDIOERNEIEKLEFRVRELEQALVDRKH 2167
QY 1903 -----EOAEDKXDAARKTIDITEK-1SNEBOLQOATNLKETLYEREL-1QCKE 1952
DB 2168 FGAVEAKPELSLEVOLOAERDAIDRKEKETTNEBOLQEREBLENKNEVEOQALHQLBI 2227
QY 1953 QALANTEHRETLKSDLALGKME-----OERDEAKVIALTEKMSLSE 1998
DB 2228 OKKESSTRLOELEQENKLEFKODMEKGLAIKESDANSTODQVLFKGFQOITOEKVEID 2287
QY 1999 QINENVTTLKEGSEKETFYLPORPSQOSSQMEELRESIKTDQLE-----E 2047
DB 2288 QINEQVTKLO-----QOLKITTNKVIIEKNELLRIDLEQIECLMSDOECVKEN 2336
QY 2048 AEKISEATNEIKNLTAKISSLEBEILQNASILNEAVSERENIRHKKOQVSE--LEQ- 2103
DB 2337 REBEIEQLNEVIEKLOOELANIQKTSMAHSLSE--EADSLKHQLDVIAIEKALBEQO 2393
QY 2104 -----LSUTLSRDBAFAO-----SKREDEAVNKIASLAE-----IKITK 2141
DB 2394 VETANEEMTPMKVNLKETNFKMNQLOEILFSLKRE-ESVEKIQSIPENSUNVAIDHLK 2452
QY 2142 ENDEF-----RDSKESLOEQSSHLSE-----LCTYKTELQMLKOOKEDINNKLAEKVY 2190
DB 2453 DKPELEVVLTEDALKLENQTYFKSPENGKGSINLETRILQLESTVSAKDELELOQVY 2512
QY 2191 EV-----DELLO-----HLSLKEQ-----LDQIOMELRN----- 2216
DB 2513 QIKMOEQOFETEMLOKKIVNLOKIVEEKAALVSOILOEVAOYAKFCODNOTISBE 2572
QY 2217 -----KLKNVLECEKMDIMEKISVLRMQNEP-----OOEEDVAERMILBS 2260
DB 2573 PERTINQNLQLEDEGDISALTRISELOVAMTSLILEQOYEIAK-NVLEK 2631
QY 2261 RNO--EIOELMEKISAVSEBHTLLSLSSELOKETEAHNGMLNIKESLSTLSRFS 2318
DB 2632 EKKLELOKLLENENEKKEKKEKSPDVEVLKTTTELPH-----SNBESGFNELBA 2685
QY 2319 LQTEHVKLNTQLOTLINKRVVTRTAAYEDH--SLIKYE--KDLAAEK-----RH 2367
DB 2686 LRAESVATKAEILASYEKAEKLOEBLLVETNMTSLQKDSQVRDHAIEKEXLSLEKE 2745
QY 2368 DELRLD--LOCL--BOHGRKMSDSASEE--LKFEIEFLNLTFKKANIISVODDS 2419
DB 2746 DEVEVESKAKACFEPLPKLSKISASQTDGTIKISSNOTPOLVKNAGIQINLOSSES 2805
QY 2420 --EVQVFLNQVSTLOELEHKKGMQMLEFGDLHVDAKLSSEGMOENRIAST-- 2473
DB 2806 SEEVTEIISO-----FTEKIEKQELHA-----AEIDMESRHISSETJLK 2846
QY 2474 -----IOLLTKR--LKAVVO-----SKI-----QREIT-----VY 2496
DB 2847 REHYAVAVOLLKECGTLKAVIQCLRSKESGSIPELAHSDAYQTRICSSDGSQWQGIY 2906
QY 2497 LNO--FEAKLOEKKEON-----KELMRHEHGPSA-----SW 2528
DB 2907 LTHSQFDLASBERGSESATDSFKKIKGLIRAVHNSQMVLSTLESPIYSGEDHSIQ 2966
QY 2529 E-----ENARLLGLIKTVODESKLQSRIKMLENELNLVKDAMH-----KGEKVAI 2576
DB 2967 QVSEPLERKAYINTISSKDLITKMO-----LQREAEVYDSSQGHESPSDMRGELL 3021
QY 2577 LODKLI-----SRNAEELNAMOYKLTKKODNIQAMK----- 2609
DB 3022 LOQVLEERSVLLAARTEIYALGTDAVGLNLCBRIQOEQVEYOAMECLOKADRS 3081
QY 2610 -----EIEENLOKMAKAGVAYKEID-----NLKTK-----VVKIMEKIKYSKAT 2650
DB 3082 LLSIEIALHAKONGKRITTLKREBOESEKPSOELLLEVNIQOKOSQMLEMOVELLSMK--DRAT 3140

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QY 2651 DOIETVYKSCDEKKEGRLKEEDLRPAODNTTVCPKDYOKASTPPTCGGSGIYO 2710
DB 3141 E-----LOEQLSSEKQVVAELKSELQOTKLEIETTLKQKHKL----- 3179
QY 2711 STAMVLQSEKALRELSHYKKKYHHL.SRTMSSEDR-----KTKAKSDAHSSHT 2762
DB 3180 -----ELEAFLEVKDKTDEVLHNDTILASQOKSRELQMLKEKAK-----L 3223
QY 2763 GSHRSGPHKJETYRNG--PVTPERSEMPSLHSGPKSESSYKRVVSPNRSEIYQVWS 2821
DB 3224 GRSEERDKREELDLKFLSLESQQRNLQNTLLLEQOKOLNIESQOKIESQRMLYDAQLSBE 3283
QY 2822 PGKTGNHKLILSPSYGVLHKKRALSPNSENPTQVIVISPKTGLKNTLSTLFPNLSSP 2881
DB 3284 QGRNLEQVLESEFEYRIREMSSTIDRRRELHAQLOQSDGTQSGRPPPLESDLEKLOKO 3343
QY 2882 C--KOQVOENLN--SPKGLFVRSK 2904
DB 3344 LEEKSRIVEELNTEKTKLDSLOTR 3369

RESULT 3
US-10-171-311-8
; Sequence 8, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamackar, Shubhangi
; APPLICANT: Glatz, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoersch, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 3917
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-171-311-8

Query Match 6.9%; Score 1015; DB 15; Length 3917;
Best Local Similarity 19.6%; Pred. No. 1.6e-43;
Matches 700; Conservative 630; Mismatches 1164; Indels 1072; Gaps 148;

181 KKGKRNHYGETKMDHDSRSHTIFRMTVESRDRNDPTNSGCGAVWVSHNLVLAGS 240
DB 34 KKQKKR--KTSSSKHVSAHDLNIDQSCQENMYINSQVSESTVPIPESTIMTILHG 90
QY 241 ERASOTGAEGVRLK-----EGCN--INRSLLFLLGOYIKLSDQAGGFINYRDSKLT 291
DB 91 EITSHQGSFVLESEISTTADDCSEVNGCSFV-----RKGKPTN 132
QY 292 ILQNSLGNNAKTVIITTPVSPDETTLQLOPASTAKHVRNTPHNEVUIDDALLKRYK 351
DB 133 LIREEFQ-----VDDSYS-----EOGQDPSPTLHWNESLAKOH-- 169
QY 352 ETLDLKQOLENLESSETKA-----QAMAKEH--TOLAEIKQJHKEDEIRIMHLT 401
DB 170 ETEBLNRELEEMRVYTGIEGLOQLOFEFAIKQDGIITQLTANLQOARREDETREREL 229

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QY 402 NIVASQESODORVYKRRBYTMAPGKIONSLSHASGVSDF-----FDMLSR 447
 Db 230 EL-----TBSQKLOIOPOLQASSETLRNSTHSTAAIDLQAKOQIITHOQOLEBQH 282
 QY 448 LPSNFSK-----RAKPSDMSFPEIDSVCTERSFPDALSMDNSGIDAE 493
 Db 283 LLEDYQKKEDFTMQISFLQEKIKVYEMBODKKVENSKNBEIQEKTEIIBELNTKITEBE 342
 QY 494 ---WNLASVYTHREKT--SLHOSMIDFGQ-----ISDSVOFHDSKXENOLQYIPKOS 540
 Db 343 KKTLEIKDCLTTADKILGELQEOIVQKNQIKMKLELTSKOKEROSSEBIRKQLM----- 398
 QY 541 GMAEBCRK-----ASPEKEITS--LOQOLQSK--BEEKELVQSPFELKIALEBQL--SVKA 591
 Db 399 GIVEELQKRNKHSOPEBDIVORMEBOTQRKLEQLAEIDEMGGQIVOMKQEBLIRQHMA 458
 QY 592 KNLWAVNYSR---EHSINAEVOTDVEKEVYVRKEMSVLGDGYVNASNDLODSSVDGKRLS 648
 Db 459 QMEBKTRHKGEMENALRSYSNITVNEDOI-----LNMVAINELNLIKLODINSQEKJL 513
 QY 649 SHDECIEHRKMLEOKIVDLEEFITENLNKXSENDKOKSSEODPM-----ESTQLCEAIVA 703
 Db 514 BELGILIEKCALORQLEBDLVEELSPSREQIORARQTIAOESKLNLEAKHSISTVEDLKA 573
 QY 704 EKANLE---ELAL-----MRDNFNITILENELLKREIADLER----- 738
 Db 574 EIVASVESRKELELHGEAEVTVYKIKLEWLEKKAVALDRMAESQE-ALELEIRFQOLFS 632
 QY 739 -----SLKE-----NOETNEFEIL--EKETOKEHE 761
 Db 633 HEEELSKLDEDEIEHRIINIEKLNGLIHYKQOIGLONEMSOKIETMQPEKDNLITQ 692
 QY 762 AOLIIEIGSLKLVNAENMYNONLEE-----DLETKYLKE-----OETQL 803
 Db 693 NQIIEISIKLDOLOS--LVNSKSEEMTLQINELQKEIILROEKEKGTLEBOVEOQL 750
 QY 804 -----AELRKADNLQKVRNFDLSV--MGDESKCEIIFOLKOSLSAEAV----- 849
 Db 751 KTELLEKQMKKEENDLOEKFQALEANSILKDEKKTLEMDLKIHPVSOEELIFLDSIK 810
 QY 850 ---TRDA--QKESPLRSEN-----LELKEKMEPTSNMYNOKEKASLFEKOLETEKSN 898
 Db 811 SKSKSVWEKEIILIEBENEDLKQOCIOINEIEKORNTFSFAEKKNFEVYQELOEBYAC 870
 QY 899 YKKMEADLO-----KELQ-----SAFNEINYLN----- 921
 Db 871 LLKVADLEDSSKNQOLEYKSKLKALNEELHLQRIINPTTVKMKSVFDEKTFVAETLEM 930
 QY 922 GILLAGVPRDL-----SRVELEKAYSEFSKOLEKALEKMALENEVTLSEYK-- 970
 Db 931 GEVVEKDTTELMKEKLEVTREKTELSEQRSLDSEQLKQKHGBISPLNEKVSILKQEKQV 990
 QY 971 -FLPNEVECLKY-----OISKASEEIMLLKQEG--EHSASITSK----- 1006
 Db 991 SURCELEIILINHAENAVQCDTOVSSLLDGVVNTTSRGAIGSVSKVXKSGESKIMV 1050
 QY 1007 -----OELIMOQSEQ--ILQITDEVHTOS--KVOQTEBOYLE-----MKKMHDLF 1050
 Db 1051 EDKVSFEMMTVGEESKQEBQLILDHLPSYTKESSLATOPESENDKQKELANLVKSGONDL- 1109
 QY 1051 EKYINKSEAE-----DLIRE--MENLKGT-----MESVEVKIADTKH 1086
 Db 1110 ---FLQWEAQRICLSLVSTYHVDQVREYMEKDKALCSLKEEILFAQEEKIKELQKH 1165
 QY 1087 ELE-ETIR-----DKQOLH-----EKKYFQAMQTIPIPIPLSPSKUV 1128
 Db 1166 QELQETMTQOETGDEGKPLHLILIGLKQKAVSEECIFLQTLCSV-----LGYVYPALKC 1220
 QY 1129 EGNSSODPIEINDY-----HNILALATERNNIMVLEF----- 1160
 Db 1221 EYNADDEKMSGYISBENDEPELODYRYVEQDFQEMNHTLNLKVTEBYNNKLVLQTRLSKI 1280

QY 1161 -----ERNSLKEQV-----IDLNTQLOSLQAOISIEKSDLOKPK 1193
 Db 1281 WGOQTDKMLFERGEBNLPRKEETEPFSLSHSQMTNLBEDIIVNHKSKSLSDLEKTLKEBYV 1340
 QY 1194 QDL-----EGEVKLLLEMLLKGHL-----TDSQLSI 1221
 Db 1341 CELESILISLOOQLKETEQNVEAEIHCLOKRLQAVSESTVPSPSLPVDSVVTIESDAQRTM 1400
 QY 1222 -----EKLQLENLEVENTKLOLQOEMKNITI-----ERNE 1251
 Db 1401 YPGSCVKNINDGTIEFSGEFGVKEETNIVKLEKYOQOLEEYVAKVYSMSIAPAQOE 1460
 QY 1252 L-----OTNPFEDLKAEHDSLKQDISENIEGSIETODELRAAO 1288
 Db 1461 LSRISGKENTASSKQAHAVCQOEBQHYREMKLSODQIGFOYFETVD--VKRKEEFPKLS 1518
 QY 1289 BELREQ--KQVDSFRQ-----QLDSCVGIS----SPNHDAVANO--EKVSLGEVNS-- 1333
 Db 1519 KELGEHKEIILSNSDPHDIPESKDCVLTISEMFSKDKTFVRSIHDEISVSMDSAR 1578
 QY 1334 ---LOSEMLRGRBDLOTSKALVSELELR--AHYKSVGEVLEITTKLNGLEKEILGKS 1389
 Db 1579 QLMINEBOLEDMRQELVRYOQEHQOATELLRQAHMRQHE-----RQ 1619
 QY 1390 ESEVYLKSMLEVLKEDNNKLEKQAEYSSKENQPSLEEYFSGSKLVDEIEVLKALQKXA 1449
 Db 1620 REDQ-----BOLQEIYIKRLNQLAORSSIDENLVSE--REVLLEBELKALQSLNG 1670
 QY 1450 BEEL--EIKDRDYFELVOTANTNLVEGKLETPLOADHEDSIDRSSEEMEIKVLEKLER 1507
 Db 1671 REKLCCELRNSG---TOTQNGENQGEVE--EQTPEKELDRKEDVPPEILNE--- 1720
 QY 1508 NOYLLERLOEBKLELSNKLEITLOKEMETSVLKD-----LOOKLESLSLENIILKE 1559
 Db 1721 -RYALQKAN---NRLKILLEVYKTTAAVEETIGRHVGLIDRSSKSSQASLWRS 1773
 QY 1560 NIDTTLK---HNSDQALQK-----TOOELQAKLN--AIKAS 1593
 Db 1774 EAEASVKSCHAEHTRVYDSEIIPSYSGDMRPNDINMMSKYTEBGTESQRLVNSGFGCT 1833
 QY 1594 DNCPIOTQ-----KETSADCVHPLKEKILLLTEELHOKTNEOKL 1633
 Db 1834 EIDPENELMUNISSRLQAAVEKLLLEAISFTSSQLEHAKVQOTELMRSPKQCATESL 1893
 QY 1634 -----LHEKNEL--EQAOVELKCEVEHLMKMSIESKSLSELOHEKHD---TEQOL 1679
 Db 1894 KCOEELRELRHEESRAREQLAVELS--KAEGVIDGVADEKTLFERQIOEKTDIIDRLEOEL 1952
 QY 1680 LALKQOMVYVQEKKELOOTHEHLTAEBVDHLKENIELGLNFKNEAQKTTQEQCLNENE 1739
 Db 1953 LCASNRIQLELEBOQOIOEBRELLSROKEANK--AEAG-----PVEQOLLOETE 1999
 QY 1740 ELEQSOHRLQEIIEELMSLKDKDESALFETLKESEQVNLNLOQEMEMWALEEELKNSORT 1799
 Db 2000 KLMKEKLEVOQAOAEKVRDLOKQYKALE-----IDVEQOYVR--FIELEQENITELM 2049
 QY 1800 VIAERDQLODDLRESVENSIEFTODDLRYAQALQOQKQVQELTQISVL----- 1849
 Db 2050 DLROQNALKEKOLEKMRKFLDEQAIDREHERBDFVQO--EIQKLEQOLKVPRFQOISEHQ 2107
 QY 1850 QEKISLENOMLYNAVATYKETLSEBDLANQSKOHLFSIETFLSLSKKEKFPAL----- 1902
 Db 2108 TREVEQLANHHKEKTDKCEILLSEQLOORDIOERNBEIEKLEFFVRLEQALLVEDRKH 2167
 QY 1903 -----EOAEKDADARKTIDITEK--ISNIEBOLQOATNLKETLYERESL--IQCKE 1952
 Db 2168 FGAVAKELSLVQOLOKBRALDRKEKEITNLEBQLOFPEELEKNKEVEYQOLHMOLEI 2227
 QY 1953 QALANTEHLRETLKSKDLALQME-----QERDEANKVIALTEKMSLSLE 1998
 Db 2228 QKKESTRLOLEQENKLPKQDMEXLGLAIKESDAMSTODQHVLFGRKFAQIIOEKEVEID 2287
 QY 1999 QINENVTLKGEGEKEFTFYQRPSSQOSSQOMELRESLTKTQLOLE-----E 2047

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Db 2288 QINEVOTKLO-----QOLKITTDNXYIEEKKEKELLIRDLFQIECLMSDQECVKN 2336
Qy 2048 AEKEISEATNEIKNITAKISSLEEBEILQNASILNEAVSERENLHNSKQOLVSE---LEO- 2103
Db 2337 REEBEIQOLNEVIEKIQOELANIGOKTSMNASHLSF---EADSLGHQDLVDVIAEKLALAEQ 2393
Qy 2104 -----LSLTKSRDHAFAQ-----SKREKDEAVNKIASLAEE-----IKILTK 2141
Db 2394 VETANEEMTFMKNVKJKEFNFKNNQLOTFELFSLKREB-ESVEKIQSIPENSUNVAILDLKSK 2452
Qy 2142 EMDEF-----RDSKESIOESSHSEF-----LCTYKTELOMKKQKQEDINNKLAEKVK 2190
Db 2453 DKPELEVVLTDLKSLSENQTFKSPFENGKSGIINETRLLOLESTVSAKDLTQCYK 2512
Qy 2191 EV-----DELLQ-----HLSLKEQ-----LDPOIOMELNNE----- 2216
Db 2513 QIKDMQEGQFETEMLOKKIIVNLOKIVEKVAALVQIOLEAVQETAKCQDNQITISSE 2572
Qy 2217 -----KLRVIELCEKMDIMEKEISVLRMONEP-----QOEEDVAERMDILES 2260
Db 2573 PERTNIONLQNRDELDGSDISALTLRISIELESQVVMHTSLILEKQVIAEK-NVLEK 2631
Qy 2261 RNQ--EIOELMEKISAVYSEOHLLSSLSSELOKETAHKGCMNLIKESISLTSFSG 2318
Db 2632 EKKLELOKLEEGNEKQREKEKRSQDVEVLTTELPH-----SNEESGFVNELEA 2685
Qy 2319 LQTEHVKLTNTOLOTLINKFKVAVRTAAVKEDH-SLIKDYE-KDLAAEOK-----RH 2367
Db 2686 LRRESVATKBLASYSKEKAEKLOEBELLVKEETNMSTLOKXDSQVRDHLAEKELSTLEKE 2745
Qy 2368 DELRLQ---LOCL-EQGRKMSDSASE---LKFCIEFELNELFRKANITIOSVDDPS 2419
Db 2746 DETEVDSKKAQCFEPPIKLSKSIASQDTGTLKISSNSQTPQILVKNQIQINLOSECS 2805
Qy 2420 --EVOVFLNQGSTLOEBELHKKGFQOMLEBFGDLNVDKAKLSSEGQOENRRLAST---- 2473
Db 2806 SEEVTEIISQ-----FTEKIEKQELHA-----AEIIDMSRHISETEYTK 2846
Qy 2474 -----IQLTKR--LKAVVO-----SKI-----OREIT-----VY 2496
Db 2847 REHYVAVOLKKEBCGTLKAVILOCLRSKESGSIPELAHSDAYOTREICSSGSDMGQGIY 2906
Qy 2497 LNO---FEAKLOEKEON-----KELMRMEHHPGA-----SYM 2528
Db 2907 LTHSGQFDLASBEGSEBSATDPSFKTKIGLIRAVHNEGMOVLSLTSBPYDGEDHSIQ 2966
Qy 2529 E-----EENARLLGLIKTVODESKKLOSRIKMLENELNIVXDAMH-----KGEKVAI 2576
Db 2967 QVSEPMLEKAVINTISSLKDLITKQO---LQREAEVYDSQSHESFSDMRGELLILA 3021
Qy 2577 LQOKL-----SNNAEAEIANMVKLTUKQDNILQAMK----- 2609
Db 3022 LQOVFLSEBSVLLAARTTELTAIGTDAVGLINCLFORIOEQVEYOAMECILOKADRRS 3081
Qy 2610 ---ELENLOKNAVAKGAVPYKEID-----NLKTR-----VVKIEMEKIKYKAT 2650
Db 3082 LLSLEIOALHAQMGKRITLKEQOSEKPSQELLEENIQOKOSOMLEMOVELSSMK-DYAT 3140
Qy 2651 DEEIVAVKSLDEKBEGLRLKEELRRAQADNDTTVCVPKDYOKASTPVTTCGGSGGIVQ 2710
Db 3141 E-----LOQOLSEKVVVAELKSELAQTLLETLTKAQHKILK----- 3179
Qy 2711 STAMVLQSEKALREBELSHYKKKYVHLSRTWSSEDR-----KTKTAKSDAHSHT 2762
Db 3180 -----ELEAFLELVKDKTDEVHNLNDTILASQOKSREIOWALEKKA-----L 3223
Qy 2763 GSSHGSPHKITETTYHNG-PVTPERSEMPSLHSGPKSESTKRVVSPNREIYSQVLMS 2821
Db 3224 GRSEBRDEBELEDLKFSLSESQKRMQNLNLLLEQOKOLNSESQKLTESQRMVLYAQOLSEE 3283
Qy 2822 PGKTMHNGHILSPSGVUGLHKKRALSPNNSMPTQVNIIPGKTGLHKNLTESTLFDNUSSP 2881

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Db 3284 QGRNLEQVLESEKVRIREMSSITDRERELHAQLOLOSSDGTQSNRPPLPSEDLLELOKQ 3343
Qy 2882 C--KQKQVQDNLN-SPKXGLFVPSK 2904
Db 3344 LEEKSRIVELLNETEKYKLDLQTR 3369

RESULT 4
US-10-171-311-2
Sequence 2, Application US/10171311
Publication No. US20030087270A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Chen, Yan
APPLICANT: Zhao, Xumei
APPLICANT: Monahan, John
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Glatt, Karen
APPLICANT: Gannavarapu, Manjula
APPLICANT: Hoersch, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MRI-035
CURRENT APPLICATION NUMBER: US/10/171,311
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 3907
TYPE: PRT
ORGANISM: Homo sapiens
US-10-171-311-2

Query Match 6.9%; Score 1013; DB 15; Length 3907;
Best Local Similarity 19.1%; Pred. No. 2e-43;
Matches 691; Conservative 637; Mismatches 1115; Indels 1182; Gaps 148;

Qy 181 KKGKKNHYGETKANDHSSRSHTIFRMIVSRDNPFTNSGDCGAVMVSMLNVLVLGAS 240
Db 34 KQKKKR--KTSSEKHDVSAHHDNLIDQOCNEMYINSQRBVSTVIEPSTIMRTLHSG 90
Qy 241 ERASQTAEGVRUK-----EGCN--INRSLTILGQVIVKLSQDQAGGFINYRDSKLTR 291
Db 91 EITSHGQFVELESEISTADDCSEVNGCSFVM-----RTGKPTV 132
Qy 292 ILQNSLGNKAVIYICITIVSPFETLSTLQFASTAKHVNTPHVNEVLDEALLRYRK 351
Db 133 LREERFG-----VDSYS-----EQGADSTTHLEMESELAGKH-- 169
Qy 352 EILDLLKQLENLSSSETKA-----QAMAKEH--TOLAEIKOLHKEREDRIWHLT 401
Db 170 EIEELNLELEMEVVTGTEGLQLOEFFAIKQRDGIITQLTANLQARREKQETREFL 229
Qy 402 NIVVASQESQOQRYKRRVYTWARGKIONSLHAGVSD-----FMLSR 447
Db 230 EL-----TEQOKLQIQFOLOQASETLRNSTHSTADLLQAKQOILLTHQOOLEODH 282
Qy 448 LPQNFSK-----KAKFSDMPSFEIDSVCTEFSDFPDALSMDNSGIDAE 493
Db 283 LLEDYQKKEDFTMQISPLQEKIKYVEMQDKVENSNEEIOEKETIIEELNTKIEBE 342
Qy 494 ---WNLASKYTHREK--SLHOSMIDFG-----ISDSVQFHDSKENOLQYLPKDS 540
Db 343 KTLLEKDKLTADKLLGELQEDIVQKQEIKNMKLELTNSKOKROSSEEEKOLM--- 398
Qy 541 GDWABCRK-----ASPEKEITS-LQOQLOSK-EEEKKELVQSFELKIMLEBQL--SVYA 591

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Db 399 GTVEBELQKNNHKSQFETDI VQMEBQETQKLEQLAELEDMVGGQIQVMKQELIRQHNA 458
 Qy 592 KULEWNTSR---EHSINA EVOTDVEKEVVRKEMSVLGSGYNASNSDLODSSVDGKRUS 648
 Db 459 QMEKKTTRKRGEMENALRSYSNITVNEDOI K-----LNMVA INELNIKLODINSQEKIK 513
 Qy 649 SSHDCIEHRKMLQOKI VDLPEEIEHLNKSSENDKQSEODFM-----ESTOLCEAIMA 703
 Db 514 BELGILIEBKALQROLEDVBELSFRQIQARPTIAEQSKLNEAKHSLSITYEDLKA 573
 Qy 704 EKANALE---ELAL-----MRDNFDNIILENETLKELIADLER----- 738
 Db 574 EIVSASESKELKLEHAEVNTYKIKLEMLKEKNAVLDRAHMSQD-ALBELURQTLFS 632
 Qy 739 -----SLKE-----NOETNEFEIL-EKETQKEHE 761
 Db 633 HEEELSKLEKDELEIHRINIEKLNGLIHYKQOIDLQONEMSO KLETOPEKMDLITQ 692
 Qy 762 AOLIEIGSLKVLVENAMYNQNLB-----DLKTKLKE-----QEIOL 803
 Db 693 NOLIEISKLDQLOS--LVNSKSEMTLOINELQKEILEIROEKEKGTLEQVOEQL 750
 Qy 804 -----AELRKRADNLQKKVRNFDLSV--MGDSEKLCBEI POLKOSLDAEAV----- 849
 Db 751 KTELLEKQMEKENDLQEFQADLEAENSLKDEKLTLEMDLKIHPVSGEERLIFDSTK 810
 Qy 850 --TRDA--QKESCFLRSEN-----LELEKMEBDTSNNYNOKEKASLFEKOLETEKSN 898
 Db 811 SKSKSVMEKEIEIILEENEDLKQOOCIQINEIEKORNTFPAEKNFVAYQOLOEYAC 870
 Qy 899 YKQKMAADQ-----KELO-----SAFNEINYLN----- 921
 Db 871 LKLVQDLEDSKNQKOLEYKSKLKALNEBELHQRINPTTVKXKSVFDEKTFVATLEEM 930
 Qy 922 GILACKVRPDL-----SRVELEKVSFEPSKOLEKALEKNALENEVTCLSEYK--- 970
 Db 931 GEVAVKOTTELMKLEVTREKLEBLSQRSLDSEQLKQKHGELSFLENEVSKLOKEQV 990
 Qy 971 -FLPNEVECLKN-----QISAKSEBIMTLKQEG-EHSASITSK----- 1006
 Db 991 SLRCELEIILINHNAENVQSCDTQVSLDDGVMTMTSGAEGSVSKVKSFGESKIMV 1050
 Qy 1007 -----QEIIMQSEQ---IQLTDEVYHTOS--KVQOTBEQYLE---MKKHNDLIF 1050
 Db 1051 EDKVSFEMMTVQESBKOBOLILDHLPSYKSESSLRATOPSENDKQKELINLVKSSONDI- 1109
 Qy 1051 EKYIRNKSEAB-----DLRE-MENLKGT-----MESVEVKIADTGH 1086
 Db 1110 ----RLOHEAQRICLSLVYSTHVDQVREYMEKDKALCSLKEELI PAOEEKIKELQKH 1165
 Qy 1087 ELE-ETIR-----DKEOULH-----EKYFFQAMOTIFPITPLSDLPSPSKLV 1128
 Db 1166 QLELOTMTOETGDSGKPLHLLIGLQKAVSEGCYFLOTLGSV-----LGSYVPAKLC 1220
 Qy 1129 EGNSDPPIEINDY-----HNLIATERRNIMVCLF----- 1160
 Db 1221 EVMNADKENSQDIYISENEDPELODYRYEVODFQEMNHHTLANKVTEBYNLTALQTRLSKI 1280
 Qy 1161 -----EBNSLKEQV-----IDLNTQLOQLQOSLEKSDLOPK 1193
 Db 1281 WGOQTDQMKLEFGEENLPKEETEPILSIHSQMTNLBIDVNHKSKLSSLODEKTEKLEBOV 1340
 Qy 1194 QDLF-----EGEVKLLMEMLKGLH-----TDSQLSI 1221
 Db 1341 QELBLSLSLOQQLKETEONFAELHCLQKRLQAVSESTVPSPSLVDVSVITRESAQAQTM 1400
 Qy 1222 -----EKLOENLEVTREKLOTLQOEMKNIT-----ERNE 1251
 Db 1401 YPGSCVKKNIDGTIEFSGEFVGKEFTNIVKLEKQYOELBEEVAKVIVSMSIAFAQOTE 1460
 Qy 1252 L-----QTNFEDLKAHEDSLKQDSESENI EOSIETQDELRQAQ 1288

Db 1461 ISRISGKENTASXQAHAVCOEQOHYFNEMKLSQDQIGFQTFETVD--VKFEKFPKLS 1518
 Qy 1289 BELREQ-KQVDSFFQ-----QLDQSVGIS-----SPNHDAVANQ---EKVSLGEVNS-- 1333
 Db 1519 KELGHEGKEILLNSDPDHPIDIPESKDCVLTISEMPSKDTFTVROSIDELISVSSMDAR 1578
 Qy 1334 ---LOSEMIRGEBRDLQTSCKALVSELELLR-AHYSVEGENVLFTTKLNGLEKITLGS 1389
 Db 1579 QMLNBEQLEBMRQOLVQOYQEHQAOTELLROAHNRQHE-----RO 1619
 Qy 1390 ESEVVLKSMLENLKEDNNKLEQAEYSSKENQSLFEVFGSQKLVDEIVLKAQLKAA 1449
 Db 1620 REDQ-----EQLOEIRKILNQLAQRSSIDENILVSE---REVILBELALQKQSLAG 1670
 Qy 1450 EERL--EIKDRPYFELVQTANTNLVSGKLETPLOADHEDSDIDRSSEMEIIVLOEKLER 1507
 Db 1671 REKLCCCELRNS--TQTONGENQGEVE---EOTFKEKELDRKEDVPPEILSNE--- 1720
 Qy 1508 NOYLLERLOEBKLENSKLEILOKEMETSVLLKOD-----LOQKESLSENIILKE 1559
 Db 1721 -RYALQKAN-----NRLKILLEVAVKTTAAVEITIGRAVLGILDRSSKQSSASLIMRS 1773
 Qy 1560 NIDTTLK--HNSDTQAOLOK-----TOEQLQAKNL---AIAAS 1593
 Db 1774 EABASVKSQVHEHRTVTDSEI PSYSGSDMPRNDIMNMSKYTEBGTELSQRVRSQFAGT 1833
 Qy 1594 DNCPI TOE-----KETSADCVHPEEKIYLLITBELHOKTNEOKL 1633
 Db 1834 EIDPENEBIMLNISRLQAAVEKLEALSETSQLEHNAKVOTELMRESFRQKOBATESL 1893
 Qy 1634 -----LHEKNEL-BOAOVELKCEVHLKMSMIESKSSLESLOHEKHD---TEOOL 1679
 Db 1894 KQEBELREBLHEESARQOLAVELS-KAEGVLDGADEKTLFERQIOETKDIDBLEOEL 1952
 Qy 1680 LALQOMOVVTOEKKELQOTHEHTLAEBVDHLKENITELGPNFKNQAQKTTKEOCLYNENK 1739
 Db 1953 LCASNRLOLELAEQOQIOEBRELLSRQEKAN-K-ABAG-----PVEQOLOETE 1999
 Qy 1740 ELEQSOHRLOCEIEBELMSLKDKESALETLSEBQVNLNOEMMMLNMBELKNSORT 1799
 Db 2000 KLMKEKLEVOCAEYVRDLOKQVLALE-----IDVEQVSR-FIELEQKXNTIELM 2049
 Qy 1800 VIAERDQLODDRESVENSIETQODLRKAQOELQOQKQVQELTQIS-----VIOE 1851
 Db 2050 -----DLROONQALEQLEKMRKFLDEQAI DREHERDVFQO 2085
 Qy 1852 KISLENOMLYNVATVKEITLERDIDLQOSKQHLFSEIETLSLSEKE-----FAEQ 1904
 Db 2086 EIQKLEQOL--KVPRFPQISE-----HQTRVEQOLANHLKEKTDKSGELLSSQ 2134
 Qy 1905 AEKDKADARKTIDITEKISINEBOLLQOATNLKETLYERE-SLIQCKEOLALNT-BHL 1961
 Db 2135 LQORDIOERNEIEKLEFVRELEQALLVSADTFQVDEBRKHFGAVEAKPELSLEVOLOAE 2194
 Qy 1962 RETLSKRLALAKMQE---RDEANKVIALTEKMSLLEQOINNVTTLKEGEBEKEFT 2017
 Db 2195 RDAIDRKEKETTLNEBQEOFREBELNKNNEVQOQLOMLOLEIKKESSTRLOELEBENKLF 2254
 Qy 2018 YLQRPSSQOSSQOMELRESLTKDQLEBAE-----KEISATATIEIKYLTAKISSL 2069
 Db 2255 -----KDMKELGLAIKESDAMSTQOQHVLFQFAQILOKEVEIIOQLNCOVTKL 2304
 Qy 2070 EBEILQNASITINEAVSERENLRHSQOVLSEBOLSLTLKSRDHAFAQSKREKBAVANKI 2129
 Db 2305 QOOL-KITTONKVIEE-----KNELIRULETQIECLMSDOECVKANREBEIQLNEV 2355
 Qy 2130 A-----SLAEIKILTLEMEDFBRSKSLSQOSSHLSBELCTYKT- 2169
 Db 2356 IETLQOELANTIGOKTSMNAHSLSEBQSLKQOLDVIAEKLALQOQVETANEEVTFMKV 2415
 Qy 2170 -----ELQMLKQOQKEDINNLKAKVEVDE-----LLQHLSSLKEQDLOIQM 2211
 Db 2416 LKETNFKMQLTOBELFSIKRERESV-----EKIQSIPENSUNVVAIDHLSKQKPELEVULT 2470

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QY 2212 E-----LRNEK-LRNYELCEKMDIMEKEISVLR-----MONEQO 2245
DB 2471 BDALKLENOYTFKSFEEENGKSIINLETRLLQLESTVAKADELTQCYKQIKMDEQOQ 2530
QY 2246 QEDDVAEMDILESNOEIOELM-EKISAVYSECHTLLSSLSSELQKET--EAKHCHWL 2302
DB 2531 FE-----TEMLQKKIVNLQKIVEEKVA-----ALVSQIOLEAVOEYAFPCOD 2573
QY 2303 N-----IKES-----SLSSTLSRSPSLOTENHAKNTQOTLTKKPKVY 2341
DB 2574 NQTISSPERTNIQNOLREDELSGDISALTIRISELSQVEMHTSL--ILEKQVBI 2631
QY 2342 RPAAYKEDSLIKDYEKDLAEQKRDHRLQIOCLEHQGRKWSASASELK----- 2393
DB 2632 AEKNVLEKEKLELOKLEEGNEKKQREKE-----KKRSPQDVHVLKTTTELPHS 2681
QY 2394 -----FCIEFL-----NELFKRNIISQVODPSEYQVFL 2425
DB 2682 NEESGFNELEALRAESVATKELASYKEKAEKLOELLVKETN-MTSLQKDLQSVRDHL 2740
QY 2426 NOVGSTLQ-----EELEHKKG----- 2441
DB 2741 ABAKEKJLSEKDETEVQESKACPFEPPIKLSIASQTDGTLKISSNOTPQILVAK 2800
QY 2442 -----FMQMLEPFGDLHVDAKKLSGMOENRRIAST----- 2473
DB 2801 NAGIOINLOSCSESEVTEIISOFTERIEKMOELHA-----AHLDMESRHISEETLKR 2855
QY 2474 -----IQLITKR--LKAVVO-----SKL-----QREIT-----VYL 2497
DB 2856 EHYVAQVLKEBEGITLKAVIDCLRSKEGSIPELAHSDAYQTRIELSSDSDGMDGGITL 2915
QY 2498 NO--FEAKLOEKEQN-----KELMRMEHSPSA-----SVME 2529
DB 2916 THSOGFDIASEGGESSESATSPFKKIKGLRAVINEGQVLSLTSEPSOGEDHSIQ 2975
QY 2530 -----EENARLLGIKTVODESKLQSRITKMLENELNVKDDAMH-----KGEKVAIL 2577
DB 2976 VSEPMLEERKAYINTISSKLDTTKMQ-----LQREABVYDSQSHESPSDMGELLAL 3030
QY 2578 QDKL-----SRNAEALNAMQVLYTKKONLQAAK----- 2609
DB 3031 QOVFLERSVLLAAPTETLALGTTDAVGLLNCLEGRIOGVEYQAAMECLQKADRSLL 3090
QY 2610 --EIEMLQKVAAGAVPYKEID-----NLTKT-----VVKIEMEKIKYSKATD 2651
DB 3091 LBEIOLHLOMNGRKITTLKREGESEKPSQELLEYNIOQKOSQMLEMQUELSSMK--DRATE 3149
QY 2652 QETAYVKSQLEDEKEGLRRLKEELRRAQADNDTTVCVPRDYOKASTFPVTCGGGSGIYOS 2711
DB 3150 -----LOEQLSSEKMWVAELKSELAQTKLETTLLKAQHHLK----- 3187
QY 2712 TAMLVLOSSEKALERLSHYKKYHHLSTRMSSSEDR-----KTKYAKSAHSHHG 2763
DB 3188 -----ELEAFRLVKKOXTDEVHLLNLTSLASEQKSRBLQWALEKEKAK-----LG 3232
QY 2764 SSHRGSPPHTEYTRHG--PVTPERSEMPSLHLSGPKSESSTKRVAPNRSSEIYSQLVMP 2822
DB 3233 RBEERDELEBDLKFELESQKQKNDLNLLEQOKULNESQOKISQKMLDQAQSEBQ 3292
QY 2823 GKTGMHKLILSPKVGYLHKKRALSPNRSSEMPTOHVISPGKTGLHKLTESTLFDNLSPC 2882
DB 3293 GHNLELOVLESEKVAIRREMSSTLDRERELHAQLOQSDGQSRPPLPSEDLKLELOKOL 3352
QY 2883 --KQOKVQENLN--SPKGLFPDVSK 2904
DB 3353 BEKHSRIVELNTEKYKLDLSQTR 3377

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RESULT 5
US-10-171-311-6
; Sequence 6, Application US/10171311

```

; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoersch, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 3925
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-171-311-6

Query Match 6.9%; Score 1013; DB 15; Length 3925;
Best Local Similarity 19.1%; Pred. No. 2e-43; Indels 1182; Gaps 148;
Matches 691; Conservative 637; Mismatches 1115;

QY 181 KKEKNRHHGETKMDHSSRSHITPRMIVESRDRDPTNSENCDAVMSHLNVLGLGS 240
DB 34 KKQKKR--KTSSSKHDVSAHDLNIDQSCNENYINSSQVESTVPESTIMRTLSHG 90
QY 241 ERASOTGAEGYRLK-----EGCN--INRSLFLLGOVIKULSDQAGGFINYRDKLTR 291
DB 91 EITSHQGFVSLESEISTTADDCSEVNGCSFVM-----RTGKPTN 132
QY 292 ILQNSLGNNAKVIITTPVPSFDETLSTLOPASTAKVRNPNHYNEVLDDPALLKRYRK 351
DB 133 LUREBEFG-----VDDSYS-----EQAQDSPTLHEMMESLAKQH-- 169
QY 352 ETLDKKOLENLESSSETKA-----QMAKEEH--TOLLAETIKOLHKEDEIRIMHLT 401
DB 170 EIEELNRELEBRVYTGIBGLQLODFEFAIKORGOITTOLTANQOARREKDEIMRETL 229
QY 402 NIVVASQESQODQVKRRRVYMAPGKIQNSLHAGVSD-----FDMLSR 447
DB 230 EL-----TEQSOKLQIOFQOLQASETLRNTHSSTAADLLQAKQOILTHQOLEBODH 282
QY 448 LQGNFSK-----KAKSDMPSPFEIDSDCTESPDDDLASMDMSNGIDAE 493
DB 283 LLEDYQKKEDFTWQISFLQEKIKYVEMEQDKVENSKEEIOEKTETIIEELNTKIIIEE 342
QY 494 ---WNLASVTRHEKT--SLHOSMIDFGQ-----ISDSVQFSDSKENOLQVLPKDS 540
DB 343 KTTLELKDKLTTADKLGLGELQEIYQKQOELKNMKELELNSQKROSSSEELKOLM---- 398
QY 541 GDMAECRK-----ASFKEKITS--LOQLOQSK--EEBEKELVQSFELKIALEBQL--SVKA 591
DB 399 GTVEELQKRNHNDQSFETDVIQRMEOGTORKLQRAELDEMYGGOIYQMKOLIRQHWA 458
QY 592 KULEWVYTSR---EHSINAEVOTDYEKEVYKREMSVNLGDSGNVANSNLODSSVVGKRLS 648
DB 459 QMEEMKTRHKGEMENALRSYSNITVNEQIK-----LNNVALNELNLIKLODINSQKEKJL 513
QY 649 SSHDECIEHRKMLEQKIVDLDEEFENLNKKSSENDQKSSQODPM-----ESTQLCEAIWA 703
DB 514 BELGILIEBKALQROLEDVLELSFSREQIORARQITAEQDSKLNENAKHSISTYEDLKA 573

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QY 704 EKANLE---ELAL-----MRONFNUIIENETLKREIADLER----- 738
 Db 574 EIVASERKELELHKAEBVTNYKIKLEMLEKNAVLDRMAESOE--HELELRLTQOLFS 632
 QY 739 -----SLKE-----NORTNEFEIL--EKETOKEHE 761
 Db 633 HEEELSKUDELEIHRINIEKLNGLHYKQOIGDLONEMSKOITFMQFEXDLITKQ 692
 QY 762 AQLIHEIGLSKLVENAMYNONLEE-----DIETKTKLKE-----OEIOL 803
 Db 693 NOLIIETSKDLQOOS--LVNKSSEMTLOINELQKEIIEILQEBEKEGTLLEQOEIOL 750
 QY 804 -----ALRKRADLOKKVRNFDLSVS--MGSEKLCCEIIFOLKOSLSAEV----- 849
 Db 751 KTELLEKQMEKENDLOERFAQLEAENSLKDEKTLLEBMLKIHPPVSGEELIFLDSIK 810
 QY 850 --TRDA--QKECSFLRSEN-----LELKEKEDTSMVYNOKERKAASLFERQLETESKN 898
 Db 811 SKSKDSVWEKEIETIIEENEDLKQOCIOUNEIEIKORNTFPAEKNFVYQELQEBYAC 870
 QY 899 YKKNEDADLO---KELQ---SAFNEINYLN----- 921
 Db 871 LLKVADLJDSKNQOLEVYKSKLALNEBHLQRIINPTVKKKSVFDEKTFVAETLEM 930
 QY 922 GLLAKGVPRDL-----SRVELEKVSFESKOLEKALEKNALENYTCLSEYK-- 970
 Db 931 GEVVEKDTTELMEKLEVTREKLELBSORLSDSEQLKONGEISFLNEBVKSLKQEKQOV 990
 QY 971 -FLPNEVECLKN-----QISKASEIMULKQEG--EHSASITSK----- 1006
 Db 991 SLRCELEIITINHNAENVQSCDTQVSSLLDSVVTMTSRGABGSVSKVKKSGESKIMV 1050
 QY 1007 -----QEIIMOQOSEQ---ILQLTDEVTHTOS--KVQOTEBOYLE-----MKKMHDLF 1050
 Db 1051 EDKVSFEMMTVGEESKQEQOLILDHLPSTVKESSLATQPSBNDKQKELANLVKSPOND- 1109
 QY 1051 EKYIRNKSEAE-----DLRRE--MENLKGT-----MESVEVKIADTKH 1086
 Db 1110 -----RLQWMAORICLSLVSTHVHDQVREYEMENKDKALCSLKEBILFAOEBEKIKELOKIH 1165
 QY 1087 ELE--ETIR-----DKEOULH-----EKKYFQAMQOTIPIPIPLBSLSPSKIV 1128
 Db 1166 QLEIQTMTQETGDEGKPLHLILIGKLOKAVSESCSYFQTLQSV-----LGYVTPALKC 1220
 QY 1129 EGNSSODPIEINDY-----HNLIALATERNNIMVCLT----- 1160
 Db 1221 EVNADKENSQDYSISNEDEPRLQDYRYVQDPOEAMHTILNKVTEYKVLVLOTRLSKI 1280
 QY 1161 -----ERNSLKEQV-----IDLNTLOQLQOISIEKSDLOKPK 1193
 Db 1281 WGOQDTGAKLEFGEENLPKEETEPFLSHSQMTNLBIDIVNHHKSLSLQDLEKTKLEBOV 1340
 QY 1194 ODLE-----EGEVKLLLEMLKGLH-----TQSQLSI 1221
 Db 1341 QELBLSLLOOQLKETEONVEALHCLQKLOAVSESTVPSPSLPVDVSVITESDAQRTM 1400
 QY 1222 -----EKLOLENLEVTLEKLOLQOJEMKNITR-----ERNE 1251
 Db 1401 YPFGCVKKNIGDTIFSGEFGVKETNTYKLEKQOEBLEEBVAKVIVMSIAQAQOTE 1460
 QY 1252 L-----QTNFEDLKAEDHSLKODLSENIEOSIETQDELRAAQ 1288
 Db 1461 LSRISGKENTASSKQAHAVCQOEQHUFENEMKLSQDQIGFOFFETVD--VKFKEBFPKLS 1518
 QY 1289 EBLRQO--KQVDSFQO-----QLDQCSVGIS-----SPNHDAVANQ---EKVSLGEVNS-- 1333
 Db 1519 KELGHEKEIILSNSDPHDIPESKDCVLTISEMFSKCTFIVROSIHDELISVSSMDASR 1578
 QY 1334 ---LOSEMLRGERDLEQTSCKALVSELELLR--AHYKSVAGEBULETITKUNGLKEKILGKS 1389
 Db 1579 QLMNEBOLEBMRQELVROYQOEHQOATELLRQAHNRQME-----RQ 1619

QY 1390 ESEVYLKSMLENTLKEDNNKLEKQOAEVSSKENQFSLSEEFSGSQKLVDEIVLKAQLKAA 1449
 Db 1620 REDQ-----EQLOEITKRLNQLAQRSSINDENLVSE---RETVLELEMLKQSLSLAG 1670
 QY 1450 EERL--EIKDRDYELVQNTANTVVEGKLETPLOQDHEEDSIDRSSEMEIKVYLGEXLER 1507
 Db 1671 REKLCEELRNS--TQTONGENOGEVE---EQTFKEKELDRKPEDVPEILSNE--- 1720
 QY 1508 NOYLLERQOEKLETSNKLEITLOKEMETSVLLKD-----LOOKLESLSSENIILKE 1559
 Db 1721 -RYALQOKAN-----NRLKILILEVVKTTAAVEETIGHVGLGIDRSSKQSSASLIMWS 1773
 QY 1560 NIDTTLK---HNSDQOALQOK-----TOELOLAKNL---AIAAS 1593
 Db 1774 EEAASVSKCMEHETRVYDESIPTSSGSDMPRNDINMMSKYTEEGTELSQRLVRSQFAC 1833
 QY 1594 DNCPIITOE-----KETSADCVHPLKEKILLITBELHOKTNEOEKL 1633
 Db 1834 BIDPENEELMNTISSRLQAAVEKLELAISETSQOLEHAKVTQTELMRESFRQOEATEEL 1893
 QY 1634 -----LHEKNEL--EQOVELKCEVDBHLMKMSIESKSSLSLSLOHEKND---TEOOL 1679
 Db 1894 KQOEBLREBLHESFARQOLAVELS--KABGVIDGVADEKTLFPERQIOEKTDIIDRLEOBL 1952
 QY 1660 LALQOQOVVQEKKELOQTHEHLTAEVDBHLEKENTELGJNFGNAQOKTKTEQCLNEMK 1739
 Db 1953 LCASNRLOEBLEBOQOIOEBRELLSRQOKANK--AEAG-----PVEQOLQETE 1999
 QY 1740 ELEQSOHRLQCEIEBELMSLKDQESALTEKSEQKVINLNOEMEMVMLEBELNQSORT 1799
 Db 2000 KLMKEKLEVOQOAEKVPRDLOKQVAKLE-----IDVEQOVR--FIELEQEKNTLEM 2049
 QY 1800 VIAERDQLODDLRESVEMSIETODDLKRAQEAQLQOQKQKQVQELTQIS-----VLOE 1851
 Db 2050 -----DLROONQALKEQLTEKMRKFLEQOAIIDREHERDVFOQ 2085
 QY 1852 KISLEENQMLVNAVATKELISRRDNLNOSKQLPFEIETLSLKEKE-----FALEO 1904
 Db 2086 EIQKEEQOL--KVPRFQPISE-----HOTREVQOLANHLKEKTDKCSCELLSKQ 2134
 QY 1905 AEKDKADARKITDITEKISNIEBOLLQOATVLYKTELYERE--SLIOCKEQOLANT--EHL 1961
 Db 2135 LQRODQERNNEIEKLEFVRVRELOALVLSADTQFQVBERKHNAGVAERPELSLEVQOLAE 2194
 QY 1962 RETLSKDALQAKMEQO---RDEANVIALTEKSSLSLEQINENVTTLKEGESEKETE 2017
 Db 2195 RDAIDRKEKEITNLEBOEQOFRELEKNKEBVOQJHMOLEIQKKESTRLOQLEQENKLF 2254
 QY 2018 YLQRPSSKQOSSQMELESLKTKDLOBEAE-----KEISATNEIKVLTAKISL 2069
 Db 2255 -----KDMKELGLAIKESDAMSTQODHVLFGKFAQIIOEKEVEIIDQINBOVTKL 2304
 QY 2070 BEELQONASILNEAVSERENLRHSKQOLVSELEQSLTKLSKDHAFAOSKREKDEAVNKI 2129
 Db 2305 QOOL--KITTDKVLE---KNELIRDELTOIECLMSQOECVAKNREIEIOLNEV 2355
 QY 2130 A-----SLAEBIKILYKEMDEFDRSKESLOQSSHLSSELCTYKT- 2169
 Db 2356 IEKLQOELANIGOKTSMNAHSISEBADSILKQDLVIAEKLALBEOQVETANEMTFMKV 2415
 QY 2170 -----ELQMLKQOKEEDINNKLAEVKAVDE-----LLQHSLSLEQOLDQIOM 2211
 Db 2416 LKETNFKMNQLOLEFLSKRERESEV---EKIOIIPENSUNVALDHSKDPRELEVLVT 2470
 QY 2212 E-----LANEK--LBNVELCEKMDIMEKEISVRL-----NONERO 2245
 Db 2471 EDALKSLENQYTFKSFENGKSIINLETRLILQLESTVSADKDELTQCYKOIKMOBOQO 2530
 QY 2246 QOEDDVAERMDILLESRNOEIOELM--EKISAVYSEQHTLLSSLSSELQET--EAKHQCML 2302
 Db 2531 FE-----TEMLQOKKIVNLOKIVEKVA-----ALVSOIQLEBAVQVAKFCOD 2573
 QY 2303 N-----IKE-----SLSSITLSRSFGSLQTEHVKANTQLOTLNKFVVY 2341

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Db      2574  NOTISSEPERTINIONIMOLREBELGSDISALTLRISSELSOVEMHTS--ILKEQVBI 2631
QY      2342  RTAAVKEDSHLKDVEKDLAEOCKRDELRLQOLCEHGRKMSDASELK----- 2393
Db      2632  AEKVLKKEKLLLEOKLLEGNKKOREKE-----KKRSPDVVLKTTTELPHS 2681
QY      2394  -----FCEIEFL-----NELLFKKANIIOVODDFSEVOFL 2425
Db      2682  NEESGFNELALRAESVATKAELASYKEKEKLOELLVKEFN-MTSLQKDLSCVRDH 2740
QY      2426  NOVGSILQ-----ELEHKKG----- 2441
Db      2741  AAKEKLSILEKEDETEVOESKKACMFEPILKLSKSIASQTDGTLKISSNOTPOLIVK 2800
QY      2442  -----FMOLBEFGDLHVDAKKSEGMQENRIAST----- 2473
Db      2801  NAGIOLNLOSECSSESVTEIISOFTKIKRMOELHA-----AELDMESRHISFETTLK 2855
QY      2474  -----IOLLTKR--LKAVVO-----SKI-----OREIT-----VYL 2497
Db      2856  EHYVAVQLLKEBGTGLKAVIQLCRSKESGSIPELAHSDAYQTRREICSDSGSDMGQIYL 2915
QY      2498  NO--FEAKLOEKEON-----KELMRMEHGPSA-----SVNE 2529
Db      2916  THSOGFDIASBESGESATDSFPKKIKGLRAVNEGVOVLSLTPESFYSDGSDHSIQ 2975
QY      2530  -----EENARLLGLKTVODESKLQSRILKMLENLNVKDDAMH-----KGEKVALL 2577
Db      2976  VSEPMLEEKAVINTISLKLDTTMO-----LQRAEVDYDSQSSESSDMRGELLAL 3030
QY      2578  QDKLL-----SRNAEALNMOVKLTAKODNLQAMK----- 2609
Db      3031  QGVFLSEERSVLLAAPTETLTALGTTDVGGLNCLBQRIOGVEYQAMECLOKADRSL 3090
QY      2610  --FIENLOCMVAKGAVPYKEID-----NLTKR-----VKIMEKIKISKAD 2651
Db      3091  LSEIALHAKQMMGRKTLTRKEOSEKPSQELLEYNIOQKOSOMLEWVLSMK-DRATE 3149
QY      2652  QGIAVLYKSCLEDBEELRLKEELRAQADNDTTVCVPDYOKASTFPYTCGGSGSIYOS 2711
Db      3150  -----LQEBLSEKVVAAELKSELAKTLETTLLAQKHNLK----- 3187
QY      2712  TAMLVLOSEKALERELSHYKKYVHLSRTMSSSEDR-----KKTAKSDAHSSHTG 2763
Db      3188  -----ELBAFRLVLEKDKTBEVHLNDTLASEQKRELOMALEKEKAK-----LG 3232
QY      2764  SHRGSFHKTEYTRHG-PVTPERSEMPSLHLSPKKSESSTKRVSPNSETYSQLVMP 2822
Db      3233  RSEERDKLELEDLKFLSESQKQKRNLOLNLLEQOKLNEEQKLESQEMLYDAQLEBQ 3292
QY      2823  GKTGMHKLHLSPSKVGVLHKKRALSPNRSMPPTQHVISPQGTGLHKKULFTSTLFDNLSPC 2882
Db      3293  GKNLEIQLVLESEKAVIREMSSTLDRERELHAQLOQSSDGTGGRPLPSEDLKELQKDL 3352
QY      2883  --KQOKVQDENLN-SPKGLFDVYSK 2904
Db      3353  EEKHSRIVELLNETEKYKLDLSQTR 3377

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; CURRENT APPLICATION NUMBER: US/10/082,830
; ;
; ; CURRENT FILING DATE: 2001-10-29
; ; PRIOR APPLICATION NUMBER: 60/243,802
; ; PRIOR FILING DATE: 2000-10-27
; ; NUMBER OF SEQ ID NOS: 282
; ; SOFTWARE: Patent In Ver. 2.1
; ; SEQ ID NO 260
; ; LENGTH: 2383
; ; TYPE: PR1
; ; ORGANISM: Homo sapiens
; ;
; US-10-082-830-260
;
Query Match      6.7%; Score 993; DB 15; Length 2383;
Best Local Similarity 21.2%; Pred. No. 1,1e-42;
Matches 562; Conservative 472; Mismatches 929; Indels 690; Gaps 101;

QY      370  KAQAAKEEH--TOLLAIRK--QJHK-BREDRIWHLNNIVVASSQESQODQVRKRRV 423
Db      227  KTOELEKKAHERSÖLLIOKSGDLEKAELODRVELSALTLQOSKONEDYKMTKALRE 286
QY      424  TWAPGKIONSLHAGVSDFDMLSRLPNGFSKKAKESDMPSEIDSDVCTEFSDFDALS 483
Db      287  T-----VEILETHTHEHEASL- 305
QY      484  MMDSGIDAENWLASKVTHREKTSLHOSMIDPQI-----SDSVQFHDSSK 529
Db      306  -----SRNAOEKLSIQOVIKDITQVWEAGDNIAGSGHENSLEL-DSGI 350
QY      530  ENQOLYLPKDSG-----DMAECKASPEKEITSLOOQLOSKSEER 569
Db      351  FSQFYQADAKALTLVRSVLTTRRQAVODLRQOLAGCQEA-----VNLLOQHDMQEBEG 405
QY      570  KELVOSFEL-----KIALEBQLSVYAKNLEMTNSREHSINAEVQTVKEVVR 619
Db      406  KALRQRLQKLTGERDPLAGQTVDLQGEVDSLSKERELLQKARE-----LR 451
QY      620  KMSVILGSGVYASND-----LQDSVQKRLSSHD--ECIEHKKMLEQKIVDLBEFTE 673
Db      452  QOLEVLEQEAURLRRVNELOLQGSAGQKEEQEELHLAVRERERLOEMLMGEA--- 508
QY      674  NUNKSENDKOKSSBODFMESIOL-CEAIIHMAKANALBEALMRNFDNIILENETLKE 732
Db      509  ---KQSELSIELITREALFESHLGELLROQTEVTALARAOSINELSESENTIKTE 565
QY      733  IADERSIKENQETNEFEILEKETQKEHAQILHEIGSLKLVENAMYNQNLLEBLETK 792
Db      566  VADLRAAAVKLSALMEBALALDKVGLNQOLQLEENOSVCSHMAEAQARNALQVD--- 621
QY      793  TKLKEQELQLALELKRADNLQKVRNPDLSVSMQDSSEKLCBEIRIQLKQSLSDAEAVTRD 852
Db      622  -----LBAEKR-----REALWKNTHLEQLOKABEAGAE 652
QY      853  AQKESFLRSEVLELEKEMEDTSMNWNQEKAASTFEKOLETEKSNYKMEADLOKELQS 912
Db      653  LQADRLDIOEKEEYQKULSESR---HQDEAATTOLE-QLHQBARKQEBVLARAQEKKA 708
QY      913  AENEINYNGLLAGKVPDDLRSVLEKKVSEFSQLEKALEE-----KNALEN 961
Db      709  LVREKAALEVRLOA-VERDRQDLAEQLOGLSASAKELLESSLFEAQOONSIVIEVTQGLEV 767
QY      962  EYTCISEYK-FLPNVECEKQNOISKASEEIMLLKQEGESASIIISKQELIMOQEQILO 1020
Db      768  QIOTVTOAKEVIOGEVRCKLELDTE-----RSQAEQERDAARQ-LAQBQDGKTA 818
QY      1021  LTFDEVTHQSKVQOTEEOYLEMKKMHDDLFEKYIRNKSABEDLREMENTLQTMSEVEYK 1080
Db      819  LEOQKAAHEKVENQLRKWEKERSMHQ-----QBLALABSELBEKKWELMR 865
QY      1081  IADTHHELEETIRDKQOLLHEKKYFFQAMQTIPTTPSLDSLPFSKLVGNSQDPIEIND 1140
Db      866  LKEQOTEMALQAGEEBERTQAESALCQWQ----- 895
QY      1141  YNLIATLATERNNINWCTEENSILKEQVYIDNTQLOSLQASISKSDLOKRPDLEGE 1200

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Db      896 -----LETE-----KERVSLLETLITQOTQKELADASQOERLRQDM---K 931
Qy      1201 VKLLEME---LLKGLTDSQSISTEKLQLENLEVEITEKLTQLOEMKNITIEENELQTNB 1257
Db      932 VOKLEQETITGLITQLOEAOBELKEMARQH---RDLALAOEESSTLLQDKMDLOKQVE 988
Qy      1258 DLKAEHDSLKODLSENIEQSIENODELRAAOEELRQXQLVDSFRQQLDCSGVSSPMH 1317
Db      989 DLKSO--LVAODDSQRLVEQ-EVQEKLTRETQENRQKEL-----ERKASITLISLMK 1039
Qy      1338 DAVNAOEKVSLEGVNSLOE---MLRGERDELQTSCKALVSELELRAHVKSEGENLEI 1374
Db      1040 E-----QRLVLLOEASIRQOELSAIRQDMQOEAQOEBEKELSAQWELLRQVKEKEDFL-- 1093
Qy      1375 TKLLNGLEKEIIGKSESESVLKSMLENKEDNNKLEQOAEYVSKENQPSLEEVPSGSK 1434
Db      1094 -----AOEAOLEELASHITEQOL-----RASLMAQEAQAQOLRLRSTES---- 1136
Qy      1435 LVDELIEVLKAOLKABE-RLEIKDRYFELVQTNANNLVEGKLETPLOADH-----BE 1486
Db      1137 ---QLEALAAEQOQNGOAOQOALASVLSALQALGSVCSRPBLSGGDSAPSVWLEP 1193
Qy      1487 DSIDRSEBMEIKVLGEKLERNOYLLERLOEBEKLETS-NKL-EILOKEMETSVLLKDLQ 1544
Db      1194 DONGARS-----LFRGRLITLALSAVAVSAHLKHLQMDLKTQOTRDVLRDY- 1241
Qy      1545 OKLESLSBENITLKENIDITLKHNSDTQOQLOKTOEQLAKNLAIASDNCPTQOKET 1604
Db      1242 QKLEERLTDTAEKQVHTELQ---DLQRLQSONOEKSK-----WEGKQN 1284
Qy      1605 SADC-VHPLBEKILLTTELHOKTNEQOELKHEKLEBOAYELKCEVHLMKSMESKS 1663
Db      1285 SLESLEMEHETWASLOSLRRAELQRMGAQGERELLQAKENLTAQVHNLQAAVAEVA 1344
Qy      1664 SLESLOHEKHTDEQOLLALQOQOVVTOEKE---LOOTHEMLTAEVDLKENIELGNLF 1720
Db      1345 QASAGIIEEDRTARSALKLKNBEVESREBAQALQOEGELKVAGKALQENLAL---- 1400
Qy      1721 KNEAOQTTKEOCLLNENKELEQSOHLOCEIIEELMKSLEKESALLETLKESQKVINLN 1780
Db      1401 -----LQTLAREEBEVELTRGQIOELEKQREMQKALBELLSLDKK---RN 1444
Qy      1781 QEMEVNMLEBELKMSQRTVIAERDQLODDLESEVMSLEFODDLKRAQOALQOQKDY 1840
Db      1445 QEVDLQOQIOELEKC-RSVL-----EHLMAVO-----ERQOKLTVOREQR 1486
Qy      1841 EL-----TSOISVLOKISLLE--NOMLVNATVKTLSERDDLNSKQHLFSEIETLSIS 1894
Db      1487 ELEKRETOENVLEHOLELEKKQVIE-----SQRGOVODIKQOLV-LDECLALE 1536
Qy      1895 LKEKEFALE-----QAEKDKADARKTIDITEKISNIEBO-----LLOQATNL 1937
Db      1537 LEENHNKMECCQOKLKELEGQRETQVVALTHLTLDLEBSQGLQOQSIHDLSEHSTVL 1596
Qy      1938 KETLYERSLQCK---EQLALNTEHLERTLKSDALAKMGOER---DEANKVYA 1988
Db      1597 ARELOEROEAVKSGREQIEELOROKENHLODLERRDOEL-MQOKRIVQLEQRQRTKI 1655
Qy      1989 LTEKSSLEBOQINE---NVT-----LKEGEGEKETFYQRSKQOSSQOMELRKS 2037
Db      1656 LEBDEEQIKLSIREGRELTQORQIMOERAEERGK-----PSKARQS-LEHMKIT 1705
Qy      2038 LKTKDLOLEAEKEISEATNEIKNTLAKISLEEBELQNASITLNAVSE---RENLRHS 2093
Db      1706 LRDKKEVEGCOQENHLELOELKDQOQOGLHRKVGEISLLSGREQEVIVLQOQLOQA 1765
Qy      2094 KOQVSEIQLSLTKSRDHAFOSKREKDEAVNKIASIEIKILTKEMDEFDRSKESL 2153
Db      1766 REQ--GEIKEQSL-----QSQIDEAQRALAQDQDELEALQOEOQOQOQCEBERV 1811
Qy      2154 QEOSHLEBEL---CTYKT---ELQMLKQCKEDINNKLAEKVAVDELQHLSTLKEQL 2206

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Db      1812 KEKADALQALBQAMTLTKERHGEIJDHKEQARBLEEELAVEGRRV-----QALEEVL 1864
Qy      2207 DOIQWELNREKLRNVELCEKMDIMEKEISVLFMQN--EPOE-----EDDAERMD 2256
Db      1865 GDLRAESR-----EOBKALLQOQCAQOAEHEVEYTRALDQSWLOQA 1908
Qy      2257 ILESRNOEIOELMEKISAVYSEQHTLISLSSELOKETEAHGMCLINIKESLSTLSRSP 2316
Db      1909 VKERDQDELEALRAE-----SQSRHBEAARAR-----AEALOELGKXH 1949
Qy      2317 GSLQTEHVYKLTQLOTLNKFVYVRYTAUVKEDSHLIDYEXDLAEQKRHDE----LR 2371
Db      1950 AALQ-----KEQHILLEQ-----AELSRSLSEASTATQ 1977
Qy      2372 LOLQCLEQHGKRWSSASSELKFCETIEFLNELLFKKANIGQVODFSEVQVFLQVQST 2431
Db      1978 ASLDAQOASRQ---LEBALRIOEGEIODOL-----RYQBDVQOLOQALQO--- 2021
Qy      2432 LOEELHKKGFQWLEEFQDLHVDAKKLSEGGQENRRIASTIOLTLTKRLKAVOSKIQ 2491
Db      2022 RDEELRHQOERQOLLEK-----SLAQVOENMIOEKUNIGORE--EEIRGLHQS--VR 2072
Qy      2492 EITVYLANFEAKLOEKKEQNKELMRMBHGPSASVMEENARLIGILTYODESKLQOS 2551
Db      2073 ELQTLAQKEQIILBELRETQQRNNLEALPHSKTSPMEQSKLDSLEBRLORELERLQA 2132
Qy      2552 RIKMLENE-----LNLVQDAMHGK--EKVALDQKLSRNAEALNMOVL 2597
Db      2133 ALRQTEAREIEWEKAODLALSLAQTKASVSSLOEAMFLQASVLERSEQO----- 2184
Qy      2598 TKQODNLOAMKEINLQOMVAKGAVPYKE-----EINLKTQVVKIEMEKI 2645
Db      2185 RLQDELELTRALK-BKLSPGATSTALCSREQOQVQGEVGEVBEPSDPGMEKOS 2242
Qy      2646 YSKATDOEIALYKSLCEDEKEBGLRLKEBLRRAQANDTVCVPRQYQKASTFPTCCGG 2705
Db      2243 W-----RQLEHLQCAVARLEIDRSLLQHN-----VQLRSTLE---QDG 2279
Qy      2706 SGIVOSTAMLV--LOSEKALEREIS-HYKKYVHLSRTWSSSEDRKKTAKASDAHSHT 2762
Db      2280 RGQKNSDAKCAVLEQKEVULLQAOQLTLERKQKODYITSAQTSRRE-----L 2325
Qy      2763 GSHRSGPHKTETTHNGVTPERSSEMPSLHLGSPKSSSTSRVVSPPRSEIYQOLWSP 2822
Db      2326 AGLHNSLSHSLIAVAQAP-----BATVL-----BAETRL-----DESLQSLTSP 2366
Qy      2823 GKTGMKHILSPS 2835
Db      2367 GPVLDHP---SPS 2376

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RESULT 7
US-10-116-712-670
; Sequence 670, Application US/10116712
; Publication No. US20030194764A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Switzer, Ann
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.568
; CURRENT APPLICATION NUMBER: US/10/116,712
; NUMBER OF SEQ ID NOS: 670
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 670
; LENGTH: 1232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-712-670

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Query Match      6.4%  Score 946;  DB 12;  Length 1232;
Beet Local Similarity 24.9%  Pred. No. 1.3e-40;

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QY 351 KEILDKQOLENLESSSETKAQAMAKEBHDTOLAEIKOLHKEREDRIWHLTNIIVASSOE 410
Db 349 AELNLKQOVQOL-----QVLL----- 365
QY 411 SOQDORVKRRRVTAWPAKIONSLSHAGVSDPDMLSRLPGNFSKAKAFSDMSPFEIDDS 470
Db 366 -----LQAHG-----CTLPGSITVE-----PS----- 382
QY 471 VCTERSDFPDALSMWDSNGIDAEMNLASKYTHREKTS--LHOSMIDFGOISDSVOFHDSS 528
Db 383 -----ENLOSIMEKN-----QSLVEENKLSRGLSEACQTAQMLERIIITWEOA 426
QY 529 KENOLOYLPKDSGDMAECCR--ASFEKEITSLQOOLOSKE--BEKKELVOSFELKIALEBO 586
Db 427 NE-----KONAKLELRQHAACKLDLOKLVETLEDOELKEVETICNLQOLITQLSDE 479
QY 587 LSVKAKNLEMYNBSREHSINAEVQTDVEKEVVRKEMSVLGDSGYNASNDLDDSSVDGR 646
Db 480 -----TYACMAAIDTAVEGEAQTSPF-----TSRSSDAFTQHAIR 518
QY 647 LSSSHDECEHRKMLEQKTVLDEEPTENLKK--SENDKO--KSESDFMESIQLCRAIMAE 704
Db 519 QAOMSKEIVELNKALALK-----EALARKWQDQSOLOPIQOYQDNI----- 561
QY 705 KANALEELALMRDNFDNITLENETLKREIADBERSIKENOETNEPEILEKEKOEKEHQAOL 764
Db 562 KEPELEVINLOKEK--EELVLELOJAKKDQNAQKLESERRRKLQOLEGQIADLKK----- 615
QY 765 IHEIGSLKLVENAEWYNOONLEEDLETCKLKEOEIOALERKRADNLOKKVRNEDLSV 824
Db 616 LNEOSKRLKTKSTERTVSKLNOET---RMKKNQOVOL--MKOMEDAE--KFRQW---- 664
QY 825 SWGSEKLCCEEIFOLKQOSLSDAEAVTRDAQKSCFLRSNLELKEKEDTSMWYNQEKKA 884
Db 665 ---KOKEDKEVIOJKE-----RDRKQO-----YELLKERNFQOSVNLRRKTBE 706
QY 885 ASLFEKOJETESKNKKMADLOKELQSAFNEINIYNGU--LAGKVPRLLSRVELEKVV 942
Db 707 AAANKRKLKDALOKOREV--ADRRKKTQS-----RQMEGTARUKMVLGEIEMVST 757
QY 943 SEFSKOLEKALEEKNALENEVTCLSEYKFLPNEVECKLNQISKASBEIMLLKOEGBHSAS 1002
Db 758 BEAKHNLNDLEDRKILADQVAKKE-----KKEGSENP 793
QY 1003 IISKOEIIMQESQOILQUTDEVTHTQSQVQOTEROYLEMKWMDLFEKYIRNKSEAD 1062
Db 794 KLRRRTFSLTEVRGQV-----SESED 814
QY 1063 -LLREMEULKGTWSEVEVKIADTKHEL--EETIRDKEO-----LHEK--KYFF--QA 1108
Db 815 SITKOIESLETMEFRSAQIADLOOKLDAESEDPRKORMENIATILKCAKLYIGEL 874
QY 1109 MOTIPIPIPLSDSLPPSKLVEGNSODPIEINDYHMLALATERNNIMVCLTERNSLKEO 1168
Db 875 VSSKIQVSKLESLSQSKTSCADMOKM--FEERNHFAEJETELOALVAMEOQH--QEK 930
QY 1169 VIDLNTQLOSLQAOSEIK-----SDLOKPROLDEBEVLLLEEM 1207
Db 931 VLYLISQOQ--QSQMAEKQLESSEKQOQLSTLKCODELEKKNREVEQNOQ--QLLRN 987
QY 1208 ELKHLHLDQSLSIKLOLEN--LEVTREKLOTOLOEMKNITIERN--ELQTNFEDLK-- 1260
Db 988 EIKOKLTLLOVASQOKHLPKDITLSPSSFEYVQPKPKPSRVKKEKFLQOSMDIEDLKVC 1047
QY 1261 -----AEHDSLKQDSENIEOSIETODELRAAOEELR-----EOKLOVDSFPOQLLD 1307
Db 1048 SEHSVNEHEDGDDDEGDDEEWKPTKLVNYSRKINIQGSCCKMGKNKOC--GCKKQASD 1105
QY 1308 CSVG--ISSPNHDAVANOEKVSLGEVNSLOSEMRLGERDELQTSICALVSELELRAHVKS 1366
Db 1106 GCVDDCCBPBKRNNOQOGKDSLGTVERBQ-----DSSESPK-----LE----- 1143

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QY 1367 VEGENLEITRKUNGLEKEILGKSESEVLKSM--LENLEKE-----DNKKLEQAE 1414
Db 1144 ---DPEVTGSLSTFNP--VCAITPNSKILKEKCDVQVLSKTPAPSPFDLPBLKHVAT 1198
QY 1415 EY-----SSKENOFSLEEVFGSQOKLVDE 1438
Db 1199 EYQENWAPGKKKKRALASNTSPFSGCSPIEE 1230

RESULT 9
US-10-116-712-669
; Sequence 669, Application US/10116712
; Publication No. US20030194764A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Switzer, Ann
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.568
; CURRENT APPLICATION NUMBER: US/10/116,712
; CURRENT FILING DATE: 2002-04-07
; NUMBER OF SEQ ID NOS: 670
; SOFTWARE: FaalSEO for Windows Version 4.0
; SEQ ID NO 669
; LENGTH: 1232
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-116-712-669

Query Match      6.4%; Score 941.5; DB 12; Length 1232;
Best Local Similarity 24.5%; Pred. No. 2,2e+40;
Matches 375; Conservative 262; Mismatches 492; Indels 403; Gaps 60;

QY 3 EGDAAKVCVRVPLIQRE--QGDQANLQWKAGNNTISOVDGT-KSFNFDVNSHESTSQ 59
Db 6 KQIPVRVALRCRPLVPKEISEGCQWCLSFVPEBPQV--VVGTDKGFYDVFDPDSTEQBE 63
QY 60 IYQELAVPIRSALOGNYGTFAYQGTSSGKTYTMMG-----TPNSLGIITPOLAOEYF 112
Db 64 VNTAVAPLRIKGVFGYNATVLAAYQGTSGKTYSGMGAYTAEQENEPVGVIPVYQLLF 123
QY 113 KLIOEIPNREFLLRYSMEIYNETVTKDILCDDRKRPLEIRDPFRNVVADLTLELVWV 172
Db 124 KEIDKSDPEFTLKSYIEIYNEIEILDLCPSREAOQININREDPREGKIYVLTETVAV 183
QY 173 PEHVIOWKKEGKNRHYGETKNDHSSRSHTIFRMIVESRDRNDPTNSENCDAVWVSHL 232
Db 184 ALDVTSCLEQGNNSRTVASTMANSQSSRSHAFITSLQKKSKDNSS-----FRSKL 236
QY 223 NIVDLASGERASQTAEGVRLKEGCNINRSFLICQVTKKLSGQAGGFINYRDSKLTRI 292
Db 227 HLVDLAGSEROKRTVABEDRLKEGINIRGLCLGNVISALGDDKKGGFAPYRDSKLTRL 296
QY 223 LQNSLGSNAKTYIITIPV--SPDETSLTQFASHTAHVNTPHVNEVLDEALKRYR 350
Db 227 LQNSLGSNAKTYIITIPV--SPDETSLTQFASHTAHVNTPHVNEVLDEALKRYR 350
QY 237 LQNSLGSNAKTYIITIPV--SPDETSLTQFASHTAHVNTPHVNEVLDEALKRYR 350
Db 237 LQNSLGSNAKTYIITIPV--SPDETSLTQFASHTAHVNTPHVNEVLDEALKRYR 350
QY 351 KEILDKQOLENLESSSETKAQAMAKEBHDTOLAEIKOLHKEREDRIWHLTNIIVASSOE 410
Db 349 AELNLKQOVQOL-----QVLL----- 365
QY 411 SOQDORVKRRRVTAWPAKIONSLSHAGVSDPDMLSRLPGNFSKAKAFSDMSPFEIDDS 470
Db 366 -----LQAHG-----CTLPGSITVE-----PS----- 382
QY 471 VCTERSDFPDALSMWDSNGIDAEMNLASKYTHREKTS--LHOSMIDFGOISDSVOFHDSS 528
Db 383 -----ENLOSIMEKN-----QSLVEENKLSRGLSEACQTAQMLERIIITWEOA 426
QY 529 KENOLOYLPKDSGDMAECCR--ASFEKEITSLQOOLOSKE--BEKKELVOSFELKIALEBO 586
Db 427 NE-----KONAKLELRQHAACKLDLOKLVETLEDOELKEVETICNLQOLITQLSDE 479

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QY 587 LSVKAKNLEMYNNSRHSINAEVOTDVEKEVVRKENSVLGDSGYNASNDLODSSVDGKR 646
DB 480 -----TVACMAAIDTAVEOEAOVTSPE-----TSRSSDAFTTQHAKR 518
QY 647 LSSSHDECIEHRKMLEOKIVDEEFLENLTK-SENDKO-KSSQODFMESIQCEAIMAE 704
DB 519 OQOMSKEVELKALALK-----EALARKKTONDSQLOPQYOYODNI----- 561
QY 705 KANALEELAKMRDNFNPIILENETLKREIADLERSKENOEENFEILKEKTOKEHAOL 764
DB 562 KPELEVINLOKKEK-BELVLEIOTAKKANOAKLSRRKRLLOLEGOIADLKK----- 615
QY 765 IHEIGSLKLVNEMNYNOLLEDEFTKRLKKEOEIOIAELRKRADNLOKKVVRNFDLSV 824
DB 616 LNEOSKTLTKKESTERTVSKLNOEI-----RMKNQOVRQO--WRQMEDAE-KFRQW---- 664
QY 825 SNGDSKLCCEBIFOLKQSLSDAEAVVRDAQKESFARSNLELKEKEDTSMWYNQKEKA 884
DB 665 ----KQKRDKEYIOLKE-----RDRKRO-----YELLKERNFQOSVNLRRKTE 706
QY 885 ASLFEKOLETEKSNYKMEADLOKELQSAFNEINYNGE--LAGKVPRLLSRVELEKKV 942
DB 707 AAAANKRLDALOKQREV-ADKRKETOS-----RGMENRARKYKMLNGEIEVMYST 757
QY 943 SEFSKOLEKALEEKNALENEVTCLSEYKFLPNEVECLKNQISKASEEIMLKQEGHSAS 1002
DB 758 BEAKRHLNLDLEDRKITADQVAOLKE-----KXESGENPPP 793
QY 1003 IISKEIIMQOSEOQLOLTDVETHOSKVQOOTEBOYLEMKKHMDLFEKYIRNKESEAD 1062
DB 794 KURRRTFSLEVRGOV-----SESED 814
QY 1063 -LLREMENTKGTWESVVKIADTKHBL-----EETIRDKEQ-----LLHEK--KYFP-QA 1108
DB 815 SITKOLESJETEFERSAQIADLOQLDAESDRKQEMENATILKCKALKYILGEL 874
QY 1109 KOTIFITPLSDSLPSPSKLVEGNSQDPIEINDYHNILALATERNNIMVCLETERNSLKEQ 1168
DB 875 VESKIOVSKLESLSKOSTKSCADMQKML-FEERNHFAELETTELQALVMEQOH---QEK 930
QY 1169 VIDLNTQLOSLQASIEK-----SDLOKPRQODEEGEVKLLLM 1207
DB 931 VYLLSLOLO--OSQMAEKOLESVSEKEQOOLSTLKCQDBELKMKRVECEQONO-QLRREN 987
QY 1208 ELIKGLHLDTSQLSIEKLOLEN--LEVTETKLOLQOEMKNITIERN--ELQTNFEDLK-- 1260
DB 988 EIIKQKLTLLQVARSQKHLPKXOTLLSPDSFEYVQKPKRSRYKEKFLQESMDIEDLKVC 1047
QY 1261 ----AEDSLKODLSENIEQSIETODELPAQOEELR-----EOKOLVDSFRQOILLD 1307
DB 1048 SEHSVNEHEDGDGDDEGDDEBWKPTKLNVVNSRKNIOGSCSKGMCNKKOC--GCRQOKSD 1105
QY 1308 CSVG-ISSNNHDAVANQEKVSLGEVNSLOEMLRGERDELQTSCKALVSELELRAHVNS 1366
DB 1106 CGVDDCCCDPTKCRNRQOGKQSDLSITVHTO-----DSSESFK-----LE----- 1143
QY 1367 VEGENLEITRKLNGLEKEILGKSESEVLKSM--LENLKE-----DNKLEQAE 1414
DB 1144 ----DPEVTPGLSFFNP--VCATPNKSLIKEMCDVQVLSKTPRAPSPFDLDELGHVAT 1198
QY 1415 EY-----SSKENQPSLEEVSSQOKLVE 1438
DB 1199 EYOENKAPGKKKKRALASNTSPFSGSGPIEBE 1230

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RESULT 10
US-10-205-823-419
; Sequence 419, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.

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; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbatcheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glatz, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 419
; LENGTH: 1979
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-419

Query Match 5.9%; Score 872; DB 15; Length 1979;
Best Local Similarity 21.5%; Pred. No. 1.6e-36;
Matches 500; Conservative 404; Mismatches 788; Indels 634; Gaps 92;

QY 266 LGOVKKLSDDQAGGFIVRDSKLRILLQNSLGNKAVIITCTIPVSPDELTSLQFAS 325
DB 12 LGO-----SLQGGGSLASTLGOISNFTKMDL----- 38
QY 326 TAKHVRNTPHNVLEVD-----EALLKRYKEILDLKQOLENLESSSETKAQAMAKESH 379
DB 39 ----MEGEBVAVELPDRKTEIEAIIHLRSENRLKKTCTDLEKHA-SEIQIKQOS 93
QY 380 TOLLAEIKQLHKEERDRIWHLNIVASSQESQDQRYKRRVTWAPKQIONSLSHASY 439
DB 94 TSYRNLOQO---KEVEISHL-----KARQIALQDQDLKLOSAQSVPS-----GAGV 137
QY 440 SDFDLMSLRPGNFSKAKAFSDMPSPEIDDSVCTEFSPDLDLSMWDNSGIDAEWNLASK 499
DB 138 -----PATYASSSF-----AYG 149
QY 500 VTHREKTSLHQSMIDFGQISDVQPHDSKENOLOYLPRDSG---DMAECRKA-----SF 551
DB 150 IGH-HPSAFHDDMDPGDISSQO-EINRLSVESRLEBEVGHMWHIAQTSKAOGTDND 207
QY 552 EKEITSLOQLOSKKEBEKELVQFELKIALEBOLSV--KAKNEMVTNSRHSINAEV-609
DB 208 QSEICKLQNI-----KELKONRSQEIJDQHMSVYLQNAHQOKLEISRRH---RE 257
QY 610 QTDVKEVVRKEMSVLGSQGYNASNDLODSSVDGKRSSSHDECIEHRKMLEOKIVDE 669
DB 258 LSYDERIELE-NLLQCGGSGVITDLSKIYEMQTIQVLOIVKVESIKRQEO---LE 312
QY 670 EFIEMLNKK--SENDKOKSEQODFMESIOLCEAIMAEKANALEELAKMRDNFNPIILEN 726
DB 313 DKIKOINKKLSAENDR-----DILRRQO--EQUNVEKQIEMEC----- 350
QY 727 ETLKRIADLERSLKENOETNEFEILEKTOKEHAOLIHETIGSLKLVNEMNYNOL 786
DB 351 ENLKLECSKLOPSAV----- 365
QY 787 EDLEFTKTLKKEOEIQLAELRKRADNLOKKVVRNFDLSVSGDSKLCCEBIFOLKQSLSDA 846

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Db 366 -----KOSDPTMEKERILAQASAV-----EEVFRLOQALSDA 397
Qy 847 ---EAVTRDAQKCSFLRSENLELKEMETSWMYNQKRAASLFEKQETESKNYKMA 904
Db 398 ENEIRLSSLDNDSNLAEDNLKWKRIE-----VLEKEKSLSQEKE 439
Qy 905 DLQKELQAFNINYLNGLAGVPRDLLSRVLELEKKEVFSKQETEKALEEKNALENEVT 964
Db 440 ELQMSLLKLNNEY-----VIXSTATRD-----ISLSEHLDLKLNLEAKQELN-----Q 485
Qy 965 CLSEVKFLPNEVECLKNQISKASEEIMLKQEGESHASIISKOEIIMQDSQOILQLTDE 1024
Db 486 SISEKETILAEIEBLDRQOQATKHMILIKQO-----LSKQO-----NEGDSIISLQKD 535
Qy 1025 VTHTSKYOQTEBOYLEMKKHNDLPEKITRNKSEADLLREMEINKGTMESV----- 1077
Db 536 LNDEKKRVHQLDDMDITKELDVQKEKLIQSEVALNDLHLTKQKLEDEVNMLVDQUNKS 595
Qy 1078 ---EYKIDTKHELETIRDKQOLHEKKYFQAMQTIPIPIPLSDSLPSPKLVESGNSQ 1134
Db 596 QESNVSTQKENLEKHEIRONE----- 618
Qy 1135 PIEINDYHNLJALATERNNINWCLETERNS-----LKEQVIDLNTQLOSLQASIEKSD 1188
Db 619 -----ELSRIRNELMQSLNDSNSNFKDTLKEREADEVNRLKQNLSELEQUNEN 667
Qy 1189 LQKPKQDLBEGEVKULLEMKHLKHLTD-----SQLSIEK-----LQLENEVTEKL-- 1235
Db 668 LKKVAFVYMENEKVLVACEVDRHQLEBCLAGNNOISLEKNTIVETLKEKEIEIHELQW 727
Qy 1236 ---QLOREMK-NITIER--NELQTNFBDLKAHNSL-----KOD-----LSENTBO--- 1276
Db 728 AKKRLEENKYEKTEIELSNNRNINTSALQLEHEHLIKLNQKQMEIAELKKNIBQMDT 787
Qy 1277 -SIEQDELRAAQOELREQOVLDSFRQOLDCSVGISSPNHDAAVANOKEVSLGEVNSIQ 1335
Db 788 DHKFKDVLSSS---LEEQKQLT-----QLI-----NKEIEIEKLKERS 824
Qy 1336 SEMLEGERDELOTSKALVSELELIRAHKVSVEGENLEITTKLNGLEKILKSEBSVYL 1395
Db 825 SKL-----QEBLDKYQAL-RKNEIILRQTE-----EKDRSLGSMK-----EENMHL 865
Qy 1396 KSMLENLEKEDNN-----KLKEQAEVSSKENQES-----LEEVFSSQKLVDEIELV 1442
Db 866 QEEERLEBESRTAPVADPKTLDVTEVLASVSQNTIKHEHLBEIKHNOKIIDQONS 925
Qy 1443 KAQL--KAAERLEIKDRDY-FELVQNTANTNLVEGKLETPLOADHEEDSIDRSEMEIK 1499
Db 926 KMQLQSLQEQKKEKDEFRYQHEQNNANTHOLF-----LEKDEIKSLQKTIQOIKQ 978
Qy 1500 VLGEKLE--RNQVLLERLOEBELSNKLEILQ-KEMETSVLLDDLOQKLE-SLSS- 1553
Db 979 LHEERQDQTDNSDIFQETKVQSLNIBNGSEKHDLSKATERLVAIGIKEREHELKILNEM 1038
Qy 1554 NIILKENIDTTLKHSIDTQAO-LQKTQOQLQAKMLAASDNCPTQOKETSACQVNL 1612
Db 1039 NISLTKQIDQSLKDEVGKLTQIIOQKDEIQ-ALHARISSTSH---TQD----- 1083
Qy 1613 EKKILTEELHQKTEQNEQKLEHKNLEBQAOVELKCEVENHMKMSISKSLSELOHE- 1671
Db 1084 ---VYTLQOQLOAYAMERKAVAVLNEKTRNSHLKTEYHKMDVIAAKAELIKLODEN 1140
Qy 1672 -----KHDTL-----QQLLAKQOMQVVTQEKEL 1696
Db 1141 KKLSTRESSQDMFRETIONLSRIIREKIDIBALQSCQTLVLAVLQTSSTGNBAGVN 1200
Qy 1697 QOHTHLTAUVHLKENIELGANFKRBAQKTKKEQCLINENKELEQSHRLOCEI----- 1752
Db 1201 SHQFELLQERDKLQOQVKMEWK---QQVMTVQNMQHEBAQOEBELHQAQAVLVDS 1257
Qy 1753 EELMSLKDKEGALFETKESEQVINLQMEMMMLMELEKNSQRTVAIEBDQOQDDLR 1812

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Db 1258 DNNSKLOVDYTGILQSYEQNETKLNFGQELAQVQHSIGOLCNTRKDLLGLKDIISPOL 1317
Qy 1813 ESEVMSIETODDLRKA-----QEALQOQKDVQELTQISOIVLQEKISLLENOM 1860
Db 1318 SASLITPQSAECLRSKSEVLESESELQOEBELIRKSLQEDATITRTIQENNHLSDBI 1377
Qy 1861 LVNVAIVKETSERDDLQNSKQFLPSEIETLSLSKEKEFALEQAQEKADARKTIDIT 1920
Db 1378 ---AATSELERKEHQOTSEIKQLEKQDVLOKLLKEKD-LIKAKSDQLSSNE--NFT 1431
Qy 1921 EKISNIEBOLQO-TNLKETLY-----ERESLQCKEQLALNTFLRET---- 1964
Db 1432 NKVN--ENELRQATNTNKEKRLILLEMIDIGLKGNEKIVEYRQKETEYQALQOETNMKF 1489
Qy 1965 -----LKSQDLALGKMEORDEA-----ANKVIALTEKMSLSLEQOINEN 2003
Db 1490 SMLREKEPECHSMKEKLAIEFQDLKEKQGTGLNOLNANVSKMOETTVFOORDDV 1549
Qy 2004 VTLKEGEQEKETFLQO---RPSKQSSQWELRESLTKTDLOLEEA-EKEISEATNE 2058
Db 1550 MIALQKQMENTALQNEVQRLDKREFRQNOELERLNLH---LSEDSYTRHALAEDR 1605
Qy 2059 IKNTAKISLSEBELQANSILNEAVSERENLRHSKQOVLSEL-EQLSITLKSQDHAFAQ 2117
Db 1606 EAKLRKKVTVLEKELVSSNM-----ENASHQASVQVESLQOQLNVVSKORDET--- 1655
Qy 2118 SKREKDEAVNKIASLAEIKILTKEMDERFQSKESLOQSSHL-SEELCTYTELOMLQ 2176
Db 1656 -----ALQUSQOEVQKQYALSLALQVLEFFQOEBKAMYSAELEKQO 1700
Qy 2177 QKEDINNKLAEKVEDEHLQHLSLKEQLDQIOMELNREKRLNELCEKMDIMEKEISV 2236
Db 1701 -----LIAEWKKAENLEKGVISLQCLDBANALASAS---RLTQDLVKEQOIE 1749
Qy 2237 LRLMONEQOEE-DDVAER-MDILESNOEIOELMEK-----ISAVVSEQHTLLSSLS 2288
Db 1750 LK-RQNELRQEWLDDVQKMLANSSEKGVKVLNRLFIHFHTPKNQRHEVRLMS 1808
Qy 2289 ELQKETEAKHGMNLIKESLSTLS--RSFGSLQTEHYKYNLQDTLLN-KKVVYRTPA 2345
Db 1809 ILGVRREMEBOLFHDQGSVTRKMTGWLGGSKSVNPLRPNQOSVANSFSELVFKFL 1868
Qy 2346 VKEDSLIKDYEKDLAEOKRHDELRLQOCLQCHGRKMSDSASE 2391
Db 1869 ETEHPSIIPPKLTV-----HD-----MKPLDSGGRKKRDPINAE 1903

RESULT 11
US-09-820-843A-113
; Sequence 113, Application US/09820843A
; Publication No. US20030039963A1
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEIN
; TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
; FILE REFERENCE: 063915
; CURRENT APPLICATION NUMBER: US/09/820,843A
; CURRENT FILING DATE: 2001-03-30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 113
; LENGTH: 2354
; TYPE: PRT
; ORGANISM: L. major
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: AC005802_5 L6202.3
; NAME/KEY: misc feature
; OTHER INFORMATION: gi|6899670
US-09-820-843A-113

Query Match 5.6%; Score 821; DB 11; Length 2354;
Best Local Similarity 19.4%; Pred. No. 8; Se-34;

```

Matches 514; Conservative 474; Mismatches 1013; Indels 646; Gaps 91;
 Oy 333 TPVNEVLDDDEALLKRYREIIDLK-----KOLENESSESTKQAMAKEEHTOLIA--- 384
 Db 123 SPOPASVSTATLVHVEEDAVSTKPSVEADHLNLSIITLLOQLNDEGNALMAALS 182
 Oy 385 EIKOLHKEEDRIWHLTNIVASSQ-----ESQODQVKRRVTAAPGIQNSLHAS 437
 Db 183 AAEQLRTAKEB-----NTALKSTAHLLQORLDTATQORAELEAVARLAADRDEARQOL 236
 Oy 438 GUSDPMLSRLPGNFSEKAKFSMPSPFIDSVCTEFSDFDALSMDNSGIDAMNLA 497
 Db 237 AANAEELQORLDTATQORA-----ELEAVARLAADRDEARQOLAN-----A 279
 Oy 498 SKYTHREKTSLHQSMDIFGOISDVQFHDSSKENQOYLPKDSGMAEGRKSAFEKEITS 557
 Db 280 EELQORLDTATQOR-----AELEAVARLAAD-GDSARQOLANAE----- 320
 Oy 558 LOQOLOSKEEKEKELVOSFELKIA-----ELEBOLSVKAKNLEWVNSREHSINAEVQ 610
 Db 321 LOORLDTATQORAEI-----EAVARLAADRDEARQOLANAEELQORLDTA-----TOOR 371
 Oy 611 TOVEKEVVKEMSVLGDSGMASNSD--LQDSSVDGKRILSSHDEIEHRKMLECKIVL 668
 Db 372 AELEAQLARL-----AADRDEARQOLANAEELQORLDTATQORAELEAVARL 420
 Oy 669 BEEFIEIANKSENDKOSSEODFMESIQCEAIMAKKANALEBTALMRNFDNIIENET 728
 Db 421 AANAEELQORLDTATQORAELEAVARLAADRDEARQOLANAEELQORLDT 472
 Oy 729 LKREIADLE---RSJKEOETNEFEILEKETOKHEHAOLTHEIGSKLVENAEVNYON 784
 Db 473 ATQORAELEAVARLAADRDEARQ-----OLANAE-----E 504
 Oy 785 LEEDELTCKKLKEQIOIALBELKRADNLQKVRNFDLSVMSGDSKLEBEIFOLKOSUS 844
 Db 505 LOORLDTATQORAELEAVARLAANAELO-----QRLD 538
 Oy 845 DAEAVTRDAQECSFPRSENLLEKEMBDTSMWYNOKERASLFEKOLETEKSNYKMEA 904
 Db 539 TATQORAELEAVARLAADRDEARQOLANAEELQORLDTATQORAELEAVARLAANAE 598
 Oy 905 DLQKELQSAFNEINYLINGLAG-KVPRDLISRVLEKVKVSEFSKOLEKLEBNALENEV 963
 Db 599 ELQORLDTATQORAELEAVARLAADRDEARQOLANAEELQORLDTATQORAELEAV 657
 Oy 964 TCLS-----EYKLPNEVECLKNQISKASSEIWLKQEGHSAIISKOIIMQESQEI 1018
 Db 658 ARLAADRDEARQOLANAEELQORLDTATQORAELEAVARLAADRDEARQOLANAEEL 717
 Oy 1019 LQLTDEVTHTQOSKVQOOTEBOYLEMKIMHDLFEKYIRNKSSEADBLIREMENTLKGTMESVE 1078
 Db 718 QORLDTAT-----QORAELEAVARLAADRDEARQOLANAEELQORLDTATQORAELE 771
 Oy 1079 VKIADTKHELEETIRDKQOLHEKKYFQAMQOTIFPTPLSDSLPSPKLVGNSQDPTI 1138
 Db 772 AQLARLAADRDEARQOLANAEELQORLDTA-----TOORAEI 809
 Oy 1139 NDYHNLIALATEERNNTWCLETERNSLKEQVIDLNTQLOSLQOSITEKSDLOKPKQDLE 1198
 Db 810 E--AQVARLAADRDEARQOLANAEELQORLDTATQORAELEAV-----VAALADRDE 861
 Oy 1199 GEVKLLLEMBELKGHITDSQLSIEKQLENLLEVTEKQLTOLOEMKNITIERNELQTNFED 1258
 Db 862 AROQOLANAEELQORLDTATQORAELEAVARLAANAEELQORLDTATQORAELEAVAR 921
 Oy 1259 LKAHDSLKQDUSENTEQOSTETODELRAAQEELREOKQVLDSFRQQLDSCSVGISPPNHD 1318
 Db 922 LAADRDEARQOLANAE-----LOQRLD----- 945
 Oy 1319 AVANQKSVLSIGEVNSIQSEMTLGERDELOTSKALVSELELLRAHVKSVEGENLEITTKKL 1378
 Db 946 -TATQORAEI-----EAQVARLAADRDEARQOLANAELO-----QRLDTA--- 986

Oy 1379 NGLKEKELKSGSEBSVLKSMLENTKEDNNKLEQ-----AEEYSKKNOPSLBEVPSGOK 1434
 Db 987 -----TOORAELEAVARLAADRDEARQOLANAEEL-----QO 1020
 Oy 1435 LVDEIEVLKQOLKAAEBELEIKDRDYFELVGTANTNVLGKLEPFLQADHEDSDIDRSE 1494
 Db 1021 RLDTATQORAELEAVARL-AADRDEARQOLANAEELQORLDTATQ-----ORA 1069
 Oy 1495 EMEIKVLEKLERNOYLLERLOEKELESNKLEILOKEMETSVLKKDLOOKLESLSLEN 1554
 Db 1070 ELEAVARLAADR-----EARQOLANAEELQORLDTATQORAELEAVARLAADG 1121
 Oy 1555 IILKENIDT--LKHSDDTOAOLQTOEQLOLANKLAIAASDNCPTIOKETSADCVHP 1611
 Db 1122 DEARQOLANAEELQORLDT-----ATQORAELEAVARLAADRDEARQOLANAE--E 1173
 Oy 1612 LEEKILLTEBELHQCTNEOKELHEKNLEBOAQUELVKCEVEHLMKSMIESKSLS 1667
 Db 1174 LOORLDTATQORAELEAVARLAADRDEARQOLANAEELQORLDTATQORAELEAVAR 1233
 Oy 1668 LOHEKHDTEQOLLA-----LKQOMQVVTQEKKELOQTHEHLTAEDVHLKENIELGPNFE 1723
 Db 1234 LAADGDEARQOLANAEELQORLDTATQORAELEAVARLAADRDEARQ-----QLANAEEL 1291
 Oy 1724 AQOQTTKEOCLINENKELBESOHRLQCEIIEBLMSL-----KDXSA 1765
 Db 1232 QORLDTATQ-----QRAELEAVARLAANAEELQORLDTATQORAELEAVARLAADRDEA 1347
 Oy 1766 LETTKESQKVININQOEWMLMEELKNSQRTVIAERDLODDLRSEVMSIETODDL 1825
 Db 1348 ROQLANAE--LOORLDTATQORAELEAVARLAADRDEARQOLANAE--ELOQRL 1401
 Oy 1826 RKAQELAQOQKQVQELTSOISVLQEKISLLENQMLYVAVTKETLSERDDLQSGOKHLF 1885
 Db 1402 DTATQORAELEAVARLAANAEELQORLDTATQORAELEAVARLAADR--EARQOLA 1458
 Oy 1886 SEIETLSLSEKKEPALQOEKDKADAARKTIDITEK---ISNIEE--QLLOQNTLKE 1939
 Db 1459 ANAEELQORL--DTATQORAELEAVARLAADRDEARQOLANAEELQORLDTATQORA 1515
 Oy 1940 TLVERESLI-----OCKQOLNTEHLRETLKSK-----DLAQKMOERDEANAKYI 1987
 Db 1516 ELEAVARLAADRDEARQOLANAEELQORLDTATQORAELEAVARLAADRDEA----- 1570
 Oy 1988 ALTERMSSLEEOINENVTTLKEGEKETFYLO-----RPSKQSSQWMEELRESLTKXD 2042
 Db 1571 --ROQLANAEELQORLDTATQORAELEAVARLAADRDEARQOLANAEELQORLDT-- 1626
 Oy 2043 LOLEBAEKEISATNIEIKNLTAKISSLEBEIILQNASILNEAVSERENLRHSQOLVSELE 2102
 Db 1627 -----ATQORAELEAVARL-----AADRDEAR--QOLANAE 1657
 Oy 2103 QLSLTKSRDHAFAFSKREKEAENVKIASLAEIKILTKEMDEFPSKESLQOSSHSE 2162
 Db 1658 ELQORL-----DTATQORAELEAVARLAADRDEAR-----QOLANAE 1696
 Oy 2163 ELCTYKTELQMLKQOKEDINNKLAEKVKEVDELLQHSLSKQLODOIQWELNEKLRNVE 2222
 Db 1697 EL--QORLDTATQORAELEAVARLAADRDEARQOLANAEEL--QORLDTATQORAE 1750
 Oy 2223 LCEKMDINEKEISVLR-----LMONEQOQEDDVAEMMDLIESNOSTIOELMEKI 2272
 Db 1751 LEVENAVALLREEREARGETAVAGBOVOYRELVEEBEECKEKERMWCLIESVQAQLE--A 1806
 Oy 2273 SAVYSEQHTLSSLSSELQKETE-KHQMNLKESLSSTLSRSGSLQTEHVAKINTQO 2331
 Db 1807 SAAKQOQROEVAKANEVOERLDSMARCTIAHEGAPQPADRDALROLANLREBVKLS 1866
 Oy 2332 TLINKFKVYVRT-AAVKEDHSLIKDYEKDLAAEQKRHDELRLQLOCLBQHGKWSDSASE 2390
 Db 1867 ---EKQKMERVIIPQVRERQMLE-----AAEBGRAD--LEARLVDBAGLRSRPAAS 1914

QY 2391 ELKFEIEFLNELLEFKKANIIOVDDFSEVOFLVQVSTLQOELEHKKGFQWLEBFG 2450
 DB 1915 T---NEVNLRYRLALOEH---EAAQNRCTTLEA---QVASLTSDR----- 1950
 QY 2451 DLHVDAKLSSEGQENRRIASTIQLTLRLKLAVVOVKIQREITVYLVNFEAKLOEKKQ 2510
 DB 1951 -----DNGRQOESADL-----SEAQRHLD-----NVQE----- 1973
 QY 2511 NKELMRMEHHPSPASVMEENARLLGLIKTYODESKQOSRIKMLENL----- 2560
 DB 1974 -----RDMAHH---RCAALEEQNAAMASELQAVAKLRQASVKAASSLMTRLSASSGAGV 2026
 QY 2561 -----NLVKDDAMHK-GEKVALIIOBKLSRNAEAELNMQVLTQKQDNLOQAMKE 2610
 DB 2027 SARVAVGSSAVPQAAPRHDALIAVGBRLBERGAMRLBEGVELRRARPLEVLAIE 2086
 QY 2611 IENLOKMAKGAVPYKEEIDNLKTKVVKIEMEKIKYSKATDOELAYL---KSCLEDEKEG 2667
 DB 2087 -----KLIGDRRTSDAEVATEPTQV---RRNAASHRLDSREAQLDERAARLEKEEQ 2137
 QY 2668 LRLRLKEELR-----RAQ-----ADNPTVC--VPKDYQKASTPPVTCG 2703
 DB 2138 LRLVARELQTKSRALQVLYARALNRPQVTLTLTADGDTSTPDTFQOQOQGTPTP--- 2193
 QY 2704 GSGGIVQSTAMVLQSEKALEREISHYKKYKHYHLSTRWSSEDRKKTAKSDAHSHTG 2763
 DB 2194 -----LREPVSLDEVAHY-----GRTAGAAV----- 2216
 QY 2764 SSHRSPHKTEITYRHGVPYTERSEMPSLHSGPKSESSTKRVSPN---RSEIYSQLVM 2820
 DB 2217 SSGGLASPL-----PREPRARVHVRAVEATGTEDTQVRLTATEAVRDLVEHILE 2268
 QY 2821 SPKGTGM 2827
 DB 2269 SNGLOGV 2275

RESULT 12

US-09-874-923-120
 ; Sequence 120, Application US/09874923
 ; Patent No. US20020081320A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Campos-Neto, Antonio
 ; APPLICANT: Webb, John R.
 ; APPLICANT: Dillon, David C.
 ; APPLICANT: Skeiky, Yashir A.W.
 ; APPLICANT: Bhatia, Ajay
 ; APPLICANT: Collier, Rhea
 ; APPLICANT: Probst, Peter
 ; APPLICANT: Brannon, Mark
 ; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
 ; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
 ; FILE REFERENCE: 210121.420C8
 ; CURRENT APPLICATION NUMBER: US/09/874,923
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 120
 ; LENGTH: 2310
 ; TYPE: PRT
 ; ORGANISM: Leishmania major and chagasi
 US-09-874-923-120

Query Match

5.5%; Score 811; DB 9; Length 2310;

Best Local Similarity 19.4%; Pred. No. 2,7e-33;

Matches 475; Conservative 450; Mismatches 926; Indels 596; Gaps 84;

QY 558 LQQQLQSKSEEEKKEIVQSEELKIA-----ELEBOLSVKAKLEKWTNSRSHSINAEO 610
 DB 204 LQQRDLTAIQQRAEL-----EAQVARLAADRDEARQQLAANAELQQRDLTA-----TQQR 254
 QY 611 TDVEKEVVRKEMSVLQDSCYNASND--LQDSSVQDKRSLSSHDECIEHRKYLEQKIVDL 668

DB 255 ALEBARVARL-----AADRDEARQQLAANAELQQRDLTAQORAELEAQVARL 303
 QY 669 EEFITENLKKSEENDQKSEODPFMESIQCEAIMAKANAELALL-----MDNDPNTLL 724
 DB 304 AANAELQQRDLTAQORAELE-----AQLAR--LAADRDEARQQLAANAELQQRDLTAQO 358
 QY 725 ENETLKREIADLERSLKENEQTEFEILEKETQKEHEAQLHIEIGSL-----KLVE 776
 DB 359 QAELAEQAVARLAANAELQO-----RLDTATQORAELEAVARLAADRDEARQQLAA 411
 QY 777 NAEWYNQNLLEEDLETKYLKQEIQLAELRRRADNLQKRVNFDLSVSGSEKICEEI 836
 DB 412 NAE-----ELQQRDLTAQORAELEAQVARLAANRDEAR-----QQLAANA 452
 QY 837 POLKQSLSDAEAVNTDAQKQCSFLASENLEKXKEDTSMWYNOKEKASLSPEKQLETK 896
 DB 453 EELQQRDLTAQORAELEAQVARLAADRDEARQQLAANAELQQRDLTAQORAELEAV 512
 QY 897 SNYKXMEADLOKELOSAPNEIYVNLGLAGVPRDLISVELEKVS-----EPKQL 949
 DB 513 ARLAADRDEARQQLAANAEE-----LQQRDLTAQORAELEAVARLAANAELQO 565
 QY 950 EKALEEKNALENEVTCLESEKFLPNEVECLKNQISKASEEIMLTKQEGEHSAS1ISKOEI 1009
 DB 566 DTAQORAELEAQVARLA-----NAEELQQRDLTAQORAELEAVARLAADRDEARQ 619
 QY 1010 IMQOSEQILQLTDEVYTHQSKVQOOTEEOYLEMKMHDDLFKKYTRNNSSEADLLREMN 1069
 DB 620 QLAANAELQQRDLTA-----QORAELEAQLARLAADGDEARQQLAANAELQQRDL 673
 QY 1070 LKGTWSEVVKIADTKHLEETIRDKOELEKKKFFQOMQTFPIPTPLSDSLPSKULVE 1129
 DB 674 ATQORAELEAVARLAADRDEA---RQQLAANAELQQRDLTA----- 713
 QY 1130 GNSQDPIEINDYHNLIALATERNNIMVCLETERNSLKEQVIDLNTQLOSLQASIE--KSD 1188
 DB 714 --TQORAELE--AQARLAADRDEARQQLAANAELQQRDLTAQORAELEAVARLAAD 769
 QY 1189 LQKPKQDLEEGEVKLLLENELIKGHLTDSQSLSEKQLLENLEVTKL---OTLOEMKN 1244
 DB 770 GDEARQQLAANAELQQRDLTAQORAELEAVARLAADRDEARQQLAANAELQQRDL 829
 QY 1245 ITIERNELQTNFEDLKAEHDSLKQDL---SENIQESIETQOELRAA-----QBE 1290
 DB 830 ATQORAELEAQLARLAADGDEARQQLAANAELQQRDLTAQORAELEAVARLAADRDE 889
 QY 1291 LREQKQLVDSFRQQLDSCSVGISSPNHDAVANAQEVSLGEVNSLQSEMJRGERDELQTS 1350
 DB 890 ARQQLAANAELQQRDL-----TATQORAELE-----EAQLARLAADRDEARQ 933
 QY 1351 KALVSELEL-----LRAHYKVEGENLEITTKYL---NGLEKEITLKSESEVYL 1395
 DB 934 AANAELQQRDLTAQORAELEAQVARLAADRDEARQQLAANAELQQRDLTAQORAE 993
 QY 1396 KSMLENLKEDNNKKLEQ-----AEEYSKKNQSLSEVVSQKLVDEIVLKAQJKAEE 1451
 DB 994 EAQLARLAADRDEARQQLAANAEL-----QQRDLTAQORAELEAQA 1037
 QY 1452 RLEIKRDVFEIVQNTANNLVEGKLETPLOADHEEDSIDRSESEMIKLGSEKLERNOYL 1511
 DB 1038 RL-----AANAELQQRDLTAQO-----QAELAEAVARLAADRDE 1072
 QY 1512 LERLOEKLEISNKLLEIQKEMETSVLLKDLQOKLESILSENITLKENIDTTLKHSQT 1571
 DB 1073 -----EARGQQLAANAELQQRDLTAQORAELEAVARLAANAELQQRDLTAQORAE 1127
 QY 1572 QAQLOK-----TQOELQAKNLAIAASQNCPTQKEKTSADCVHLEEKI 1616
 DB 1128 EAQVARLAANAELQQRDLTAQORAELEAVARLAADRDEARQQLAANA----- 1177
 QY 1617 LLLTEELHQKTQEOEKLHEKKELEQAQVELKCEVEHLMKSW-----IESKSLSESLQ 1669

Db 1178 -----EELQORL---DTATQORAELEAVARLANAAEELQORLDTATQORAELEAQLARLA 1230
 Qy 1670 HEKHDTBOQLA---LKQOMQVVTQOEKELQOETHLEVDHLEKENIEIGLNFKNQAQ 1725
 Db 1231 ADRBEARQOLAAANAEELQORLDTATQORAELEAVARLANAAEELQORLDTATQORAELEAQLARLA 1284
 Qy 1726 OKTTBOCLINENNELFOSQORLOCELEELMKSLKDKESALETLKESQKVININQEMEM 1785
 Db 1285 QRELEERVARLAADRBEARQOLAAANAEELQORL---DTATQORAELEAVARL----- 1335
 Qy 1786 VMELEBKNSQRTVIAERDOLDDRESVEMSTETODDRKQOEALQOQKDVQELTSQ 1845
 Db 1336 -----AADGEARQOLAAANE---ELQORLDTATQORAELEAVARLAN 1377
 Qy 1846 ISVLOEKISLEENOMLYNATVETTESRDDLNQSKQHLSEIETLSLSKEKEFALBEQ 1905
 Db 1378 AEELOQRLDTATQORAELEAVARLANADR---EARQOLAAANAEELQORL---DTATQOR 1431
 Qy 1906 EKDKADARKTIDITEK-----ISNIEE--OLLOQANTULKELYERESLT-----QCKEOL 1954
 Db 1432 AELEAVARLANADRBEARQOLAAANAEELQORLDTATQORAELEAVARLANADGEARQOL 1491
 Qy 1955 ALNTEHLRETLKSK-----DLALGMEQERDEAANKVIALTERKSSLEEQINENVTTL 2007
 Db 1492 AANAEELOQRLDTATQORAELEAQLARLANADBEA-----RQOLAAANAEELQORLDTA 1544
 Qy 2008 KESEGETEYLO----RPSKOSSQOMELRESLTKDOLUEBAEKETSEATNEIKOL 2062
 Db 1545 TQORAELEAVARLANADGEARQOLAAANAEELQORLDT-----ATQORAELE 1590
 Qy 2063 TAKISSLEEELQNASILNEAVSERENLRHSQOLVSELEQSLTLKSRDHAFANQSKRK 2122
 Db 1591 EAVARL-----AADRBEAR---QOLAAANAEELQORL----- 1619
 Qy 2123 DEAVNKIASIAEBEIKILTKEMDFRDSKESLOESSHLESLCTYTELQMLKQCKEDIN 2182
 Db 1620 DTATQORAELEAQLARLANADRBEA-----QOLAAANAEEL---QORLDTATQORAELE 1669
 Qy 2183 NKLAEKVKEVDLLOHLSLAKEDLOLOMELRNEKIRNTELCBKMDIMEKESIVLR--- 2238
 Db 1670 AQLARLANADGEARQOLAAANAEEL---QORLDTATQORAELEAVARLANREBEARGETA 1726
 Qy 2239 -----LMQNEPQOEEDVAERMIDLESRNQOIEQIMEXISAVYSCQHTLLSSLELOK 2292
 Db 1727 VAGEQVQLVRETYEEBEELKEBWKLESVQAQURE---ASAQAQOQREVAKAKAEVQE 1782
 Qy 2293 ETEA-HKQOMLNKESLSSTLSRFSGLQTEHVKNLTOLQTLNKKVYRT-AAVKEDH 2350
 Db 1783 RUDSMARRCIEHGDAPORADGRDADLQOLANIREEVKLS---EKQKAMERVIPIGRERQ 1839
 Qy 2351 SLIKDYEKDLAEBOKHDELRLLOQLBQHRKMSASASEELKFCIEIEFLANLEFKKANI 2410
 Db 1840 MLE-----AAEBQAD--LEARLVDEAGDLRSRPAST---NEVNLVRLAQLQH- 1885
 Qy 2411 IOSVODDFSEVQVFLNQGSTLOEELHKKGFQWMELEFQDGLHVDKAKLSEMOENRRI 2470
 Db 1866 -EAAQNRCTTEA--QVASLTSR-----DNROQESADL 1917
 Qy 2471 ASTIQLITRLKAVVOSKIQREITYLANQFEAKLOEKKEONKELRRMHHGPSATVEE 2530
 Db 1918 -----SEAQRHLD-----NVOE-----RDMANH--RCALAE 1942
 Qy 2531 ENARLLGLITVODESSKKLOSRIKMLENEL-----NLVKDAMRK- 2570
 Db 1943 ONAANAASELQAVKALROASVASSIMTRLASASSGAGVSARVAVGSSAAPPQAPARD 2002
 Qy 2571 GEKVALLODKLNRNAEELNMOYKLTKKQDNLOQAMKELIENLOKMAKAGAVPYKEID 2630
 Db 2003 AELIAVEGERLBERGEAMRLLAEGVELRBRARPLRVLAE-----KLIGDRITSAAEEVA 2057
 Qy 2631 NUKTVVVIEMEKIKYKATDOETAYL---KSCLEDKXEGRLKLEIR----- 2676
 Db 2058 TEPTIV---RRNAASHRLDSREAQDERRARLRKEQOQLRVARLEQTSRALQVLYA 2113

Qy 2677 -----RAQ-----ADNDTTCV--VPKDYOKASTFPTVCGGSGGIVQSTAMVLQSEKXA 2723
 Db 2114 RALNRQVAVSLTLTADGDDTSYPTDTPQOQOQGTTRP-----LEBPYVS 2156
 Qy 2724 LEBELSHYKKYHHLSRTWSSSEDRKTKYAKSDAHSHTGSSRCSPHKTEYRHQPYTP 2783
 Db 2157 LDSEVAVY-----GRTGAAY-----SSGLASPL-----PREP 2184
 Qy 2784 ERSEMPSHLGSPPKSSSESTKEVSPN---RSEIYSQVMSPGKTM 2827
 Db 2185 PARAVYHRAVEATGTEDTQVRLTATAYRVLVLEYHLESNGLOV 2231

RESULT 13
 US-09-991-496-120
 Sequence 120 Application US/09991496
 Patent No. US20020169285A1
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Campos-Neto, Antonio
 APPLICANT: Webb, John R.
 APPLICANT: Dillon, David C.
 APPLICANT: Skeiky, Yaser A.W.
 APPLICANT: Bhactia, Ajay
 APPLICANT: Colter, Rhea
 APPLICANT: Probst, Peter
 APPLICANT: Brannon, Mark
 TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
 FILE REFERENCE: 210121.420C9
 CURRENT APPLICATION NUMBER: US/09/991,496
 NUMBER OF SEQ ID NOS: 137
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 120
 LENGTH: 2310
 TYPE: PRT
 ORGANISM: Leishmania major and chagasi
 US-09-991-496-120

Query Match 5.5%; Score 811; DB 10; Length 2310;
 Best Local Similarity 19.4%; Pred. No. 2.7e-33;
 Matches 475; Conservative 450; Mismatches 926; Indels 596; Gaps 84;
 Qy 558 LQOQLOKSEKKEKELVOSFEIKIA-----ELEBOLSVAKNLEMTNSRHSINAEO 610
 Db 204 LQORLDTATQORAELEAVARLANADRBEARQOLAAANAEELQORLDTA-----TQOR 254
 Qy 611 TDVEKEYVRKMSVLDGSGVYASNSD--LQDSSVDGRKLSSHDECTEHRKMLEOKIVDL 668
 Db 255 AELEAVARL-----AADRBEARQOLAAANAEELQORLDTATQORAELEAVARL 303
 Qy 669 EEFLENINKSEENDKQSSBODFWESIQLCEAIWAEKANLEELAL-----MRONFVITL 724
 Db 304 AANAEELQORLDTATQORAELEAVARLANADRBEARQOLAAANAEELQORLDTATQ 358
 Qy 725 ENETLKREIADLERSKENQETNEFEETLEKETQKHEBAQULIHEIGSP-----KCLVE 776
 Db 359 QRAELEAVARLANAAEELQO-----RUDTATQORAELEAVARLANADRBEARQOLAA 411
 Qy 777 NAEYNNQNLBEDELTKTKLKEOEIQLAEIRKPADNLOKVRNFDLSVSGNSEKLCCEI 836
 Db 412 NAE-----ELQORLDTATQORAELEAVARLANADRBEARQOLAAANAEELQORL 452
 Qy 837 FOLKOSLDAEAVTRDQKCESFLRSENLELKEKMEPTSNWYNQKEKVASLFEKOLETERK 896
 Db 453 EELQORLDTATQORAELEAVARLANADRBEARQOLAAANAEELQORLDTATQORAELEAV 512
 Qy 897 SNYKMEADLOKELQSAFNEINYLINGLILAGKVPDDLRSVLEKKYS-----EFSKOL 949
 Db 513 ARLAADRBEARQOLAAANAE-----LQORLDTATQORAELEAVARLANAAEELQORL 565

QY	950	EKALEKALENEVTCSEYKFLPNBVCCKNOJISKASEBIMLKQEBHSA311SKOEI	1009
Db	566	DTATQORRELAQVARIJLA-----NABELOQRDLTATQORAELEAVARVILAARDERQ	619
QY	1010	IMOESEBILUTPEVHTQSKVOQTEQYUEMKMGHDLPEFKYIRNSBADDLREMEN	1069
Db	620	QJANAEELQORLDAT-----QORAELEQJRLAADGBEARQJLANAEELQORLD	673
QY	1070	LKGTMESEVXIADTKHELEETIRDKEOJLHEKKYFQAMQTIPEITPLSDLPPSKLVE	1129
Db	674	ATQORAELEAVARILAARDREDA-----RQJLANAEELQORLDTA-----	713
QY	1130	GNSODPIEINDYHNILALATERNNIMVLETFERN3LKQVINDLTQLOSLQASIE-KSD	1188
Db	714	--TOORAELE--AQJRLAARDREARQJLANAEELQORLDTATQORAELEAVARILAAD	769
QY	1189	LQKRODIEBEVUKLLEMEJLKGHJTSQSIEKJQJENJEVTEKU-----QTOJEBEKN	1244
Db	770	GDEARQJLANAEELQORLDTATQORAELEAVARILAARDREARQJLANAEELQORLD	829
QY	1245	ITIRNELOTNPEDLKAEHDSJLKODL---SENIEOSIETODELRAA-----QOE	1290
Db	830	ATQORAELEQJRLAADGBEARQJLANAEELQORLDTATQORAELEAVARILAARDRE	889
QY	1291	LREQKOLVDSFRQJLLDSCVGISSEPNHDVANOEVKSJGEVNSJQSEWJLGERDELQTC	1350
Db	890	ARQJLANAEELQORLD-----TATQORAELE-----EQJRLAARDREARQJL	933
QY	1351	KALVSELEL-----LRAVKSJGEGNLEITTKL-----NGLEKEIJGSEBSVL	1395
Db	934	AANAEELQORLDTATQORAELEAQVARIJLAADGBEARQJLANAEELQORLDTATQORAE	993
QY	1396	KSMJENLKEDNNKKEQ-----AEYSSKENOFSEBEVSGSQKLVDEJELVKAJKAEE	1451
Db	994	EAQJRLAARDREARQJLANAEEL-----QJRLDPTATQORAELEAQVA	1037
QY	1452	PLEIKRDYFELVOTANTNLVEKJLETPJLQADHDEBDSIDRSESEMEIKVJLCEKERNQYL	1511
Db	1038	RL-----AANAEELQORLDTATQ-----QORAELEAVARILAARDR-----	1072
QY	1512	LERIQEBKLESNKLEIIOKEMERSVLLKDLQOKLBSJLENNIIEKENIDTTJLKHSDT	1571
Db	1073	-----EABQJLANAEELQORLDTATQORAELEAVARILAANAEELQORLDTATQORAE	1127
QY	1572	QAOLQK-----TOOEJQJAKULJALASPNCPITQEKTSADCVHPLEEKI	1616
Db	1128	EAQVARIJLANAEELQORLDTATQORAELEAVARILAARDREARQJLANA-----	1177
QY	1617	LLLTLEELHQKTNEOEKJLHEKNELEQAVELKCEVEHJLMKSM-----IESKSSLESJQ	1669
Db	1178	-----EELQORL-----DTATQORAELEAQVARIJLANAEELQORLDTATQORAELEAQJRLA	1230
QY	1670	HEKJIDTEGQJLLA-----LKQOMQVVTQEKKEJLQJTHEHTAEVDHJKENIEJGLNPKNEAQ	1725
Db	1231	ADREBARQJLANAEELQORLDTATQORAELEAQVARIJLANAEELQORLD-----TATQ	1284
QY	1726	QKTKKEQJLLENKELEBOSQRLQCEJIEJELMKSLKJDKESALETJESQKQYINJQEWEM	1785
Db	1285	QORAELEAVARILAARDREARQJLANAEELQORL-----DTATQORAELEAVARIL-----	1335
QY	1786	VMEJMEELKNSQRTVIAERDQJLDLRESVEMSIETQDDEKQABALQOQKQYQJELTSQ	1845
Db	1336	-----AADGBEARQJLANAE-----ELQJRLDPTATQORAELEAQVARIJLAN	1377
QY	1846	ISVJQEKJLLENQJLVAVATYKJELSRDDJNSQKJLSEJIEJTL3LSJLKEKEPALEQA	1905
Db	1378	AEEJQORLDTATQORAELEAVARILAARD-----EABQJLANAEELQORL-----DTATQOR	1431
QY	1906	EKJVDARAKTIDJTEK-----ISNTEE--OLQOQJTNJKEJTYEBSJLI-----QCKEQJL	1954
Db	1432	AEEJQVARIJLAARDREARQJLANAEELQORLDTATQORAELEAVARILAARDGBEARQJL	1491
QY	1955	ALNTEHJLEJTKSK-----DLJGKJGQBERDEANKVIALJTEKMSJLEBQJENINVTTL	2007

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Db      1492  AANAEELQORLDTTQORAELEAQLARLAADRDREA-----RQOLAAANAEELQORLDTA 1544
Qy      2008  KEGEKEKETFYLO-----RPSKOQSSQSSOMELRESLTKDLOLEAEKELISEATNEIKNL 2062
Db      1545  TQORAELEAVARLAADGDDEARQOLAAANAEELQORLDT-----ATQORAEEL 1590
Qy      2063  TAKISSEBEELONASILNEAVSERENLRHSKOOLUSELOSLTSLKSRDHAFQOSKREK 2122
Db      1591  EAVVARL-----AADRDREA---QOLAAANAEELQORL----- 1619
Qy      2123  DEAVNKIASLAEEIKILTKEMDEFRDSKESLOESSHLSBELCTYKTELOMLKOQKEEDIN 2182
Db      1620  DTAIQORAELEAQLARLAADDEAR-----QOLAAANAEEL---QORLDTATQORAELE 1669
Qy      2183  NKLAEKYKEVDELQHLSTLKEQLODOIOMELRNEKLRNYLCEKMDIMEKISVLR----- 2238
Db      1670  AQLARLAADGDDEARQOLAAANAEEL---QORLDTATQORALEVEMAVLAREBERARETA 1726
Qy      2239  -----LMQNEPQOEEEDVAERMIDLESRNOEIOELMEKISAVYSEQHTLSSLSSELQK 2292
Db      1727  VAGQOVOLYRETVEEEECLKEEBRWCTESRAVQOLRE-----ASAAAKOOROEAAKANEVOE 1782
Qy      2293  ETER-HHGHMLNITESLSTLSRFGSLQTEHVKYKLTQLOTLNKFVVVVRT--AAVEDH 2350
Db      1783  RLDSMARCEIAHEGDAPQADGRDRLQALANIREEVKLS--EKOAMERVIPGVERQ 1839
Qy      2351  SLIDYERKDLAABOKRDELRLOLQCEHQGRKXSDSASELKFCEIEFENELFFKKANI 2410
Db      1840  MRLE-----AAEQRAD---LEARLVDEAGDLSRRAAST--NEVNLVRDLAQSH-- 1885
Qy      2411  IQSVQDDFSEVOVFLNOVGSTLOEELEHKKGFQMWLEEFCDLHVDAKKLSEGMQOENRRI 2470
Db      1886  -EAAQNCRCTLEA---QVASLTSDR-----DNGRQOESADL 1917
Qy      2471  ASTQQLTKRLKAVQOSKIQREITVYLNQREPAKLOEKKENKELMRMEHNGSASVMEE 2530
Db      1918  -----SEAQRHLD-----NVQE-----RDMANH--RCALLEE 1942
Qy      2531  ENARLLGILKTVODESKKLOSRIKMLENEL-----NLVYKDAMHK- 2570
Db      1943  ONAAMAELOAVKAKLRQASVYKASSLMTRLSSASSSGAGVSARVRVGGSSAVQOAPHRD 2002
Qy      2571  GEKVAILODKLISRNAEELNAMOVLTKTKODNLOAKMEIENLOKVVAKAVPYKEID 2630
Db      2003  AELIAEYGERLRERGEAMRLLAEGVELREBARPLERVLAE-----KLIGRRTSDABEVA 2057
Qy      2631  NLKTRVVKIEMEKIKYKATDOELAYL---KSCLEDKEEGLRUKELR----- 2676
Db      2058  TEPTOV-----RRNAHSRHLDSREAOJDERBAARLRKEEQOLLEVARBELQKSRALOVLVA 2113
Qy      2677  -----RAC-----ANDDTTVC--VPKDYOYKASTFFPTCGGSGGIQVSTAMVLVLOSEKA 2723
Db      2114  RALNRFOVTSLLTLADDDTSYPTPOOQOQGRTP-----LREPVYS 2156
Qy      2724  LERELSHYKKKYVHLSRTWSSSEDRKKTAKSDAHASHHTGSSHRGSPHKTETVYRHGEVTP 2783
Db      2157  LDSEVAVY-----GRTAGAAV-----SSGLASPL-----PREP 2184
Qy      2784  ERSMPBLHLGSPKXSSSTKRIVSPV---RSEIYSOLVMSPKGTGM 2827
Db      2185  PRAMVHRAVEATGETEDTQVRLTAATEAVYADVLYEHILIESNGLOV 2231

RESULT 14
US-09-820-843A-114
; Sequence 114, Application US/09820843A
; Publication No. US20030039963A1
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEIN
; FILE REFERENCE: Q63915

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; CURRENT APPLICATION NUMBER: US/09/820, 843A
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.0.
; SEQ ID NO: 114
; LENGTH: 2310
; TYPE: PR
; ORGANISM: L. major
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: AC005893_12 L6202.3
; NAME/KEY: misc feature
; OTHER INFORMATION: g1|6899664
US-09-820-843A-114

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Query Match      5.5%; Score 811; DB 11; Length 2310;
Best Local Similarity 19.4%; Pred. No. 2,76-33;
Matches 475; Conservative 450; Mismatches 926; Indels 596; Gaps 84;

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QY 558 LQOOLQSKKEEKEKELVOSFELKIA-----ELEEOUSVAKNLEWVNSREHSINAEO 610
DB 204 LQORLDTATQORAELE-----EAQVARIADADRDEARQOLAAVAEELQORLDTA-----TQOR 254
QY 611 TDVEKEVVRKEMSVLGDGYNASND--LQDSSVDGKRLSSSHDECIEHKKMLEQKIVDL 668
DB 255 AELEAVARL-----AADREARQOLAAVAEELQORLDTATQORAELEAVARL 303
QY 669 EEFTEINLKSSENDKOKSSODPMESIOLCEAIMAEKANAELAL-----MRDNFDNILL 724
DB 304 AANAEELOQRDLDTATQORAELE-----AQLAR--LAADREARQOLAAVAEELQORLDTATQ 358
QY 725 ENETLKREIDRLERSLKENOETNEFELLEKEKTOKEHEAQLIHEIGSL-----KKLVE 776
DB 359 QRAELEAVARILAAVAEELQO-----RLDTATQORAELEAVARILAADREARQOLAA 411
QY 777 NAEMYNQNLSEDELETYKTLKEOEIOLAEELRKADNLOKKVRFDLSSVSGSEKICEBI 836
DB 412 NAE-----ELQORLDTATQORAELEAVARILAAADR-----QOLAAVA 452
QY 837 FOLKOSLSDAEAVTRDAQKSCFLRSBENLEKEMEDTSWNVQKEKAASLEKQULETEK 896
DB 453 EELQORLDTATQORAELEAVARILAADREARQOLAAVAEELQORLDTATQORAELEAV 512
QY 897 SNVKKEADLOKELQSAFNEINVLNGLAKVPRDLRSVELLEKYS-----EESKOL 949
DB 513 ARLAADREARQOLAAVAE-----LQORLDTATQORAELEAVARILAAVAEELQORL 565
QY 950 EKALEKNALENEVTCISEYKFLPNEVECLKNQISKASEEIMLKQEGEHSASITISKORI 1009
DB 566 DTATQORAELEAVARILAA-----NAEELQORLDTATQORAELEAVARILAADREARQ 619
QY 1010 IMQOSEQLQLTDEVTHTQSKYQOTEBQYLEMKKRNHDLFEKYIRNKSEADLLREMEN 1069
DB 620 QLAANAEELOQRDLDTAT-----QORAELEAQLARILAADREARQOLAAVAEELQORLDT 673
QY 1070 LKGTMSVEVKAJADTGHLEETIRDBKOLLHKKYFQAMQTIPTPLSDBLPSKULVE 1129
DB 674 ATQORAELEAVARILAADREARQOLAAVAEELQORLDTA----- 713
QY 1130 GNSQDPIEINDYHNTJALATERNNIMVCLTERNSLKEQVIDLNTQLOSLQASIE--KSD 1188
DB 714 --TQORAELE--AQARILAADREARQOLAAVAEELQORLDTATQORAELEAVARILAAD 769
QY 1189 LQKPRQDLEEGEVKULLMEELLKGHITDSQSLSEKLOLENLEVTETKL-----QTLQEMKN 1244
DB 770 GDEARQOLAAVAEELQORLDTATQORAELEAVARILAADREARQOLAAVAEELQORLDT 829
QY 1245 ITIEHNEIQTINFEDEKAEHDSLKODL-----SENIQESIETQDELRAA-----QOE 1290
DB 830 ATQORAELEAVARILAADREARQOLAAVAEELQORLDTATQORAELEAVARILAADRE 889
QY 1291 LREQKQVLDSFRQOILLDCSVGISPNHDAVANOQEVSLGEVNSLOSEMILGERDELQTSQ 1350

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DB 890 AROQLAANAEELOQRDL-----TATQORAELE-----EAQARILAADREARQOL 933
QY 1351 KALVSELEL-----LAAHYKSVGEWLETTKKL-----NGLEKEITLKSESEVYL 1395
DB 934 AANAEELOQRDLDTATQORAELEAVARILAADREARQOLAAVAEELQORLDTATQORAELE 993
QY 1396 KSMLENLKEDNNKLEKQ-----AEEYSSKENQPSLEBEVFGSQKLVDELEVLAAOLKAABE 1451
DB 994 EAQARILAADREARQOLAAVAEEL-----QORLDTATQORAELEAVOYA 1037
QY 1452 RLEIKDRDYFELVQANTNLVGEKLETPLOQADHEEDSIDRSEEMEIKVLGKELRNQYL 1511
DB 1038 RL-----AANAEELOQRDLDTATQ-----QRAELEAVARILAADRD--- 1072
QY 1512 LERLOEKLELSNKLLEILOKEMETSVLKDDLOQKLESLSENITLKENIDITLKHSDT 1571
DB 1073 ----EAROQLAANAEELOQRDLDTATQORAELEAVARILAAVAEELQORLDTATQORAELE 1127
QY 1572 QOQLOK-----TQOELQAKNLAIAASDNCPTTQEKETSADCVHPLEEKI 1616
DB 1128 EAQVARIADADRDEARQOLAAVAEEL-----TQORAELEAVARILAADREARQOLAAVA 1177
QY 1617 LLLTEELHOKTNEOEKLLHEKNELEAOVLEKCEVEHLKSM-----IESKSSLESLO 1669
DB 1178 ----EELQORL-----DTATQORAELEAVARILAAVAEELQORLDTATQORAELEAQLARLA 1230
QY 1670 HEKHDTBOOLLA-----LKOQMOVVTOEKKELQOQTHEH.TAEVDHUKENIELGLNFKMAQ 1725
DB 1231 ADRDEARQOLAAVAEELQORLDTATQORAELEAVARILAAVAEELQORLDTA-----TATQ 1284
QY 1726 QKTTKEQCLLNENKLEOSQRLQCEIELEMLKSLKXESALETTKESEOKVININQEWEM 1785
DB 1285 QRAELEAVARILAADREARQOLAAVAEELQORL-----DTATQORAELEAVARIL----- 1335
QY 1786 VMLMEHELKNSQRTYIARQDLODDLRSVMSLETQDDLRKQABALOQKQKYOELTSQ 1845
DB 1336 ----AAGDEARQOLAAVAE-----ELQORLDTATQORAELEAVARILAAVA 1377
QY 1846 ISVLQEKISLENQMLYVAVATVKEITLSERDILANSKQHLFEIETLSLSEKKEFALQEA 1905
DB 1378 ABELOQRDLDTATQORAELEAVARILAADRD---EAROQLAANAEELOQRL-----DTATQOR 1431
QY 1906 EKQADAAKRTIIDTEK-----ISNIEE--QILQATNLKETTLYERESILI-----QCKEOL 1954
DB 1432 AELEAVARILAADREARQOLAAVAEELQORLDTATQORAELEAVARILAADREARQOL 1491
QY 1955 ALNTEHLERETLKSK-----DLALGKMEODERDAANKVIALTEKMSLSLEQINENVTTL 2007
DB 1492 AANAEELOQRDLDTATQORAELEAQLARILAADREARQOLAAVAEELQORLDTA 1544
QY 2008 KEGEKEKETFYLO-----RPSKQOSSOMELRESLTKDLOLEAEKEISEATNEIKNL 2062
DB 1545 TQORAELEAVARILAADREARQOLAAVAEELQORLDTA-----ATQORAELE 1590
QY 2063 TAKTSSLEBELQNASILNEAVSERENLRHSKQOLUSELQOLSTLKSRDHAPQASKREK 2122
DB 1591 EAVARIL-----AADREARQOLAAVAEELQORL----- 1619
QY 2123 DEAVNKIASLAEBEIKLITKEMDEFRDSEKESLOESSHLSSELCVTYKTELQMLKQOKEDIN 2182
DB 1620 DTATQORAELEAQLARILAADREARQOLAAVAEEL-----QOLAAVAEEL-----QORLDTATQORAELE 1669
QY 2183 NKLAEKVEYDELLQHLSSLSKEQLODOIOMELRNEKLNVEELCEKMDIMEKEISVLR----- 2238
DB 1670 AQLARILAADREARQOLAAVAEEL-----QORLDTATQORAELEAVEMVILREREAGETA 1726
QY 2239 -----LMQNEPQOEEDVDVARMIDLESRNQOELQEMLEKISAYVSEQHTLSSLSSELOK 2292
DB 1727 VAGEQVOLYRETVEEBCECLKEERWCLSESRVQALRE-----ASAAKQOOREVAAKANAEVOE 1782
QY 2293 ETEA--HKGCMILNTKESISTLSRSFGSLQTEHAKLTQLOTLNKKFVVVYRT--AAVKEDH 2350
DB 1783 RUDSMARCTIAHGSDAPQRADGRDADLRQOLANIREVUKLS---EKQKAMERVLPGVREKO 1839

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QY 1824 DIRKAOEALQOQKDKVQVBLTQSI SVLQEKI SLLENOMLYNVATVKETLSERPDLNOSKOH 1883
 Db 1470 ALTKSSKDLVCGNQSELODLSIKSVSEIKNFENK--YN---CETTSLKDEIEBKOK- 1522
 QY 1884 LFSLETTLSLSLKEKEFFALEQAEKADARKTIDITEKISNIEEQLLOQATNLKETLYE 1943
 Db 1523 ---EIVTLQTELDKDR---ISEVEKERAMISENSETVIKESYSDKIKSLESKINSIKEN--- 1573
 QY 1944 RESLIQCKEQALANTEHLRETLKSKDLALGKMEQERDEA----ANKVIALTERMSSLEEQ 1999
 Db 1574 ----HSKE---ITTHNEQKTSIKQDIA--KLSQDHESAQTQLEDKENQKELKASLEKH 1623
 QY 2000 INENVTTLKEGEGEKETFYLQRPSSQOQSSQMEELRESLTKDLOLEBAKEISEATNEI 2059
 Db 1624 NTESATSIIE-----KNNQIKELSETIKSLKTELKTSGDALKQSQKEY 1666
 QY 2060 KMLTAKISLSEELILQNASILMEAVSERENLRHSKQOLVSELEQLSLTLKSRDHAFQSK 2119
 Db 1667 KTLKTKNSDTE-----SKLEKQLELEKVK-----SDLOTADEKLKGITEREIALK 1712
 QY 2120 REKDEAVNKIASLAEIKILTYKEMDEFKDSKESLQFQSSHLSEELCTYKTELQMLKQKE 2179
 Db 1713 SELETVKNSGLSTTSLSLALTKTVKSLKEKEKELOFLSGNKSKELEDYIQKHSDISKXK 1772
 QY 2180 DINNKLAEKVKEVDELLOHLSLKEQLDOIQMEELNREKLRNYELCEKMDIMEKEI---S 2235
 Db 1773 ALTDELEKERTKQFDDSKKLTLENDLTSTKKELETEKTQTSKFKNLEERKDKKEIVKLNK 1832
 QY 2236 VRLMONEPOQOEEDVAERMIDLESRNQIQLMEKISAVS--EQH 2280
 Db 1833 ELELLKNDNSGAKKELSEKVSKLDS--EIEILSKLEDPKKSVMKOH 1876

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